

GenCore version 5.1.7  
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OM protein - nucleic search, using ~~frame plus p2n model~~

Run on: April 1, 2006, 04:29:01 ; Search time 10735.5 Seconds  
(without alignments)  
2853.949 Million cell updates/sec

Title: US-10-628-525A-21  
Perfect score: 2893  
Sequence: 1 CVAELSRDLGLPEPIAG.....LLGRANEARHVKRLHVGPCR 539

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Command line parameters:  
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-Q=/abes/ABSSWEB spool/US10628525/runat\_31032006\_095113\_16622/app\_query.fasta\_1  
-DB=GenEmbl -QFMT=fastap -SUPFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdd -LIST=150  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abes06h  
-USER=US10628525 @CGN 1.1 4375 @runat\_31032006\_095113\_16622 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: gb.ba.\*
- 2: gb.in.\*
- 3: gb.env.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pr.\*
- 9: gb.ro.\*
- 10: gb.sts.\*
- 11: gb.sy.\*
- 12: gb.un.\*
- 13: gb.vi.\*
- 14: gb.htg.\*
- 15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2893	100.0	1620	6	AR106498 Sequence
2	2861	98.9	1749	6	BD071187 Plant lik
3	2861	98.9	1752	6	AR106494 Sequence

4	2832	97.9	2008	6	BD249566
5	2832	97.9	2008	6	AR340014
6	2832	97.9	2357	15	AP036891
7	2832	97.9	2491	6	BD249559
8	2832	97.9	2491	6	AR340007
9	2818	97.4	2383	6	A93359
10	2818	97.4	2383	6	AR174874
11	2818	97.4	2383	6	AR411327
12	2782	96.2	2592	15	AF168786
13	2757	95.3	2990	6	AR049919
14	2757	95.3	2992	6	A63308
15	2655	91.8	1528	6	BD249560
16	2655	91.8	1528	6	AR340008
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18	2525.5	87.3	2533	6	E06904
19	2525.5	87.3	2533	15	RICSSS
20	2525.5	87.3	2585	15	AF165890
21	2511.5	86.8	1926	6	AX653976
22	2511.5	86.8	2623	15	AK109458
23	2507.5	86.7	2547	15	AY299404
24	2473.5	85.5	2421	15	TAE292522
25	2470.5	85.4	2575	15	TAE292521
26	2467.5	85.3	2591	15	AF091803
27	2467.5	85.3	2862	6	AX031272
28	2466.5	85.3	2239	6	A93350
29	2466.5	85.3	2239	6	AR174875
30	2466.5	85.3	2239	6	AR535116
31	2466.5	85.3	2239	6	BD008446
32	2466.5	85.3	2771	6	BD209997
33	2466.5	85.3	2771	6	BD54865
34	2466.5	85.3	2771	6	AX010492
35	2324	80.3	2055	15	TAD48227
36	2299	79.5	1802	15	BD018427
37	2043	70.6	1415	6	BD249565
38	2043	70.6	1415	6	AR340013
39	1981	68.7	2440	15	AB126832
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41	1936	66.9	2329	15	AY128273
42	1930	66.7	2280	15	BT012843
43	1910	66.0	2360	6	A51207
44	1910	66.0	2360	6	AR112888
45	1910	66.0	2360	6	CS114479
46	1910	66.0	2360	6	AR256403
47	1910	66.0	2360	15	STSTASYNT
48	1684.5	58.2	110000	15	AP008212
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50	1645.5	56.9	1758	6	A51201
51	1645.5	56.9	1758	6	AR112885
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57	1553.5	53.6	1578	15	AY570713
58	1431	49.5	1431	15	BT009026
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78	1109.5	38.4	2793	6	CS114477	CS114477 Sequence							
79	1109.5	38.4	2793	6	AR256402	AR256402 Sequence							
80	1107	38.3	2319	15	OSA308110	AJ308110 Oryza sat							
81	1103	38.1	2418	6	AR220363	AR220363 Sequence							
82	1103	38.1	2418	6	AR255139	AR255139 Sequence							
83	1101	38.1	2394	15	AF395537	AF395537 Oryza sat							
84	1099.5	38.0	2988	15	PSSTASYNT	X88790 P. sativum m							
85	1097	37.9	3049	15	AF026421	AF026421 Chlamydom							
86	1095	37.8	2010	6	BD071186	BD071186 Plant lik							
87	1095	37.8	2865	15	AF019296	BD249570 Modificat							
c 88	1093	37.8	1798	6	BD249570	BD249570 Modificat							
c 89	1093	37.8	1798	6	AR340018	AR340018 Sequence							
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91	1093	37.8	2019	6	AR340017	AR340017 Sequence							
92	1093	37.8	2248	6	BD249574	BD249574 Modificat							
93	1093	37.8	2248	6	AR340022	AR340022 Sequence							
94	1084	37.5	2348	6	AR220348	AR220348 Sequence							
95	1084	37.5	2348	6	AR535124	AR535124 Sequence							
96	1083.5	37.5	1926	6	AS1203	AS1203 Sequence 5							
97	1083.5	37.5	1926	6	AR112886	AR112886 Sequence							
98	1083.5	37.5	1926	6	CS114475	CS114475 Sequence							
99	1083.5	37.5	1926	6	AR256401	AR256401 Sequence							
100	1080	37.3	2645	15	AK066446	AK066446 Oryza sat							
101	1077.5	37.2	2793	15	TAE269504	AJ269504 Triticum							
102	1075	37.2	2433	15	AB115917	AB115917 Oryza sat							
103	1075	37.2	2433	15	AB115918	AB115918 Oryza sat							
104	1074.5	37.1	2780	15	TAE269503	AJ269503 Triticum							
105	1072.5	37.1	74136	14	CR954216_4	Continuation (5 of							
106	1070.5	37.0	2842	15	AF155217	AF155217 Triticum							
107	1070	37.0	1550	15	AV570701	AV570701 Ostreococ							
108	1068.5	36.9	2972	15	AV133249	AV133249 Hordeoc							
109	1067.5	36.9	2433	15	AB115916	AB115916 Oryza sat							
110	1066	36.8	2447	15	AB115915	AB115915 Oryza sat							
111	1066	36.8	2319	15	AK101978	AK101978 Oryza sat							
112	1066	36.8	2359	15	AF419099	AF419099 Oryza sat							
113	1050.5	36.3	1742	15	TAU66377	U66377 Triticum ae							
114	1050.5	36.3	2825	6	A93354	A93354 Sequence 5							
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119	1029	35.6	2412	6	AR755428	AR755428 Sequence							
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123	978.5	33.8	2085	6	AR049920	AR049920 Sequence							
c 124	972	33.6	1724	6	BD016979	BD016979 Starch sy							
125	970	33.5	148409	15	CR956619	CR956619 M.truncat							
126	931.5	32.2	2168	15	MEGBS	X74160 M.esculenta							
127	909	31.4	2221	15	AR029546	AR029546 Phaseolus							
128	906	31.3	1609	15	AK061803	AK061803 Oryza sat							
129	898.5	31.1	2188	15	BT013430	BT013430 Lycopersi							
130	896	31.0	2270	15	AF210699	AF210699 Perilla f							
131	893	30.9	2161	6	AK394246	AK394246 Sequence							
132	881.5	30.5	4987	15	AK072339	AK072339 Oryza sat							
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134	880.5	30.4	2478	6	AG3310	AG3310 Sequence 3							
135	880	30.4	2208	15	AB110011	AB110011 Phaseolus							
136	878.5	30.4	2176	6	AR220354	AR220354 Sequence							
137	878.5	30.4	2176	6	AR535130	AR535130 Sequence							
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139	871	30.1	2274	6	AR220357	AR220357 Sequence							
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147	863	29.8	1833	15	AX149948	AX149948 Arabidops							
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Db	541	GGATATATTATGGGACGAATTGCATGTTGTGTGTCAAATGATGGCATGGCCAGTCTATGTG	600
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Db	601	CCAGTCCCTTCCTGCTGCAAAATATAGACCAATATGGTGTATTAAGAAGCTCCCGCAGCAATT	660
Qy	221	LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu	240
Db	661	CTTGTAAATACATAATTTAGCACATCAGGGGTAGAGCCTGCAAGCACATATCTGTACCTT	720
Qy	241	GlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArg	260
Db	721	GGGTTCACCTCTGAATGTATGAGCTCTCGAGTGGGTATTTCCCTGAATGGCGAGGAGG	780
Qy	261	HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAsp	280
Db	781	CATGCCCTTGACAAGGGGTGAGCGAGTTAAATTTTTTGAAGGTGCAGTTGTGACACGAGAT	840
Qy	281	ArgIleValThrValSerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGlyGln	300
Db	841	CGAATCTGTACTGTCACTAAGGGTTATTCGTGGCAGGTCAACACTGCTGAAGGTGGACAG	900
Qy	301	GlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle	320
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Qy	321	AspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp	340
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Db	1081	AGGCCTCATGTCTCTGTATGGCTCTTAATTGGAAGGTGGATATATCAGAAGGCATTTGAT	1140
Qy	381	LeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly	400
Db	1141	CTCATTCACATTATCATACCGATCTCATGCGGAGAGATGTTCAATTTGTATGCTTGGGA	1200
Qy	401	SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys	420
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Qy	421	PheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp	440
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Qy	441	IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln	460
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Qy	461	TyrGlyThrValProValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPhe	480
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Qy	481	AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThr	500
Db	1441	AAACCTTTCTGGTGGAGATGGAGACGGGTACAGGGTGGGCATTTGGCACCCCTAAACCACA	1500
Qy	501	GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu	520
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Qy	521	LeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg	539
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RESULT 2			
BD071187			
LOCUS	BD071187	1749 bp	DNA linear
			PAT 27-AUG-2002

DEFINITION	Plant like starches and the method of making them in hosts.
ACCESSION	BD071187
VERSION	BD071187.1 GI:22616790
KEYWORDS	JP 2001519664-A/26.
SOURCE	Zea mays
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 1749)
TITLE	Guan,H. and Keeling,P.L.
JOURNAL	Plant like starches and the method of making them in hosts
COMMENT	Patent: JP 2001519664-A 26 23-OCT-2001; EXSEED GENETICS LLC
	OS Zea mays
	PN JP 2001519664-A/26
	PD 23-OCT-2001
	PF 03-APR-1998 JP 1998542940
	PR 04-APR-1997 US 60/042939
	PI HANPING GUAN,PETER L KSEILING
	PC A01H5/00,C12N15/29,C12N15/31,C12N15/54,C12N15/70,C12N15/74,PC C12N15/80,
	PC C12N15/81,C12N15/82,C12P19/04
	CC Plant like starches and the method of making them in hosts FH
FEATURES	Key Location/Qualifiers
source	FT CDS Location/Qualifiers
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	/organism="Zea mays"
	/mol_type="genomic DNA"
	/db_xref="taxon:4577"
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Alignment Scores:	
Pred. No.:	5,52e-233
Score:	2861.00
Percent Similarity:	92.5%
Best Local Similarity:	92.5%
Query Match:	98.9%
DB:	6
	Length: 1749
	Matches: 539
	Conservative: 0
	Mismatches: 0
	Indels: 44
	Gaps: 1
US-10-628-525A-21 (1-539) x BD071187 (1-1749)	
Qy	1 CyeValAlaGluLeuSerArgGlu----- 8
Db	1 TCGGTCGGGAGCTAGCAGGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCTGCTG 60
Qy	8 ----- 8
Db	61 GCGCCCCGCTGTCGCCCGGCTTCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 120
Qy	9 -----AspLeuGlyLeuGluProGluGly 16
Db	121 TCGACGG 180
Qy	17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36
Db	181 ATTGCTGGAAGGTTCCATCATCAACAGTAGTTGTGGCAAGTCAGCAAGATTCTGAGATT 240
Qy	37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56
Db	241 GTGGTTGGAAGGAGGCAAGCTCGAGCTAAGTAAGTAACAAAGCATTTGCTTTGTAACCGGC 300
Qy	57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76
Db	301 GAAGCTTCTCTTATGCAAGTCTGGGGTCTAGGAGATGTTTGTGTTTCATTGCCAGTT 360
Qy	77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96
Db	361 GCTCTTGCTGCTGCTGGTCAACCGTGTGATGGTTGTAATGCCAGATATTAAATGATACC 420
Qy	97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116







DB:	6	Gaps:	1
US-10-628-525A-21 (1-539) x AR340014 (1-2008)			
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Db	119	TGCGTTCGGAGCTGAGCAGGAGGGCCCGCGCGCGCTGCCACCGCGCTGCTG	178
Qy	8	-----	8
Db	179	GCGCCCGCTCGTGCCTCGCGCTTCCTCGCGCGCGCGCGAGCCACCGGTGAGCCGCA	238
Qy	9	-----AspLeuGlyLeuGluProGluGly	16
Db	239	TCGAGCGCGCGCGCTGCCAGCGCGCGCTGGGGGACCTCGGTCTCGAACCTGGAAGGG	298
Qy	17	IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle	36
Db	299	ATTGCTGAAGGTTCCATCGATAACACAGTAGTTGTGGCAGTGAGCAAGATTCTGAGATT	358
Qy	37	ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly	56
Db	359	GTGGTTGGAAAGGAGCAGCTCGAGCTAAAGTAACACAAAGCATTGCTTTGTAACCGGC	418
Qy	57	GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal	76
Db	419	GAAGCTTCTCTTATGCAAGTCTGGGGGTCTAGGAGATTGTTGTGTTTCAATGCCAGTT	478
Qy	77	AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr	96
Db	479	GCTCTTGTCTGCTGCTGCTACCGTGATGGTGTGTAATGCCAGATATTTAATGTGACC	538
Qy	97	SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe	116
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Qy	117	GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPhe	136
Db	599	GGCGGTGACATGAAGTTACCTTCTCCATGAGTATAGAGATTCAAGTTGAGTGGGTGTTT	658
Qy	137	ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe	156
Db	659	GTTGATCATCCTCATATCACAGACCTGGAAATTTATATGGAGATTAAGTTGGTGTCTTT	718
Qy	157	GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle	176
Db	719	GGTGATAAATCAGTTTCAGATACACACTCTTGTCTATGCTGCATGTGAGGCTCTCTTGATC	778
Qy	177	LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis	196
Db	779	CTTGAATTGGGAGGATATATTTATGGACAGAAATGTCATGTTGTCTCAATGATGGCAT	838
Qy	197	AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp	216
Db	839	GCCAGTCTAGTGCAGTCTCTTCTGTCGAAATATATAGACCATATGTTGTTTATAAGAC	898
Qy	217	SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr	236
Db	899	TCCCGCAGCATCTCTGTAATACATAATTTAGCACATCAGGCTGAGAGCTCGCAAGCACA	958
Qy	237	TyrProAspLeuGlyLeuProProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu	256
Db	959	TATCTCGACCTGGGTGGCCACTGAATGGTATGGAGCTCTGGAGTGGGTATTCCTCGAA	1018
Qy	257	TyrAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyValAlaVal	276
Db	1019	TGGCGAGGAGGATGCGCTTGACAGGCTGAGGAGTGAATTTTGAAGGTGAGATT	1078
Qy	277	ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrProGluValThrAla	296
Db	1079	GTGACAGCAGATCGAATCGTGAAGTGTCAAGGGTTATTCGTGGGAGGTCACAACTGCT	1138
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Knight,M.E., Harn,C., Lilley,C.E., Guan,H., Singletary,G.W., MuForster,C., Wasserman,B.P. and Keeling,P.L.  
Molecular cloning of starch synthase I from maize (W64) endosperm and expression in Escherichia coli  
Plant J. 14 (5), 613-622 (1998)  
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2 (bases 1 to 2357)  
Knight,M.E., Harn,C., Lilley,C.E.R., Guan,H.P., Singletary,G.W.,

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  Broglie, K.E. and Lightner, J.R.
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AUTHORS	Broglie, K.E. and Lightner, J.E.		
TITLE	Modification of starch biosynthetic enzyme gene expression to		
JOURNAL	produce starches in grain crops		
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Db	982	GCCAGTCTAGTCCAGTCTCTTCTGCTGCAAAATATAGACCATATGCTTTTATAAAGAC 1041
QY	217	SerArgSerIleLeuValIleHisAenLeuAlaHisGlnGlyValGluProAlaSerThr 236
Db	1042	TCCCCGAGCATTTCTTGTAATACATTAATTTAGCACATCAGGGGTGAGGCTCGAAGACA 1101
QY	237	TyrProAspLeuGlyLeuProProGluTyrTyrGlyAlaLeuGluTrpValPheProGlu 256



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Db 566 TCCGATAAGAAATTATGCAAAATGCATTTTACACAGAAAAACACATTCGGATTCCCATGCTTT 625
Qy 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136
Db 626 GCGGSGAACAATGAAGTTACCTTCTTCCATAGATAGAGATTCAAGTTGACATGGGSGTTT 685
Qy 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156
Db 686 GTTGATCATCCCTCATATACAGACTGGAAATTTATATGGAGATTAAGTTTGGTGTCTTT 745
Qy 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176
Db 746 GGTGATAATCAGTTCAGATACACATCCTTTGTCTATGCTGCATGTGAGGCTCCTTTGGTC 805
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196
Db 806 CTTGAATGGGAGGATATATTTATGGACAGAAATTCATGTGTTGTCTCAATGATTGGCAT 865
Qy 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216
Db 866 GCCAGTCTAGTGCAGTCTCTTGTCTGCATAATATAGACCATATGTTGTATTAAGAAGAC 925
Qy 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236
Db 926 TCCCGCAGCATCTCTGTAATACATAATTTAGCACATCAGGGTGTAGAGCTGCAAGCAC 985
Qy 237 TyrProAspLeuGlyLeuProGluTyrTrpTyrGlyAlaLeuGluTyrValPheProGlu 256
Db 986 TATCCTGACCTTGGGTTGCCACTGAATGGTATGGAGCTCTGAGTGGGTATTCCTCGAA 1045
Qy 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276
Db 1046 TGGGCGAGGAGGATGCCCTTGACAGGGTGAGGAGTTAATTTTTTGAAGGTGCAGTT 1105
Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296
Db 1106 GTGACAGCAGATCGAATCGTGACTGTGTCAGTAAAGGTTATTCATGGGAGTCAAACTGCT 1165
Qy 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316
Db 1166 GAAGTGGGACAGGGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGATTAACCGGAAT 1225
Qy 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336
Db 1226 GTAAATGGAAATTGACATTAATGATTGGAACCTGCCACAGACAAATGTTATCCCTGCTAT 1285
Qy 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356
Db 1286 TATTCCTGTTGATGACCTCTCTGMAAGGCCAAATGTAAAGGTGCATTCGAGAAGGAGCTG 1345
Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
Db 1346 GGTTTTACCTTATAGGCTGATGTCTCTGATTGGCTTTTATTGGAAGATTGGATTATCAG 1405
Qy 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396
Db 1406 AAAGGCAATTGATCTCACTTCACTATATACAGATCTCATCGGGAAGATGTTCAATTT 1465
Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416
Db 1466 GTCATGCTTGGATCTCGTCAACCAGAGCTTGAAGATTGGATGAGATCTACAGAGTGCATC 1525
Qy 417 PheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr 436
Db 1526 TTCAAGGATAAATTTTCGTGGATGGGTGGATTGATTTAGTGTTCCTGATTTCCACCAGAAATCT 1585
Qy 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456
Db 1586 GCCGGCTGGATATATGTTAATGCCATCCAGATTCGAACCTTGTGGTCTCAATCAGCTA 1645
Qy 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476
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Qy 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAla 496
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Qy 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516
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Qy 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536
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Qy 537 ProCysArg 539
Db 1885 CCATGCCGC 1893

RESULT 10
ARI174874
LOCUS ARI174874 2383 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6307124.
ACCESSION ARI174874
VERSION ARI174874.1 GI:17915194
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2383)
TITLES Kosemann, J. and Prohberg, C.
Nucleic acid molecules encoding soluble starch synthases from maize
JOURNAL Patent: US 6307124-A 1 23-OCT-2001;
FEATURES Location/Qualifiers
source
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ORIGIN

Alignment Scores:
Pred. No.: 3,66e-229 Length: 2383
Score: 2818.00 Matches: 534
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Best Local Similarity: 91.6% Mismatches: 2
Query Match: 97.4% Indels: 45
DB: 6 Gaps: 1

US-10-628-525A-21 (1-539) x ARI174874 (1-2383)
Qy 1 CysValAlaGluLeuSerArgGluAsp----- 9
Db 146 TCGGTCCGGAGCTGAGCAGGAGGGCGGCCGCCGCGCGCGATGCCACCCGCGCTGCTG 205
Qy 9 ----- 9
Db 206 GCGCCCCCGCTGCTGCGCGCTTCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 265
Qy 10 -----LeuGlyLeuGluProGluGly 16
Db 266 TTGACGCGCCGCCCGCTGCGCCGCGCGCGCTGCGGGGTCTCTGGTGTCCAACTGGAAGGG 325
Qy 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36
Db 326 ATTGCTGAAGGTTCCATCGATAACACAGTAGTTGTGGCAAGTGAGCAAGATTCAGAGATT 385
Qy 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56
Db 386 GTGGTTGGAAGAGGAGCAGCTCAGCTAAAGTAACAACAAACATGTCTTTGTAATCGGC 445
Qy 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76
Db 446 GAAGCTTCTCCTTATGCAAAAGTCTGGGGGTCTAGGAGATGTTTGTGGTTCATTGCCAGTT 505
Qy 77 AlaLeuAlaAlaArgGlyHisArgValMetValMetValMetProArgTyrLeuAsnGlyThr 96
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EMYGALFWPPEWARRHALDKGAVNPLKCAVVTADRIVTVSKYSHEVTTABGGQGL  
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 VGPCR"

## ORIGIN

## Alignment Scores:

Pred. No.: 4,62e-226 Length: 2592  
 Score: 2782.00 Matches: 523  
 Percent Similarity: 90.4% Conservative: 6  
 Best Local Similarity: 89.4% Mismatches: 10  
 Query Match: 96.2% Indels: 46  
 DB: 15 Gaps: 1

US-10-628-525A-21 (1-539) x AF168786 (1-2592)

QY 1 CysValAlaGluLeuSerArgGlu-----8  
 DB 191 TGGCTGCGGAGCTGAGCAGGAGGGTCCCGCGCGAGCGCGCGCTGCCACCGCG 250  
 QY 8 -----8  
 DB 251 CTGCTGGCGCCCGCTGCTGCCGCCCTTCTCGCGCGCGCTCGCGAGCCCGAGGGTGAG 310  
 QY 9 -----AspLeuGlyLeuGluPro 14  
 DB 311 CCGGCGTCGACACCGCGCCCTGCGCGAGCGCGTCTCGCGACCTCGTCTCCAACCT 370  
 QY 15 GluGlyLeuAlaGluGlySerIleAspAsnThrValValalaserGluGlnAspSer 34  
 DB 371 GAAGGGAATGCTGAGGGTTCATCGATGACACAGTAGTTGTGCAAGTAGCAAGATTCT 430  
 QY 35 GluIleValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheVal 54  
 DB 431 GAGATCGTGGTTCGAAAGGAGCAGCTCGAGCTAAGTAACACAGCATTGCTTTGTA 490  
 QY 55 ThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAspValCysGlySerLeu 74  
 DB 491 ACTGGCGAAGCTTCTCTTATGCAAGTCTGGGGTCTAGGAGATGTTTGTGTTTCATTG 550  
 QY 75 ProValAlaLeuAlaalaArgGlyHisArgValMetValValMetProArgTyrLeuAsn 94  
 DB 551 CCAAGTTGCTCTTCTGCTGCTGCTACCGTACCGTGTGATGTTGTAATGCCAGATATTAAT 610  
 QY 95 GlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIlePro 114  
 DB 611 GGTACCTCTGATNAGAAATACGCAAAATGCATTTTACAGAAAGACACATTTCGGATTCCA 670  
 QY 115 CysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyr 134  
 DB 671 TGGTTGGCGGTGAACATGAAGTTACCTTTTCCATGAGTACAGAGATTCAGTTGACTGG 730  
 QY 135 ValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGly 154  
 DB 731 GTGTTTGTGATCATCCCTCATATCAGACCTCGAAATTTATATGAGAGATAGTTTGGT 790  
 QY 155 AlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaalaCysGluAlaPro 174  
 DB 791 GCTTTTGGTATNATCAGTTTCAGTACACGCTCTTTGCTATGCTGCATGTGAGGCTCT 850  
 QY 175 LeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAsp 194  
 DB 851 TTGGTCTTGAATTTGGAGGATATATTTATGACAGAAATTCATGTTTGTGTGATGAT 910  
 QY 195 TrpHisAlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyr 214  
 DB 911 TGGCATGCGAGTCTAGTGCAGTCTTCTTGTGCAAAATATAGACCATATGTTGTTAT 970  
 QY 215 LysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAla 234  
 DB 971 AAGACTCCCGAGCAATCTTGTATACATAAATTTAGCACATCAGGGGTGTAGAGCCTGCA 1030

QY 235 SerThrTyrProAspLeuGlyLeuProProGluTyrTyrGlyAlaLeuGluTyrValPhe 254  
 DB 1031 AGCACATATCTTACCTTGGTGGCCACCTGAATGGTATGGAGCTCTGGAGTGGGTATTC 1090  
 QY 255 ProGluTyrAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274  
 DB 1091 CCTGAATGGGCAAGGAGGCATGCCCTTGACAGGGTGGAGCAGTAAATTTTTTGAAGGT 1150  
 QY 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThr 294  
 DB 1151 GCAGTTGTGACACAGATCGAATGTGACTGTGAGTAAGGGTTATTCATGGAGGTGACA 1210  
 QY 295 ThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsn 314  
 DB 1211 ACTGCTGAAGTGGACAGGGTCTCAATGAGCTCTTAAGCTCCCGAAGAGTGTATTAAAC 1270  
 QY 315 GlyIleValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCysIlePro 334  
 DB 1271 GGAATTTGTAATGGAATTGACATTAATGATTGGAACCTCGACCGGACAAATGTATCCCT 1330  
 QY 335 CysHisTyrSerValaAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlyLys 354  
 DB 1331 TGTCTATTATCTGTTGATGACCTCTCTGGAAGAGCCAAATGTAAAGTGCATTGCAGAG 1390  
 QY 355 GluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAsp 374  
 DB 1391 GAGCTGGTATTACCTATATAGGCTGAAGTTCCTCTGATTTGGTTTATTTGAGAGNTGGAT 1450  
 QY 375 TyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspVal 394  
 DB 1451 TATCAGAAAGGCAATGATCTCATTAACATTATCATACCATCTCATCGGAGCAGCTT 1510  
 QY 395 GlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGlu 414  
 DB 1511 CAATTTGTCATGCTTGGATCTGCTGACCCAGAGCTCGAAGCTGGATGAGATCTACAGAG 1570  
 QY 415 SerIlePheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArg 434  
 DB 1571 TCGGACTTCAAGGATATAATTTCTGTGATGGTGGTGGATTTAGTCTTCCAGTTTCCACCGA 1630  
 QY 435 IleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsn 454  
 DB 1631 ATAACCTGCGGCTCGCATATATTTGTTAATGCCATCCAGATTCGAACCTTGTGCTCAAT 1690  
 QY 455 GlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArg 474  
 DB 1691 CAGCTATATGCTATGCAAGTATGGCAGATTCCTGTTGTCATGCAACTGGGGGCTTAGA 1750  
 QY 475 AspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAla 494  
 DB 1751 GATACCTGTGAGAGACTTCAACCTTTTCGCTGAGATGGAGAACAGGGTACAGGGTGGGCA 1810  
 QY 495 PheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIle 514  
 DB 1811 TTGCAACCCCTAACCAACGAAACATGTTTGTGGACATTCGGAATTCGCAATTCGACATA 1870  
 QY 515 GlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHis 534  
 DB 1871 CAAGGAGCAAAATCTTCTCGGAAGGGCTCATGAAGAGGGGCATGTCAAAAGACTTTCAC 1930  
 QY 535 ValGlyProCysArg 539  
 DB 1931 GTGGGACCATGCCGC 1945

## RESULT 13

## AR049919

## LOCUS

## DEFINITION

## AR049919

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

AR049919 2990 bp DNA linear PAT 29-SBP-1999  
 Sequence 1 from patent US 5824790.

AR049919

AR049919.1 GI:5971911

Unknown.







ACCESSION A63308  
 VERSION A63308.1 GI:3717138  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unclassified sequences.  
 REFERENCE 1  
 AUTHORS Keeling, P.L. and Knight, M.E.  
 TITLE MODIFICATION OF STARCH SYNTHESIS IN PLANTS  
 JOURNAL Patent: WO 9720936-A 1 12-JUN-1997;  
 ZENECA LTD (GB)  
 COMMENT Other publication AU 1037197 19970627.  
 FEATURES  
 source Location/Qualifiers  
 1..2992  
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Alignment Scores: 7.34e-224 Length: 2992  
 Pred. No.: 2757.00 Matches: 523  
 Score: 90.9% Conservative: 8  
 Percent Similarity: 89.6% Mismatches: 45  
 Best Local Similarity: 95.3% Indels: 1  
 Query Match: 6 Gaps: 1  
 DB:

US-10-628-525A-21 (1-539) x A63308 (1-2992)

Qy	1	CysValAlaGluLeuSerArgGlu-----	8
Db	719	TGCGTCGCGAGGTGACGAGGAGGGCCGCGCGCGCGCTGCCACCGCGCTGCTG	778
Qy	8	-----	8
Db	779	GCSCCCCGCTCGTCCCGCGCTTCCTCGCGCGCGCGCGCGCGCGCGCGCA	838
Qy	9	-----AspLeuGlyLeuGluProGluGly	16
Db	839	TCGACGCGCGCGCGCGCGCGCGCGCGCGCGCTCGGTCTCGAACCTCGAAGG	898
Qy	17	IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle	36
Db	899	ATTGCTGGAAGGTTCCATCGATACACAGTAGTTGTGGCAAGTGCAGATTCGAGATT	958
Qy	37	ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly	56
Db	959	GTGTTGGAAAGGAGCGAGCTCGAGCTAAAGTAAACAAAGCAATTGCTTTGTAACCGGC	1018
Qy	57	GluAlaSerPro-TyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVa	76
Db	1019	GAAGCTTCCTTAATCGAAAGTCTGGGGTCTAGGAGATGTTGTGTTCATTGCCAGT	1078
Qy	76	IAlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyTh	96
Db	1079	TGCTCTTGCTGCTCGCGGTCCCGGTGATGTTGTAATGCCAGACATTTAAATGGTAC	1138
Qy	96	xSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPh	116
Db	1139	CTCCGATAGAAATATGCAATATGATTTTACCGAAAGAACATTCGGATTCCATTCTT	1198
Qy	116	eGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPh	136
Db	1199	TGCGGTGAACATGAAGTTACCTTCTCCATGATAGTAGATTCAGTTGACTGGGTGTT	1258
Qy	136	eValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPh	156
Db	1259	TGTTGATCATCCCTCATATCACAGACTCGAAATTTATATGGAGATAAGTTGGTGCTTT	1318
Qy	156	eGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuI	176
Db	1319	TGSGTAAATACAGTTACAGATACACATCTCCTTTCATGCTATGCTATGAGGCTCCTTTGGT	1378

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Qy	176	eLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHi	196
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Qy	196	sAlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAs	216
Db	1439	TGCCAGTCTAGAGCCAGTCTCTTCTGCTGCAAAATATAGACCATATGCTGTTTATAAGA	1498
Qy	216	pSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerTh	236
Db	1499	CTCCGAGCATCTCTTGTATAACATAATTTAGCACATCAGGGTGTAGAGCTGCAAGCAC	1558
Qy	236	rTyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGl	256
Db	1559	ATATCCTGACCTTGGGTGGCCACCTGAATGATGAGGCTCTGAGTGGGTATTCCTCGA	1618
Qy	256	uTrrAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVa	276
Db	1619	ATGGCGAGGAGGATGCCCTTGACAGGGTGAAGGAGTAAATTTTGAAGGTCAGT	1678
Qy	276	lValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAl	296
Db	1679	TGTGACAGCAGATCGAATCGTGAATGAGTAAAGGTTATTCATGGAGGTTCACACTGC	1738
Qy	296	aGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyI	316
Db	1739	TGAAGGTGGACAGCGCTCAATGAGCTTTAAGCTCCAGAAAGAGTGTATTAAACGGAT	1798
Qy	316	eValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHi	336
Db	1799	TGTAAATGGAAATTCATTAATGATTGGAACCTCGCCACAGACAAATGTATCCCTGTCA	1858
Qy	336	sTyrSerValAspAspLeuSerGlyLysAlaLysCysGlyGlyAlaLeuGlnLysGluLe	356
Db	1859	TTATCTGTTGATGACTCTCTTGAAGGCTAAATGTAAAGGTGCATTGACAGAGGAGCT	1918
Qy	356	uGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGl	376
Db	1919	GGGTTTACCTATTAAGGCTGATGTTCTCTGATGGCTTTATTGGAGATTTGATATCA	1978
Qy	376	nLysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPh	396
Db	1979	GAAAGCATGATGATCTCATTCACATTCATACACAGATCTCATCGGAAGAATGTTCAAT	2038
Qy	396	eValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIl	416
Db	2039	TGTCATGCTTGGATCTGGTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGATCGAT	2098
Qy	416	ePheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleTh	436
Db	2099	CTTCAAGGATAAATTCGTGGATGGGTGGATTTAGTGTTCAGTTTCCACCCGATTAAC	2158
Qy	436	rAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLe	456
Db	2159	TGCGGTGGCGATATATGTTAATGCCATCCAGATTCGAACCTTGTGGTCTCAATCAGCT	2218
Qy	456	uTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgPheTh	476
Db	2219	ATATGCTATGTCAGTATGGCACAGTCTCTGTGTGTCATGCAACTGGGGGCTTACAGATAC	2278
Qy	476	rValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAl	496
Db	2279	CGTGGAGAACTTCAACCTTTCCGTGAGAAATGGAGAGCAGGGTACAGGGTGGGCATTCGC	2338
Qy	496	aProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGl	516
Db	2339	ACCCCTAACACACAGAAACATGTTTGTGACATTCGGAACCTGCAATATCTACATACAGG	2398
Qy	516	yThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGl	536
Db	2399	AACACAGTAATAATGGGAAGGCTTAATGAAGCCAGGCGATGTCAAAGAGATTCCACGTGG	2458



QY 504 PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523  
Db 147 TT-GTGACATTTGGAACTGCAATATCTACATACAGGGAACACAAAGTCTCTCTGGGAAG 89

QY 524 AlaAsnGluAlaArgHisValIleArgLeuHisValGlyProCysArg 539  
Db 88 GCTAATGAGCGAGCATGTCAAAAGACTTCACGTGGGACCATGCCGC 41

RESULT 16  
AR340008/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 (bases 1 to 1528)  
AUTHORS  
Brogie,K.E. and Lightner,J.E.  
TITLE  
Modification of starch biosynthetic enzyme gene expression to  
produce starches in grain crops  
JOURNAL  
Patent: US 6570008-A 6 27-MAY-2003;  
E. I. du Pont de Nemours and Company; Wilmington, DE  
FEATURES  
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Location/Qualifiers  
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ORIGIN  
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Best Local Similarity: 99.8% Mismatches: 1  
Query Match: 91.8% Indels: 1  
DB: 6 Gaps: 0

US-10-628-525A-21 (1-539) x AR340008 (1-1528)

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Db 1527 CGAGCTAAAGTAACACAAAGCATTTGTTGAACCGCGGAAGCTTCTCTTATGCAAG 1468

QY 64 SerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaArgGlyHis 83  
Db 1467 TCTGGGGTCTAGGAGATGTTTGTGGTTCATTGCCAGTGTCTCTGCTGCTGCTCAC 1408

QY 84 ArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsn 103  
Db 1407 CGGTGATGGTTGTAATGCCAGATATTTAAATGGTACCTCCGATTAAGAAATTATGCAAT 1348

QY 104 AlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThr 123  
Db 1347 GCATTTTACACAGAAACACATTCGATTCGATTTTGGCGGTGAACATGAAGTTACC 1288

QY 124 PhePheHisGluTyrArgAspSerValAspTyrPheValPheValAspHisProSerTyrHis 143  
Db 1287 TTCTTCCATGAGTATAGAGATTTCAGTTGACTGGGTGTTTGTGATCATCTCATATCAC 1228

QY 144 ArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyr 163  
Db 1227 AGACCTGGAAATTTATATGGAGATAAGTTTGGTGTCTTTTGGTATAATCAGTTTCAGATAC 1168

QY 164 ThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGlyGlyTyrIle 183  
Db 1167 ACATCTCTTGTATGCTGATGATGAGGCTCTTTGATCTCTGAAATTTGGAGGATATATT 1108

QY 184 TyrGlyGlnAsnCysMetPheValValAsnAspTyrPheAlaSerLeuValProValLeu 203  
Db 1107 TATGGACAGAAATTCATGTTTGTGTCATGATTTGGCATGCCAGTCTAGTGCCAGTCTT 1048

QY 204 LeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIle 223

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Db 987 CATATTTAGCATCATCAGGGGTAGAGCTTGCAAGCACATATCTGACCTTTGGGTGGCA 928

QY 244 ProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrPheAlaArgHisAlaLeu 263

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QY 304 GluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsn 323

Db 747 GAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACGGAATTCGAAATGGAATTCATTAAT 688

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Db 687 GATTGGAACCTGCCACAGCAAAATGTATCCCTGTCTCATTTATCTGTGTGATGACCTCTCT 628

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Db 627 GGAAGGCCAATGTAAAGGTGATTCGAGAGAGCTGGGTTTACCTATAAGGCCCTGAT 568

QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 383

Db 567 GTTCTCTGATTTGCTTTATTTGAAGGTTGGATTATCAGAAAGCATTCATTCATTTCAA 508

QY 384 LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403

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QY 404 ProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423

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QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443

Db 387 TGGTTTGGATTTAGTGTTCAGTTTCCACCGAATAACTGCCGCTGCCGATATATTCTTA 328

QY 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463

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Db 267 GTTCTCTGTTGTCATGCAACTGGGGGCTTAGAGATACCGTGGAGAACCTTCAACCTTTTC 208

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Db 207 GGTGAGATGGAGAGCAGGAGTACAGGTTGGGCATTCGACCCCTAACCCACAGAAACATG 148

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Db 147 TT-GTGGACATTCGGAACCTGCAATATCTACATACAGGGAACACAGTCTCTCTGGGAAG 89

QY 524 AlaAsnGluAlaArgHisValIleArgLeuHisValGlyProCysArg 539

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RESULT 17  
CQ879887  
LOCUS  
DEFINITION  
ACCESSION  
VERSION

CQ879887 1881 bp DNA linear PAT 11-OCT-2004  
Sequence 9 from Patent WO2004/065537.  
CQ879887  
CQ879887.1 GI:54033803

KEYWORDS	Oryza sativa	QY	90	ProAsglyLeuAasnGlyThrSerAspLysAasnTyrAlaAasnAlaPheTyrThrGluLys	109
SOURCE	Oryza sativa	Db	520	CCGAGATACATCAACGGGCGCTTGAACAAAAATTTGCAAAACGCAATTTTACACTGAGAAG	579
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.	QY	110	HisIleArgIleProCysPheGlyGluHisGluValThrPhePheHisGluTyrArg	129
REFERENCE	1	Db	580	CACATTAAGATTCCATGCTTTGGCGGAGAACATGAAGTTACTTTTTTTCACGAGTATAGG	639
AUTHORS	Heim, U., Herbers, K., Sonnwald, U. and Glickmann, E.	QY	130	AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAasnLeuTyr	149
TITLE	Expression cassette for nucleic acids in plant tissue containing starch	Db	640	GATTCTCTGTTGATTGGTGTTTGTGATCATCTCATATCATAGACCTCGAAAATTTGTAT	699
JOURNAL	Patent: WO 2004065537-A 9 05-AUG-2004; Sungene GmbH & Co. KGAA (DE)	QY	150	GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla	169
FEATURES	Location/Qualifiers	Db	700	GGAGATAAATTTTGGTGCTTTTGGCGATATATAGTTTTCAGATACACACTCTCTGCTATGCG	759
Source	1..1881	QY	170	AlaCysGluAlaProLeuLeuLeuGlyGlyTyrIleTyrGlyGlnAasnCysMet	189
CDS	/organism="Oryza sativa" /mol_type="unassigned DNA" /db_xref="taxon:4530"	Db	760	GGTGTTGAAGCCCATTAATTTCTTGAACCTGGAGGATATATCTATGGACAGAAATGTCATG	819
	1..1881	QY	190	PheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyrArg	209
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	VFDHPSYRPNLIGDNFQAGDNQPRYLLCYAACERAPLLILEGGYIYGKCKMFVV	QY	270	AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr	289
	NWHAFLVLLAAKTRPGVGRDARSVLVIHNLAHQVPEPASTYPDILGLPPEWYGAL	Db	1060	AATTTTTTAAAGGCGCAGTGTGTGACAGCATCGAATGTGACTGTGTGACCGGGGTAT	1119
	EWFFEWARRHALDKGEAVNFLKGAVVTADRIIVTSQGSWEVTTAEGGQGLNELLS	QY	290	SerTrpGluValThrThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArg	309
	RKSLVINGVNDIDINDMNPSTDKFLPYHSVDLSGKAKKAELOKELGLPRLPDVPL	Db	1120	TCATGGGAGGTCAACAACCTGCTGAAGTGGCGAAGGCCTCAATGAGCTCTTAAGCTCCCG	1179
	IGFIRLDYOKIGIDILIKLAIPLMRDNIQFVLMGSDPGFCGMWSTESGYRDKRFGW	QY	310	LysSerValLeuAasnGlyIleValAasnGlyIleAaspIleAasnAspTrpAsnProAlaThr	329
	VGFSPVSHRITAGCDILLMPSEFEQGLNOLYAMQYCTVPVHCTGGLGLDVFENFP	Db	1180	AAGAGTGTATTGAATGGAATTTGAAATGGAATTGACATTAATGATTGGAACCCATCCACA	1239
	FAKGEQGTGWAFSPLTIEKNAVIGADGNFDIQITQVILGGSEARHVRKLINGPCRL	QY	330	AspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLys	349
	TV"	Db	1240	GACAAATTTTCTCCCTTATCATTTATCTGTGTGATGACCTGTCCGGAAGGCCAAGTGATA	1299
ORIGIN	US-10-628-525A-21 (1-539) x CQ879887 (1-1881)	QY	350	GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe	369
Alignment Scores:		Db	1300	GCTGAATTCGAGAAGGAGCTGGGTTTACCTATAAGCCCGCATGTGCTCTGATTGCTTT	1359
Pred. No.: 1	1.8e-204	QY	370	IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeu	389
Score: 2525.50	Length: 1881	Db	1360	ATTGGAAGATTGGACTATCAAAAAGGCATTGATTAATTAATTAATTAATTAATTAATTA	1419
Percent Similarity: 85.8%	Matches: 475	QY	390	MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrp	409
Best Local Similarity: 80.5%	Mismatches: 31	Db	1420	ATGCGGGAACAATTAATTAATTCATGCTTGGATCTGGTGACCCAGGTTTGAAGATGG	1479
Query Match: 87.3%	Indels: 51	QY	410	MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerVal	429
DB: 6	Gaps: 3	Db	1480	ATGAGATCCACAGATCAGGGTACAGGATAAATTTCTGTTGATGGTGGTTCGATTTAGTGT	1539
US-10-628-525A-21 (1-539) x CQ879887 (1-1881)		QY	430	ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu	449
QY 1 CysValAlaGluLeuSerArgGlu-----8		Db	1540	CCAGTTTCCACCGAATAACTGACAGTTGCGATATATTTGTTGATGCCATCCAGATTCCGAA	1599
Db 100 TCGTGGCGGAGCTGAGCAGGACGCTGGGTGGCGCAGCGCGCTGGCACCGCGCGCG					
QY 8 -----8					
Db 160 CTGGTGAAGCAGCCGGTCTTCCGACCTTCTCTGTGCGACGTGACGCCACCCGCGGCC					
QY 9 -----AspLeuGly-----11					
Db 220 AGCAGTCCCGCGCGCGCGGACCCCGCGCGCGCTTCCCGACTCCCGCGCTGGGGAG					
QY 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAsnThrValValAla					
Db 280 ATCGAGCCCGATCTAGAGGTCTCAGAGAAGATTCCATCGACAAAACAATTTTGTGGCT					
QY 30 SerGluGlnAspSerGluIleValValGlyLysGluGlnAlaArgAlaLysValThrGln					
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QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp					
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Db 460 GTTTGTGGTTCACTGCCAATTGCTCTTGTCTTCTGTTGTTGATGCCATCCAGATTCCGAA					

Qy	450	ProCysGlyLeuAenGlnLeuTyAlaMetGlnTyGlyThrValProValValHisAla	469
Db	1600	CTTTGTGGCCCTCAATACAGTATATGCTATGCAATATGCTACAGTGCCTGTGTTTCATGGA	1659
Qy	470	ThrGlyGlyLeuAArgAspThrValGluAenPheAenProPheGlyGluAenGlyGluGln	489
Db	1660	ACTGGAGGCTTCAGAGATACAGTGGAGAAATTTCACCCGTTTCTGAGAAGGAGAGACG	1719
Qy	490	GlyThrGlyTrrpAlaPheAlaProLeuThrThrGluAenMetPheValAspIleAlaAen	509
Db	1720	GGTACAGGCTGGGCATTCTCGCCACTAACCATTTGAAAAAATGCTGTGGCATTCGCGAT	1779
Qy	510	CysAenIleTyrlleGlnGlyThrGlnValLeuLeuGlyArgAlaAenGluAlaAArgHis	529
Db	1780	GGCAATTTTCGACATACAGGGAAACAAGTCTCTTTGGAGGGTCTAATGAAGCGAGCAT	1839
Qy	530	VallysArgLeuHisValGlyProCysArg	539
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RESULT 18			
E06904			
LOCUS	E06904 2533 bp RNA linear PAT 29-SEP-1997		
DEFINITION	cDNA encoding soluble starch synthase.		
ACCESSION	E06904		
VERSION	E06904.1 GI:2175060		
KEYWORDS	JP 1994070779-A/1.		
SOURCE	Oryza sativa		
ORGANISM	Oryza sativa		
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
TITLE	Ehrhartoideae; Oryzeae; Oryza.		
JOURNAL	Baba.T. and Shimada,H.		
COMMENT	1 (bases 1 to 2533)		
	SOLUBLE RICE STARCH SYNTHETASE GENE AND ITS USE		
	Patent: JP 1994070779-A 1 15-MAR-1994;		
	MITSUI GIYOUSAI SHOKUBUTSU BIO KENKYUSHO:KK		
	OS Oryza sativa		
	PN JP 1994070779-A/1		
	PD 15-MAR-1994		
	PF 07-JUL-1992 JP 1992179947		
	PI BABA TADASHI, SHIMADA HIROAKI		
	PC C12N15/52.A01H5/00;		
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	CC hypothetical: No;		
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Score:	2525.50	Matches:	475
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Best Local Similarity:	80.5%	Mismatches:	33
Query Match:	87.3%	Indels:	51
DB:	6	Gaps:	3
US-10-628-525A-21 (1-539) x E06904 (1-2533)			
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Qy 330 AspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyValAlaLysCysLys 349

Db 1353 GACAAATTTCTCCCTTATCATTAATCTGTGTGATGACCTGTCCGGAAGGCCAAGTGATAA 1412

Qy 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleAtrProAspValProLeuIleGlyPhe 369

Db 1413 GCTGAATTCAGAGAGAGCTGGGTACCTATAAGGCCCGATGTGCTCTGATTGGCTTT 1472

Qy 370 IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeu 389

Db 1473 ATTGGAAGATTGGACTATCAAAAGGCATGTGATTAATTAACCTTGCCATTCAGATCTC 1532

Qy 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyr 409

Db 1533 ATGCGGGACAAATTAATTCGTGATGCTGTGATCTGGTGACCCAGGTTTTGAAGATGG 1592

Qy 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPheSerVal 429

Db 1593 ATGAGATCCACAGATCAGGGTACAGGATTAATTCGTGGATGGTTGGATTAGTGT 1652

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Db 1713 CTTTGTGGCTCAATCAGCTATGCTATGCAATATGTFACAGTGCTTGTTCATGGA 1772

Qy 470 ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln 489

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Qy 510 CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529

Db 1893 GGCAATTCGACATACAGGGAACACAGTCCTCTTTGGGAGGTCTAATGAAGCGAGGCAT 1952

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Db 1953 GTCAAGCGACTTTACATGGGACCATGCCGC 1982

RESULT 19

RICSSS 2533 bp mRNA linear PLN 11-JAN-2003

LOCUS Oryza sativa mRNA for soluble starch synthase, complete cds.

DEFINITION Oryza sativa mRNA for soluble starch synthase, complete cds.

ACCESSION D16202

VERSION D16202.1 GI:450484

KEYWORDS Oryza sativa

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 2533)

AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

TITLE Baba,T., Nishihara,M., Mizuno,K., Kawasaki,T., Shimada,H., Kobayashi,E., Ohnishi,S., Tanaka,K. and Arai,Y.

JOURNAL Identification, cDNA cloning, and gene expression of soluble starch synthase in rice (Oryza sativa L.) immature seeds

PUBMED Plant Physiol. 103 (2), 565-573 (1993)

REFERENCE 2 (bases 1 to 2533)

AUTHORS Baba,T.

TITLE Direct Submission

JOURNAL Submitted (06-MAY-1993) Tadaashi Baba, University of Tsukuba, Institute of Applied Biochemistry, Temohdai 1-1-1, Tsukuba Science City, Ibaraki 305, Japan (Tel:81-298-53-6632, Fax:81-298-53-6632)

FEATURES

source 1. .2533

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114. .1994

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/product="soluble starch synthase"

1995. .2533

2487. .2492

3'UTR polyA\_signal

ORIGIN

Alignment Scores:

Pred. No.: 2,638-204 Length: 2533

Score: 2525.50 Matches: 475

Percent Similarity: 85.8% Conservative: 31

Best Local Similarity: 80.5% Mismatches: 33

Query Match: 87.3% Indels: 51

DB: 15 Gaps: 3

US-10-628-525A-21 (1-539) x RICSSS (1-2533)

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Db 213 TGCGTGGCGGAGCTGAGCAGGAGCGTGGTGGCGCAGCGCGCTGGCACCGCGCGCG 272

Qy 8 ----- 8

Db 273 CTGGTGAAGACGCGGCTCTGCGGACCTTCCTGTCGCGACGCTGACGCCACCGCGCGCC 332

Qy 9 -----AspLeuGly----- 11

Db 333 AGCGAGTCGCGGCGCGCGCGCGCGCGCGCGCTGTCGCGGACTCCGCGCGTGGGGGAG 392

Qy 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAsnThrValValValAla 29

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Qy 30 SerGluGlnAspSerGluIleValValGlyLysGluGlnAlaArgAlaLysValThrGln 49

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Qy 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69

Db 513 AGCGTTGCTTTGTAAACCGGTGAAGCTTCTCTTATGCAAACTCAGGTGAGTATAGGAT 572

Qy 70 ValCysGlySerLeuProValAlaLeuAlaLaArgGlyHisArgValMetValValMet 89

Db 573 GTTGTGGTTCACTGCCAAATGCTCTTCTCTGCTGCTCATCGTGTGATGTTGTAATG 632

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Qy	30	SerGluGlnAspSerGluIleValValGlyLysGluGlnAlaArgAlaLysValThrGln	49	Qy	390	MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyr	409
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Qy	50	SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAsp	69	Qy	410	MetArgSerThrGlnSerIlePheLysAspLysPheArgGlyTyrValGlyPheSerVal	429
Db	538	AGCGTTGCTTTGTAAACCGGTGAAGCTTCTCTATATGCAAGTCAGGTGGACTAGGAGAT	597	Db	1618	ATGAGATCCACAGAAATCAGGGTACAGGGGATAAATTCGTGGATGGGTTTGTAGTTT	1677
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Qy	110	HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg	129	Qy	470	ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln	489
Db	718	CACATTAGATTCCATGCTTTGCGGAGAACATGAAGTTACTTTTTTTCACGAGTATAGG	777	Db	1798	ACTGAGGCGCTCAGAGATACAGTGGAGAAATTTAACCCCGTTTGTGAGAAAGAGAGAG	1857
Qy	130	AspSerValAspTyrValPheValAspHisProSerTyrHisArgProGluAsnLeuTyr	149	Qy	490	GlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsn	509
Db	778	GAATTCGTTGATGGGTGTTGTGATCATCCCTCATATCATAGACCTCGAAATTTGTAT	837	Db	1858	GGTACAGGGTGGGCATTTCTGCCACTTACCATTGAAAAAAAATGCTGTGGGCATTTGGGAT	1917
Qy	150	GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla	169	Qy	510	CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis	529
Db	838	GGAGATAATTTTGTGCTTTTGGCGATATATCAGTTCAGATACACACTCTCTGTCTATGCG	897	Db	1918	GGCAATTTTCGACATACAGGAACACAGTCTCTTTGGGAGGTCTAATGAAGCGAGGCAT	1977
Qy	170	AlaCysGluAlaProLeuIleLeuGluLeuGlyTyrIleTyrGlyGlnAsnCysMet	189	Qy	530	VallysArgLeuHisValGlyProCysArg	539
Db	898	CGGTGTGAAGCCCAATTAATCTTGAACCTGGGAGGATATATCTATGGAAGAAATGCGATG	957	Db	1978	GTCAAGCGACTTTACATGGGACCATGCCGC	2007
Qy	190	PheValValAsnAspTyrHisAlaSerLeuValProValLeuAlaAlaLysTyrArg	209	RESULT 21			
Db	958	TTTGTGTGAATGATGGATGCCAGTCTTGCCAGTCTTCTGTCGCAAAATATAGA	1017	LOCUS	AX653976	1926 bp	DNA
Qy	210	ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGln	229	DEFINITION	Sequence 3846 from Patent WO03000898.		linear
Db	1018	CCATATGGTGTTCACAGGATGCCCGAGTCTCTGTCTATACATAATCTAGCACATCAG	1077	ACCESSION	AX653976		
Qy	230	GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProProGluTyrTyrGlyAla	249	VERSION	AX653976.1	GI:29156790	
Db	1078	GGTGTGGAGCCGCGCAGTACATATCTGACCTGGGATTTGCCACCTCGAATGGTATGGAGCA	1137	KEYWORDS			
Qy	250	LeuGluTyrValPheProGluTyrAlaArgHisAlaLeuAspLysGlyGluAlaVal	269	SOURCE	Oryza sativa		
Db	1138	TTAGAAATGGGTGTTTCCAGAGTGGGCGAGCGGATGCCCTTGACAGGGTGGGCGATC	1197	ORGANISM	Oryza sativa		
Qy	270	AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr	289	REFERENCE			
Db	1198	AATTTTTTAAAGGCGCAGTTGTGACAGCAGATCGAATTTGTGACTGTCCAGCCAGGGGTAT	1257	AUTHORS	Chang, H. S., Chen, W., Cooper, B., Glazebrook, J., Goff, S. A., Hou, Y. M., Katagiri, F., Quan, S., Tao, Y., Whitcham, S., Xie, Z., Zhu, T. and Zou, G.		
Qy	290	SerTyrGluValThrThrIleGluGlyGlnGlyLeuAsnGluLeuSerSerArg	309	TITLE	Plant genes involved in defense against pathogens		
Db	1258	TCATGGGAGGTCAACAATGCTGAAGGTGGGCAAGCGCTCAATGAGCTCTTAAGCTCCCGG	1317	JOURNAL	Patent: WO 03000898-A 3846 03-JAN-2003;		
Qy	310	LysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTyrAsnProAlaThr	329	FEATURES	Syngenta Participations AG (CH)		
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Query Match:				86.8%		Indels:	

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Qy	30	SerGluGlnAspSerGluIleValValGlyLyvsGluGlnAlaArgAlaLyvsValThrGln 49	
Db	340	AGTGAGCAGGAGTCTGAGATCATGATCTGAAGGAGCAAGCTCAAGCTAAGATTAACAGC 399	
Qy	50	SerIleValPheValThrGlyGluAlaSerProTyrAlaLyvsSerGlyLeuGlyAsp 69	
Db	400	AGCGTTGTCTTTGTAACCGGTGAAGCTTCTCTTATGCAAAAGTCAGGTGGACTAGGAGAT 459	
Qy	70	ValGlyGlySerLeuProValAlaLeuAlaalaArgGlyHisArgValIleValValMet 89	
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Qy	90	ProArgTyrLeuAsnGlyThrSerAspLyvsAsnTyrAlaAsnAlaPheTyrThrGluLyvs 109	
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Db	1180	AAGAGTGTATTA	AGAAATGTAATAGGAATGACAA	TAAATGATTCGAACCCATCCACA	1239
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Db	1240	GACAAAGTTCT	CCCTTATCATATTCTGTGATGAC	CTGTCCGGAAGGCCACAGTGTAAA	1299
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Qy	470	ThrGlyClyLeu	ArgThrValGluAsnPheAsnPro	PheGlyGluAsnGlyGln	489
Db	1660	ACTGGAGGCTC	AGAGATACAGTGGAGAAATTTAA	CCCCGTTCCTCGAAGAAGAGAGCAG	1719
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RESULT 22

AK109458

**LOCUS**

### DEFINITION

1  
2  
3  
4  
5  
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7  
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ACCESSION

**VERSION**  
**KEYWORDS**

**KEYWORDS**  
**SOURCE**

**SOURCE**  
**ORGANISATION**

2135

## REFERENCE

## AUTHORS



Db 1132 GGTGTGGAGCTGCCAGTACATATCTGACCTGGGATTCACCTGATGATGGAGCA 1191  
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VERSION AY299404.1 GI:31745887  
KEYWORDS Oryza sativa (indica cultivar-group)  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 2547)  
Jiang, H.W., Dian, W.M. and Wu, P.  
Oryza sativa (indica cultivar-group) putative soluble starch synthase I gene  
Unpublished  
2 (bases 1 to 2547)  
Jiang, H.W., Dian, W.M. and Wu, P.  
Direct Submission  
Submitted (15-MAY-2003) State Key Laboratory of Plant Physiology and Biochemistry, College of Life Sciences, Kaixuan Road 288#, Hangzhou, Zhejiang Province 310029, P R China  
Location/Qualifiers  
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VERSION AJ292522.1 GI:9369335  
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ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1  
Peng, M., Hucl, P. and Chibbar, R.N.  
Isolation, characterization and expression analysis of starch  
synthase I from wheat (Triticum aestivum L.)  
Plant Sci. 161, 1055-1062 (2001)  
2 (bases 1 to 2421)  
Chibbar, R.N.  
Direct Submission  
Submitted (18-JUL-2000) Chibbar R.N., Cereal Biotechnology, Plant  
Biotechnology Inatt., Natl. Research Council Canada, 110 Gymnasium  
Place, Saskatoon, Saskatchewan, S7N 0W9, CANADA  
Location/Qualifiers  
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127. .250

transit\_peptide

mat\_peptide

polyA\_signal

polyA\_site

ORIGIN

Alignment Scores:

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Score: 2473.50 Matches: 465

Percent Similarity: 92.0% Conservative: 30

Best Local Similarity: 86.4% Mismatches: 40

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DB: 15 Gaps: 2

US-10-628-525A-21 (1-539) x TAE292522 (1-2421)

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DB	409	GTGGGGAACTCGCG-----CCGACCTCTGCTC-----GAAGGGATTGCTGAGGATTC	459
QY	22	IleAspAlaThrValValAlaSerGluGluAapSerGluIleValValGlyLeuGlu	41
DB	460	ATTGACAGCAATAATTGGCTGCAGTGAGCAGAGATTCTGAGATCATGGATGCCAAGGAT	519
QY	42	GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr	61
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QY	62	AlaLysSerGlyGlyLeuGlyAapValCysGlySerLeuProValAlaLeuAlaAArg	81
DB	580	GCAAAGTCAGGGGGTGGGAGATGTTTGTGGTTGCTTACCAATTGCTCTTGTGCTCGT	639
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DB	640	GGTCACCGAGTGATGGTGTGAATGCCAAGATACCTAAATGGGCTCTGTATNAAAACTAT	699
QY	102	AlaAsnAlaPheTyrThrGluLysHieIleArgIleProCysPheGlyGlyGluHieGlu	121
DB	700	GCAAGGCATATACACTGCCAAGACACATTAAGATTCCATGCTTTGGGGATCACATGAA	759
QY	122	ValThrPhePheHisGluTyrArgAapSerValAapTyrValPheValAapHisProSer	141
DB	760	GTGACCTTTTTCATGAGTATAGACACACCTCGATTGGGTGTTTGTGATCATCCGTCA	819
QY	142	TyrHieArgProGlyAanLeuTyrGlyAapLysPheGlyAlaPheGlyAapAanGlnPhe	161
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QY	162	ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGly	181
DB	880	AGATACACACTCTTTTGCTATGTGATGCGAGGCCCCACTAATCTTGAATTGGAGGA	939
QY	182	TyrIleTyrGlyGlnAanCysMetPheValValAanAapTyrPheHisAlaSerLeuValPro	201
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QY	222	ValIleHieAanLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAapLeuGly	241
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QY	242	LeuProProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrPalaArgHis	261
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DB	1180	GCCTTTGACAAAGGTGAGGAGTTAACTTTTGAAGAGGAGGTTGTGCACAGCATCGG	1239
QY	282	IleValThrValSerLysGlyTyrSerTyrGluValThrAlaGluGlyGlyGlnGly	301
DB	1240	ATTGTGACCGCTAGTCAGGCTTATTCATGGAGGTCACTGCTGAAGGTGGACAGGC	1299
QY	302	LeuAanGluLeuLeuSerSerArgLysSerValLeuAanGlyIleValAanGlyIleAap	321
DB	1300	CTCAATGAGCTCTTAAGCTCCGAAAAAGTGTATTAATGGAATTTAAATGGAATTCAC	1359
QY	322	IleAanAapTyrAanProAlaThrAapLysCysIleProCysHieIleTyrSerValAanAap	341
DB	1360	ATTATGATTGGAAACCCACACAGACAGTGTCTCCCTCATCATTAATCTTGTGATGAC	1419
QY	342	LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg	361
DB	1420	CTCTCTGGAAGGCCAAATGTAAGCTGAATTCAGAGGAGGAGTGGTTTACCTGTAAAG	1479
QY	362	ProAapValProLeuIleGlyPheIleGlyArgLeuAapTyrGlnLysGlyIleAapLeu	381
DB	1480	GAGGATGTTCTCTGATTGGCTTTATTTGGAAGACTGCTGATTTACAGAAAGGCATTGATCTC	1539
QY	382	IleGlnLeuIleIleProAapLeuMetArgGluAapValGlnPheValMetLeuGlySer	401
DB	1540	ATTAAATGGCCATTCAGAGCTCATGAGGAGGAGGAGTGCATTTGTTCATGCTTGGATCT	1599
QY	402	GlyAapProGluLeuGluAapTyrMetArgSerThrGluSerIlePheLysAapLysPhe	421
DB	1600	GGGGATCCAAATTTTGAAGCTGGATGAGATCTACCGAGTTCGAGTTACAGAGTAATATTC	1659
QY	422	ArgGlyTyrValGlyPheSerValProValSerHieArgIleThrAlaGlyCysAapIle	441
DB	1660	CGTGGATGGGTGGATTAGTTAGTTCCAGTTTCCACAGAATAACTGCAGGTTCGATATA	1719
QY	442	LeuLeuMetProSerArgPheGluProCysGlyLeuAanGlnLeuTyrAlaMetGlnTyr	461
DB	1720	TTGTTAATGCCATPCGAGATTGAACCTTCGGGTCTTAATCAGCTATATGCTATGCAATAT	1779
QY	462	GlyThrValProValValHisAlaThrGlyGlyLeuArgAapThrValGluAanPheAan	481
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QY	502	AanMetPheValAapIleAlaAanCysAanIleTyrIleGlnGlyThrGlnValLeuLeu	521
DB	1900	AAAGATGTT-GTGGGCATTCGAAACCCGATGTGCATATTCAGGAGACCAAGCGCTCTG	1958
QY	522	GlyArgAlaAanGluAlaArgHisValLysArgLeuHisValGlyProCysArg	539
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RESULT 25  
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LOCUS  
DEFINITION  
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ACCESSION  
AJ292521  
VERSION  
AJ292521.1 GI:9369333  
KEYWORDS  
starch synthase I-1; wSai-1 gene.  
SOURCE  
Triticum aestivum  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
REFERENCE  
1

AUTHORS		Peng, M., Hucl, P. and Chibbar, R.N.		Db	616	CAACCTCAAGCTAAAGTTACACGTAGCATCGTGTGTTGTGACTGGTGAAGCTGCTCCTTAT		675
TITLE		Isolation, characterization and expression analysis of starch synthase 1 from wheat (Triticum aestivum L.)						
JOURNAL REFERENCE		Plant Sci. 161, 1055-1062 (2001)		QY	62	AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAaArg		81
AUTHORS		2 (bases 1 to 2575)						
TITLE		Chibbar, R.N.		Db	676	GCAAAAGTCAGGGGGCTGGAGATGTTTGTGGTTCGTTACCAATTCCTCTGTGCTCGT		735
JOURNAL		Direct Submission						
FEATURES		Submitted (18-JUL-2000) Chibbar R.N., Cereal Biotechnology, Plant Biotechnology Inst., Natl. Research Council Canada, 110 Gymnasium Place, Saskatoon, Saskatchewan, S7N 0W9, CANADA		QY	82	GlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr		101
source		Location/Qualifiers						
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		CGSLPALAARHVRVVMVMPRYLNGSSDKNYAKALYTGKHIPICFGSGHEVTFPHEY		Db	1096	GTCCCTTCTGTGCGAAAATATAGACCATACGCGTGTTCACAGAGATTCGCCGACACCCCT		1155
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		NCMFVNDWHAFLVPLVLAALKYRYPYVYRDSRLVINHLAQGVPEASTYDILGLPP		QY	222	ValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGly		241
		EYWGVALEWFPFMAARHLDKGEAVNFLKGAVTADRIVTVSQGYSWETVTAEGSQGL						
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Query Match:		85.4%						
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				Db	1576	GAGGATGTTCTCTGATTGGCTTTTATTGGAAGACTGGATTACCGAAGAGCATTTGATCTC		1635
				QY	382	IleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer		401
				Db	1636	ATTAAATGGCCATTTCCAGAGCTCATAGGGAGGAGCGCTGCAGTTTGTCTGCTTGGATCT		1695
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## ORIGIN

Alignment Scores:	
Pred. No.:	1,256-199
Score:	2470.50
Percent Similarity:	91.8%
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QY	42 GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61



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 ACCESSION AF091803  
 VERSION AF091803.1 GI:5880465  
 KEYWORDS  
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 ORGANISM Triticum aestivum  
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.  
 1 (bases 1 to 2591)  
 Li, Z.; Rahman, S., Koser-Hashemi, B., Mouille, G., Appels, R. and  
 Morell, M. K.  
 Cloning and characterization of a gene encoding wheat starch  
 synthase I  
 Theor. Appl. Genet. 98, 1208-1216 (1999)  
 2 (bases 1 to 2591)  
 Li, Z.; Rahman, S., Koser-Hashemi, B., Mouille, G., Appels, R. and  
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## ORIGIN

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 Percent Similarity: 91.8% Conservative: 30  
 Best Local Similarity: 86.2% Mismatches: 41  
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LOCUS Sequence 11 from Patent WO9914314.
DEFINITION AX031272
ACCESSION AX031272
VERSION AX031272.1 GI:10278604
KEYWORDS
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Aegilops tauschii
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Poideae; Triticeae; Aegilops.
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REFERENCE
Li, Z., Morell, M. and Rahman, S.
AUTHORS Regulation of gene expression in plants
TITLE Patent: WO 99/4314-A 11 25-MAR-1999;
JOURNAL GOODMAN FIELDER LTD (AU) ; LI ZHONGYI (AU) ; MORELL MATTHEW (AU) ;
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
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Block, M. and Loerz, H.
NUCLEIC ACID MOLECULES ENCODING ENZYMES FROM WHEAT WHICH ARE
INVOLVED IN STARCH SYNTHESIS
Patent: WO 9745545-A 1 04-DEC-1997;
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ORIGIN
Alignment Scores:
Pred. No.: 2,28e-199 Length: 2239
Score: 2466.50 Matches: 464
Percent Similarity: 91.8% Conservative: 29
Best Local Similarity: 86.4% Mismatches: 41
Query Match: 85.3% Indels: 4
DB: Gaps: 2

US-10-628-525A-21 (1-539) x A93350 (1-2239)
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## RESULT 29

AR174875

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

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AR174875  
AR174875.1 GI:17915195

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 2239)  
Block, M., Lorz, H., Lutticke, S., Walter, L., Frohberg, C. and  
Kossmann, J.  
TITLE Nucleic acid molecules encoding enzymes from wheat which are  
involved in starch synthesis  
JOURNAL Patent: US 6307125-A 1 23-OCT-2001;  
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Alignment Scores:  
Pred. No.: 2,286-199 Length: 2239  
Score: 2466.50 Matches: 464  
Percent Similarity: 91.8% Conservative: 29  
Best Local Similarity: 85.4% Mismatches: 41  
Query Match: 85.3% Indels: 4  
DB: 6 Gaps: 2

US-10-628-525A-21 (1-539) x AR174875 (1-2239)

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Qy	382	IleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer	401
Db	1161	ATTAAATATGGCCATTCCAGAGCTCATGAGGAGAGCAGTGCATTTGTCTGCTGGATCT	1220
Qy	402	GlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPhe	421
Db	1221	GGGGATCCAATTTTGAAGCTGGATGAGATCTACCGAGTCGAGTTACAGGATAAATTC	1280
Qy	422	ArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle	441
Db	1281	CGTGGATGGGTTGGATTTAGTGTTCAGTTTCCAGTTTCCACAGATAACTGCGAGTTGCGATATA	1340
Qy	442	LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr	461
Db	1341	TTGTAAATGGCATCGAGATTGGAACCTTGGCGGCTTTAATCAGCTATATGCTATGCAATAT	1400
Qy	462	GlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluLeuAsnPheAsn	481
Db	1401	GGTACAGTCTCTGATGTTCTATGGACATGGGGGCTCCGACACAGTCGAGACCTTCCAC	1460
Qy	482	ProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGlu	501
Db	1461	CTTTTGGTGCAAAAGGAGAGGGGTACAGGGTGGGCGTTCTCACCGCTAAACCGTGGAC	1520
Qy	502	AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu	521
Db	1521	AAAGATGTT-GTGGGCATTTGGCAACCGCGATGTTCGACATTCAGGAGGACCAAGCGCTCTG	1579
Qy	522	GlyArgAlaAsnGluAlaArgHisAlaValLysArgLeuHisValGlyProCys	538
Db	1580	GGAGGGCTCATGAAGCGAGCATGACGAAAGACCATACGTGGGACCATGTC	1630
RESULT	30		
LOCUS	AR535116	2239 bp	linear
DEFINITION	Sequence 1 from patent US 6734339.		
ACCESSION	AR535116		
VERSION	AR535116.1		
KEYWORDS	GI:53925988		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2239)		
	Block, M., Lorz, H., Lutticke, S., Walter, L., Froberg, C. and		
	Kossmann, J.		

QY	262	AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyValValThrAlaAspArg	281
Db	801	GGCCITGACNAGGCTGAGGAGTTAACTTTTGAAGAGGAGCAGTTGTGACAGCATCGG	860
QY	282	IleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlnGly	301
Db	861	ATTGTGACCGTCAGTCAGGGTTATTTCATGGAGGTCACAACCTCTGAAGGTGGACAGGCG	920
QY	302	LeuAsnGluLeuLeuSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp	321
Db	921	CTCAATGAGCTCTTAAGCTCCCGAAAAGTGTTGAAATGGAATGTAATGGAATTGAC	980
QY	322	IleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp	341
Db	981	ATTATGATTGGNACCCACACAGCAAGTGTCTCCCTCNCATTTATTCTGTCGATGAC	1040
QY	342	LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg	361
Db	1041	CTCTCTGGAAGGCCAAATGTAAGCTGAATTCAGAGAGGTTGGGTTTACCTGTAAGG	1100
QY	362	ProAspValProIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu	381
Db	1101	GAGGATGTTCTCTGATTGGCTTTATTTGAAGACTGGATTACAGAAAGGCATTGATCTC	1160
QY	382	IleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer	401
Db	1161	ATTAAATGGCCATCCAGAGCTCATGAGGAGGAGTGCAATTTGTGCTTGGATCT	1220
QY	402	GlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPhe	421
Db	1221	GGGGATCCCAATTTTGAAGGCTGGATGAGATCTACCGAGTCGAGTTTACAAGGATAAATTC	1280
QY	422	ArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle	441
Db	1281	CGTGGATGGGTTGGATTATAGTTTCCAGTTTCCACAGAATAACTGCAGGTTGCCGATATA	1340
QY	442	LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr	461
Db	1341	TTGTTAATGCCATCGAGATTGNACCTTGGGCTCTTAATCAGCTATATGCTATGCATATAT	1400
QY	462	GlyThrValProValHisAlaThrGlyLeuArgAspThrValGluAsnPheAsn	481
Db	1401	GGTACAGTTCCTGTAGTTTCATGGAACTGGGGGCTCCGAGACACAGTCGAGACCTTCAAC	1460
QY	482	ProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGlu	501
Db	1461	CCTTTTGGTGCAAAAGGAGGAGGGGTACAGGGTGGGCGTTCTCACCGCTAACCGTGGAC	1520
QY	502	AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu	521
Db	1521	AAGATGTT-GTGGCATTCGGNACCCGCGATGTCGACATTCAGGGAGCACAGCCGCTCTTG	1579
QY	522	GlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCys	538
Db	1580	CGAGGGGCTCATGAAGCGAGGCATACGAAAGACCATACGTGGGACCATGC	1630



GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 00:15:06 ; Search time 1269 Seconds  
(without alignments)  
2830.777 Million cell updates/sec

Title: US-10-628-525A-21

Perfect score: 2893

Sequence: 1 CVALSRELDGLPEPGIAGS.....LLGRANEARHVKRLHVGPCR 539

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-O=/abes/ABSWEB spool/US10628525/runat\_31032006\_095109\_16557/app\_query.fasta\_1  
-DB=N Geneseq -QWTF=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0 -  
-UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.cdi -LIST=150  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes06h  
-USER=US10628525 @CGN 1.1 1404 @runat\_31032006\_095109\_16557 -NCPU=6 -ICPU=3  
-NO\_WMAP -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 21:\*

1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*  
14: Geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2893	100.0	1620	2	Aav29759 Zea mays
2	2861	98.9	2991	8	Abx09932 DNA encod
3	2858	98.8	1752	2	Aav29756 Zea mays
4	2856	98.7	1749	2	Aav70960 DNA encod

5	2832	97.9	2008	3	AAZ50643	Aaz50643 Corn solu
6	2832	97.9	2491	3	AAZ50636	Aaz50636 Corn solu
7	2818	97.4	2383	3	AAT95785	Aat95785 Maize sta
8	2757	95.3	2990	2	AAV66832	Aav66832 Zea mays
9	2757	95.3	2992	2	AAT67285	Aat67285 Soluble s
10	2655	91.8	1528	3	AAZ50637	Aaz50637 Corn solu
11	2538	87.7	1855	13	ADX36677	Adx36677 Plant ful
12	2525.5	87.3	1881	12	ADQ37148	Adq37148 Cell prol
13	2525.5	87.3	1881	12	ADQ15732	Adq15732 Rice stre
14	2525.5	87.3	1881	13	ADQ4094	Adq4094 Rice star
15	2525.5	87.3	2533	2	AAQ45183	Aaq45183 Soluble r
16	2511.5	86.8	1926	8	ADA70523	Ada70523 Rice gene
17	2470.5	85.4	2747	13	ADT20132	Adt20132 Plant cDN
18	2467.5	85.3	2662	2	AAZ34651	Aaz34651 cDNA sequ
19	2466.5	85.3	2239	2	AAV01527	Aav01527 Wheat sol
20	2466.5	85.3	2805	3	AZ24487	Aaz24487 Wheat sol
21	2043	70.6	1415	3	AAZ50642	Aaz50642 Corn solu
22	1722	59.5	1984	3	AAC46797	Aac46797 Arabidops
23	1645.5	56.9	1758	2	AAT32325	Aat32325 Soluble s
24	1496	51.7	1294	13	ADX59939	Adx59939 Plant ful
25	1459	50.4	1300	13	ADX08949	Adx08949 Plant ful
26	1280	44.2	10336	2	AAZ34652	Aaz34652 Wheat sta
27	1193	40.9	1860	13	ADX13652	Adx13652 Plant ful
28	1130.5	39.1	2097	2	AAV29755	Aav29755 Zea mays
29	1130.5	39.1	2480	8	ABX09934	Abx09934 DNA encod
30	1125.5	38.9	2423	2	AAV70958	Aav70958 DNA encod
31	1103	38.1	2418	6	ABS52841	Abes2841 Typha lat
32	1103	38.1	2418	10	AD62716	Ad62716 Typha lat
33	1095	37.8	2865	8	ABX09933	Abx09933 DNA encod
34	1093	37.8	1798	3	AAZ50647	Aaz50647 Corn star
35	1093	37.8	2019	3	AAZ50646	Aaz50646 Corn star
36	1093	37.8	2248	3	AAZ50651	Aaz50651 Corn star
37	1084	37.5	1824	14	ABE48376	Aeb48376 Maize Bri
38	1084	37.5	2073	14	ABE48372	Aeb48372 Curcuma z
39	1084	37.5	2348	6	ABS52826	Abss2826 Curcuma z
40	1084	37.5	2348	10	AD62701	Ad62701 Curcuma z
41	1077.5	37.2	2939	3	AAC86433	Aac86433 Wheat sta
42	1077.5	37.2	2939	3	AAC86410	Aac86410 Wheat sta
43	1075	37.2	2607	8	ACC70869	Acc70869 Rice star
44	1071	37.0	1888	13	ADX63440	Adx63440 Plant ful
45	1070.5	37.0	2807	3	AAC86435	Aac86435 Wheat sta
46	1070.5	37.0	2842	3	AAC86411	Aac86411 Wheat sta
47	1069.5	37.0	2920	6	ABX88112	Abx88112 cDNA enco
48	1068.5	36.9	2951	6	ABX88114	Abx88114 cDNA enco
49	1067.5	36.9	2950	6	ABX88113	Abx88113 cDNA enco
50	1066	36.8	2607	8	ACC70868	Acc70868 Rice star
51	1053.5	36.4	2946	6	ABX88115	Abx88115 cDNA enco
52	1050.5	36.3	2826	2	AAV01528	Aav01528 Wheat gra
53	1038.5	35.9	2107	3	AAC86412	Aac86412 Wheat sta
54	1038.5	35.9	2107	3	AAC86434	Aac86434 Wheat sta
55	1029	35.6	2412	10	ADC07863	Adc07863 Rice DNA
56	1029	35.6	2412	12	ADJ40034	Adj40034 Plant cDN
57	980.5	33.9	1828	13	ADO82332	Ado82332 Plant ful
58	978.5	33.8	2007	2	AAV29754	Aav29754 Zea mays
59	978.5	33.8	2007	2	AAV70959	Aav70959 DNA encod
60	978.5	33.8	2085	2	AAT67286	Aat67286 Soluble s
61	978.5	33.8	2085	2	AAV66833	Aav66833 Zea mays
62	972	33.6	1724	6	ABA01821	Aba01821 Rice star
63	893	30.9	2161	6	ABK53210	Abk53210 Potato gr
64	891.5	30.8	1502	13	ADX60901	Adx60901 Plant ful
65	880.5	30.4	2380	2	AAV66834	Aav66834 Zea mays
66	880.5	30.4	2478	2	AAT67287	Aat67287 Soluble s
67	878.5	30.4	2176	6	ABS52832	Abes2832 Canna edu
68	878.5	30.4	2176	10	AD62707	Ad62707 Canna edu
69	871	30.1	2274	6	ABS52835	Abes2835 Typha lat
70	871	30.1	2274	10	AD62710	Ad62710 Typha lat
71	867.5	30.0	2183	6	ABK53215	Abk53215 Canna edu
72	863	29.8	1833	12	ADN73902	Adn73902 Thale cre
73	863	29.8	2115	3	AAC32824	Aac32824 Arabidops
74	851	29.4	2179	8	ABQ80055	Abq80055 Soybean g
75	849.5	29.4	1937	10	ADC53778	Adc53778 Low amylo
76	849.5	29.4	2542	2	AAV29753	Aav29753 Oryza sat
77	846.5	29.3	1937	10	ADC53776	Adc53776 Low amylo

78	842.5	29.1	2067	6	ABS52838	AbS52838 Typha fos
79	842.5	29.1	2067	10	AD62713	Tulipa fo
80	839	29.0	1818	14	ADW87816	Maize gra
81	838	29.0	1818	10	AD63600	Maize UDP
82	838	29.0	1818	14	ADW87799	Maize gra
83	838	29.0	2263	11	ADM77902	Maize wax
84	837.5	28.9	1818	8	ACC44559	Maize gra
85	833	28.8	1915	2	AAx60319	DNA seque
86	832.5	28.8	2267	2	AAx63355	Granule b
87	832	28.8	2263	11	ADM77903	Maize wax
88	831.5	28.7	1863	14	ADW87808	Corn line
89	824	28.5	2098	13	ADX09509	Plant ful
90	823	28.4	2399	8	ABQ80054	Corn gran
91	822	28.4	2297	13	ADT19869	Plant cdN
92	819	28.3	2028	10	ADP92505	Bread whe
93	812.5	28.1	2202	6	ABS52823	Curcuma z
94	812.5	28.1	2202	10	AD62698	Curcuma z
95	802.5	27.7	598	13	ACN46188	Cotton pr
96	777.5	26.9	11384	2	AAV52178	Streptoco
97	777.5	26.9	110000	10	ABS56454_09	Continuation (10 o
98	777	26.9	1431	10	ABX06832	S. pneumo
99	777	26.9	1431	13	ADT49969	S.pneumon
100	776	26.8	1434	13	ADK44636	Streptoco
101	776	26.8	1455	13	ADR93230	Novel S.
102	776	26.8	1455	14	AEAS7100	Streptoco
103	768.5	26.6	1645	13	ADx61230	Plant ful
104	768	26.6	1623	13	ADO84116	Plant ful
105	753	26.0	2595	13	ADT19099	Plant cdN
106	749.5	25.9	110000	6	ABA90521_06	Continuation (7 of
107	749	25.9	1377	13	ADT44429	Bacterial
108	749	25.9	1440	14	ACL70982	M. xanthu
109	749	25.9	4991	14	ACL64256	M. xanthu
110	745	25.8	1452	13	ADT43607	Bacterial
111	742.5	25.7	5928	8	ACC70867	Rice star
112	741	25.6	71979	13	ADW87736	Streptoco
113	741	25.6	71979	13	ADV78989	Streptoco
114	741	25.6	110000	13	ADV81204_08	Continuation (9 of
115	741	25.6	110000	13	ADV81204_09	Continuation (10 o
116	740	25.6	1479	6	ABQ90258	M. capsul
117	740	25.6	1479	6	ABQ90406	M. capsul
118	739.5	25.6	110000	6	ABN71527_08	Continuation (9 of
119	736	25.4	1431	13	ADW83394	Streptoco
120	736	25.4	2571	2	AAZ96227	S. pneumo
121	733	25.3	1428	6	ABN68223	Streptoco
122	726	25.1	5935	8	ACC70866	Rice star
123	719.5	24.9	1455	13	ADT48515	Bacterial
124	718.5	24.8	1427	6	ABK73466	Bacillus
125	715.5	24.7	2597	10	ADC07867	Rice DNA
126	689.5	23.8	1449	13	ADS50014	Bacterial
127	689.5	23.8	1449	13	ADS55529	Bacterial
128	680	23.5	1110	10	ADC08761	Wheat DNA
129	680	23.5	1110	12	ADJ43323	Plant cdN
130	680	23.5	1428	13	ADT41925	Bacterial
131	666	23.0	9024	3	AAc86431	Wheat SSI
132	663	22.9	1419	13	ADS58001	Bacterial
133	662.5	22.9	1428	13	ADT45680	Bacterial
134	654.5	22.6	1437	13	ADT44967	Bacterial
135	648.5	22.4	1461	13	ADS48236	Bacterial
136	646.5	22.3	1431	13	ADT46964	Bacterial
137	646	22.3	418	13	ADX29492	Plant ful
138	640	22.1	1431	13	ADT42428	Bacterial
139	636.5	22.0	1440	13	ADS62946	Bacterial
140	636.5	22.0	1440	13	ADS59388	Bacterial
141	636.5	22.0	1440	13	ADS62792	Bacterial
142	636.5	22.0	1440	13	ADS63283	Bacterial
143	635.5	22.0	1383	13	ADT46165	Bacterial
144	633	21.9	1434	13	ADT48834	Bacterial
145	631.5	21.8	1536	11	ACH98067	Klebsiell
146	630	21.8	2818	10	ADP92501	Bread whe
147	630	21.8	2818	14	ABA79534	waxy gene
148	626	21.6	1464	2	AAQ25978	giga. 3/2
149	626	21.6	1464	2	AAV23649	E. coli g
150	626	21.6	1464	9	ACD28044	DNA encod

ALIGNMENTS

RESULT 1

AAV29759

ID AAV29759 standard; DNA; 1620 BP.

XX AAV29759;

AC AAV29759;

XX 11-SEP-1998 (first entry)

XX Zea mays pEXS52 starch synthase gene.

DE SER; starch-encapsulating region; fusion vector; starch synthase;

XX glucosyl transferase; pEXS52; ss.

XX Zea mays.

OS Zea mays.

XX Key Location/Qualifiers

FT 1..2007

FT /\*tag= a

FT /product= "starch synthase"

XX WO9814601-A1.

XX 09-APR-1998.

XX 30-SEP-1997; 97WO-US017555.

XX 30-SEP-1996; 96US-0026855P.

XX (EXSE-) EXSEED GENETICS LLC.

XX Keeling P, Guan H;

XX WPI; 1998-240100/21.

XX P-PSDB; AAW56491.

XX Hybrid polypeptide comprising starch-encapsulating region and protein -

XX useful for, e.g. producing protein(s) resistant to degradation by stomach

XX acids.

XX Example 5; Page 51-53; 156pp; English.

XX The sequence is that of the starch synthase coiding region from pEXS52. It

XX can be used in the production of a hybrid polypeptide comprising a starch

XX -encapsulating region (SSR) fused to a payload protein. The hybrid

XX polypeptide can be used to make modified starches comprising the payload

XX protein, selected from, e.g. hormones, growth factors, antibodies,

XX enzymes, dyes, immunoglobulins, etc. The modified starch can also be used

XX to provide grain feeds enriched in amino acids. By encapsulating the

XX payload protein in starch, it is more resistant to degradation by stomach

XX acids

XX Sequence 1620 BP; 426 A; 313 C; 422 G; 459 T; 0 U; 0 Other;

XX Sequence 1620 BP; 426 A; 313 C; 422 G; 459 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,298-296 Length: 1620

Score: 2893.00 Matches: 539

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 2 Gaps: 0

US-10-628-525A-21 (1-539) x AAV29759 (1-1620)

Qy 1 CysValAlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGly 20

Db 1 TCGCTCCGGAGCTGAGCAGGAGGACCTCGGTCTCGAACCTGAAGGATTCTGAAGGT 60

Qy 21 SerIleAspAsnThrValValValAlaSerGluGlnAspSerGluIleValValGlyLys 40

Db 61 TCCATCGATAACACAGTAGTTGTGGCAAGTGAGCAAGATTCTGAGATTGTGGTGGAAAG 120  
Qy 41 GluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerPro 60  
Db 121 GAGCAAGCTCGAGCTAAAGTAACACAAAGCAATTGCTTTTGTAAACCGCGAAGCTTCTCCT 180  
Qy 61 TyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerIleuProValAlaLeuAlaAla 80  
Db 181 TATGCAAAAGCTCGGGGGCTAGGAGATGTTTGTGGTTCATTTGCCAGTGTCTTGTGCT 240  
Qy 81 ArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsn 100  
Db 241 CGTGGTCACCGCTGTGATGTTGTAATGCCAGATATTTAAATGCTACTCCGATAGAAT 300  
Qy 101 TyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHis 120  
Db 301 TATGCAAAATGCAATTTACACAGAAAACACATTCGGATTCCATGCTTTGGCGGTGAACAT 360  
Qy 121 GluValThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisPro 140  
Db 361 GAGGTTAACCTTCTTCCATGAGTATAGAGATTCACTGGGTGTTTGTGTGATCATCCC 420  
Qy 141 SerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGln 160  
Db 421 TCATATCACAGACTGGAAATTTATATGGAGATAAGTTTGGTCTTTTGGTGAATATCAG 480  
Qy 161 PheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGly 180  
Db 481 TTCAGATACACACTCTCTTGTCTATGCTGCTGCTGAGGCTCTTTGATCTCTTGAATTGGGA 540  
Qy 181 GlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuVal 200  
Db 541 GGATATATTTATGGACAGAAATTCGATGTTTGTGTTGTCATGATTTGGCATGCCAGTCTAGTG 600  
Qy 201 ProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
Db 601 CCACTCTCTTCTGTCGCAAAATATAGACCATATGTTGTTTATTAAGACTCCCGGAGCAATT 660  
Qy 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240  
Db 661 CTTGTATAATACATAATTTAGCACATCAGGCTGAGAGCTGCAAGCACATATCTCGACCTT 720  
Qy 241 GlyLeuProGluTyrTrpTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArg 260  
Db 721 GGGTGTCCACCTGAATGGTATGAGCTCTGGAGTGGGTATTCCTCTGAATGGGCGAGG 780  
Qy 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAsp 280  
Db 781 CATGCCCTTGACAAAGGGTGAGCGAGCTTAATTTTTGAAAGTGCAGTTGTGACAGCAGAT 840  
Qy 281 ArgIleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyGln 300  
Db 841 CGAATCGTGACTGTAGTAAGGGTATTCTGTGGAGGTCACTCACTGCTGAAGGTGGACAG 900  
Qy 301 GlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320  
Db 901 GGCCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACGGAATTTGTAATGGAATT 960  
Qy 321 AspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340  
Db 961 GACATTAATGATTTGGAAACCTCGCACAGCAAAATGATATCCCTGTCAATATCTGTGTAT 1020  
Qy 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIle 360  
Db 1021 GACCTCTCTGGAAGGCCAAATGTAAAGGTGCATTGCAGAAGGAGCTGGGTTTACCTATA 1080  
Qy 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380  
Db 1081 AGCCCTCGATGTTCTCTGATGCTCTTAATGGAAAGGTGGATATTCAGAAAGGCATTGAT 1140  
Qy 381 LeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
Db 1141 CTCATTCAACTTATCATACAGATCTCATCGCGGAAGATGTTCAATTTGTCTGCTTGA 1200

Qy 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys 420  
Db 1201 TCTGGTGACCCACAGAGCTTGAAGATTGGATGAGATCTACAGATCGATCTTCAAGGATATA 1260  
Qy 421 PheArgGlyTyrTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440  
Db 1261 TTTTCGTGGATGGGTGGATTAGTGTTCAGATTTCCACCGAATAACTGCCGGCTGGCAT 1320  
Qy 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460  
Db 1321 ATATTGTTAATGTCATCCAGATTCGAACCTTGGTCTCAATCAGCTATATGCTATGAG 1380  
Qy 461 TyrGlyThrValProValValHisAlaThrGlyLeuArgAspThrValGluAsnPhe 480  
Db 1381 TATGGCACAGTCTCTGTGTCATGCACTGGGGCTTACAGATACCGTGGAGAACTTC 1440  
Qy 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThr 500  
Db 1441 AACCCTTTTCGTGAGAAATGGAGAGCAGGGTACAGGGTGGCATTCGCACCCCTAACCA 1500  
Qy 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520  
Db 1501 GAAAAACATGTTTGTGACATTCGAACCTGCAATATCTACATACAGGGAACACAAGTCTCTC 1560  
Qy 521 LeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
Db 1561 CTGGGAAGGGCTAATGAAGCGAGGCATGTCAAAAGACTTCACGTGGGACCATGCCGC 1617

## RESULT 2

ABX09932  
ID ABX09932 standard; DNA; 2991 BP.

AC ABX09932;

DT 17-FEB-2003 (first entry)

XX DNA encoding maize Starch synthase I.

DE Starch; starch synthase; glucan association domain; GLASS; linker domain;  
KW LINKR; glucosyl transferase domain; GLYTR; C-terminal end; CTEND;  
KW granule bound starch synthase; GBSS; morphology; retrogradation;  
KW waterbinding; swelling potential; gene; ds.

OS Zea mays.

XX WO200279410-A2.

XX 10-OCT-2002.

XX 29-MAR-2002; 2002WO-US0009574.

XX 30-MAR-2001; 2001US-0279720P.

XX (BADI ) BASF PLANT SCI GMBH.

XX Commuri P, Keeling PL, Ramirez N, McKean A, Gao Z, Guan H;

XX WPI; 2003-040678/03.

XX New DNA encoding fusion protein consisting of 4 different functional  
PT domains selected from glucan association domain, linker domain, glucosyl  
PT transferase domain, and C-terminal end, useful for producing modified  
PT starches.

XX Claim 33; Page 222-223; 265pp; English.

XX The invention describes an isolated DNA molecule encoding a fusion  
CC protein consisting of 4 different functional domains selected from glucan  
CC association domain (GLASS), linker domain (LINKR), glucosyl transferase  
CC domain (GLYTR), and C-terminal end (CTEND) which are operably linked to  
CC one another. The DNA molecule is useful for expressing in plants  
CC polypeptides including starch synthase enzymes as fusion proteins with

CC improved affinity to starch and modified catalytic capabilities and to  
CC the in vivo and in vitro synthesis of glucan chains of modified lengths  
CC as compared to plants producing native starch or starch produced with  
CC native starch synthases. Expression of the starch synthase fusion  
CC proteins along with granule bound starch synthase (GBSS) will lead to a  
CC modified starch having an altered or improved morphology, retrogradation,  
CC waterbinding, or swelling potential of the granules, gel strength,  
CC adhesiveness, cohesiveness, hardness, elasticity, increased or decreased  
CC granule size, degree of branching, crystallinity, degree of cross-  
CC linking, and increased or decreased glucan chain lengths. This sequence  
CC encodes a starch synthase used in the invention  
XX  
SQ Sequence 2991 BP; 750 A; 660 C; 804 G; 776 T; 0 U; 1 Other;

## Alignment Scores:

Pred. No.: 1,39e-292 Length: 2991  
Score: 2861.00 Matches: 539  
Percent Similarity: 92.5% Conservative: 0  
Best Local Similarity: 92.5% Mismatches: 0  
Query Match: 98.9% Indels: 44  
DB: 8 Gaps: 1

US-10-628-525A-21 (1-539) x ABX09932 (1-2991)

QY 1 CysValAlaGluLeuSerArgGlu-----8  
DB 719 TCGTTCGGAGCTGAGCAGGGGGGGCCGCGCGCGCGCTGCCACCCCGCTGCTG 778  
QY 8 -----8  
DB 779 GCGCCCGCGCTCGTGGCGGCTTCCTCGCGCGCGCGCGAGCCACGGGTGAGCCGCA 838  
QY 9 -----AspLeuGlyLeuGluProGluGly 16  
DB 839 TCGACGCCCGCGCGCTGCCAGCGCGCGCTGGGGGACCTCGGTCTCGAACCCTGAAGGG 898  
QY 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36  
DB 899 ATTGCTGAAGGTTCCATCGATACACAGTAGTTGTGGCAAGTGAGCAAGATTCTGAGATT 958  
QY 37 ValValGlyLeuGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
DB 959 GTGGTTGGAAAGGAGCAGCTCGAGCTAAAGTAAACACAAAGCATTTCTTTGTAAACCGGC 1018  
QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
DB 1019 GAAGCTTCTCCTTATGCAAGTCTGGGGTCTAGGAGATGTTGTGGTTTCATTGCCAGTT 1078  
QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrIleuAsnGlyThr 96  
DB 1079 GCTCTTGTCTGCTCGTGTCCCGTCCCGTGTGATGGTTGTAATGCCAGATATTTAATGGTACC 1138  
QY 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
DB 1139 TCCGATAAGAAATATGCAATGCAATTTTACACAGAAAAACACATTCGGATTCCATGCTTT 1198  
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspThrValPhe 136  
DB 1199 GCGGTGAACTGAAGTTACCTTCTTCCATGAGTATAGAGATTTCAGTTGAGTGGGTGTTT 1258  
QY 137 ValAspHisProSerTyrHisArgProGlyYAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
DB 1259 GTTGATCATCCTCATATCACAGACCTGGAATTTATATGGAGATAAGTTTGGTCTTTT 1318  
QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
DB 1319 GGTGATAATCAGTTCAGATACACACTCCTTTGCTATGCTGCTGCTGAGGCTCCTTTGATC 1378  
QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspThrHis 196  
DB 1379 CTTGAATTGGGAGGATATATTTATGGACAGAAATGCAATGCTGTTGTGTCATGATGGCAT 1438  
QY 197 AlaSerLeuValProValLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216

DB 1439 GCCAGTCTAGTCCAGTCTCTTCTGCTCAAAATATAGCCATATGCTGTTTATAAGAC 1498  
QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProIleSerThr 236  
DB 1499 TCCCGCAGCATTTCTTGTATAATACATAATTTAGCACATCAGGGTGTAGAGCTCGAAGCAC 1558  
QY 237 TyrProAspLeuGlyLeuProGluTyrPyrGlyAlaLeuGluTyrValPheProGlu 256  
DB 1559 TATCTCTGACCTTGGGTTCACCTGAATGGTATGAGGCTCTCGAGTGGGTATTTCCCTGAA 1618  
QY 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
DB 1619 TGGCGAGGAGGCGCATGCCCTTGACAAGGCTGAGGAGTTAATTTTGAAGGTGCAGTT 1678  
QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
DB 1679 GTGACAGCAGATCGAATCGTGACTGTGATAGGGTTATTCTGGGAGGTCAACATGCT 1738  
QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle 316  
DB 1739 GAAGGTGACAGGGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACCGAATT 1798  
QY 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
DB 1799 GTAAATGGAATTTGACATTAATGATTGGAACCTCGCCACAGACAAATGATATCCCTGTCAT 1858  
QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
DB 1859 TATTCTGTGTAGTACCTCTCTGGAAGGCCAAATGTAAGGTGCATTGCGAAGGAGCTG 1918  
QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
DB 1919 GGTTTACCTATTAAGGCTGTGATCTCTGATTGGCTTTATTGGAAGGTTTGGATTATCAG 1978  
QY 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396  
DB 1979 AAAGGCATTGATCTCATCACTTATCATCATCAGATCTCATCGCGGAAGATGTTCAATTT 2038  
QY 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416  
DB 2039 GTCATGCTTGGATCTGGTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATC 2098  
QY 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436  
DB 2099 TTCAAGGATAAATTTCTGGTGGATGGGTGGATTGATTGATCTCCAGTTTCCACCGAATACT 2158  
QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456  
DB 2159 GCGGCTCGGATATATTGTTAATGCCATCCAGATTTCGAACCTTGTGGTCTCAATCAGCTA 2218  
QY 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
DB 2219 TATGCTATGCAATGAGCACAGTTCCTGTGTGCCATGCAACTGGGGGCTTAGAGATACC 2278  
QY 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAla 496  
DB 2279 GTGGAGAACTTCAACCCCTTCTGGTGAAGTGGAGAGCAGGGTACAGGGTGGGCATTCGCA 2338  
QY 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
DB 2339 CCCCTAACACAGAAAAACATGTTTGTGGACATTGCGAATTCGCAATATCTACATACAGGCA 2398  
QY 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536  
DB 2399 ACACAAGTCTCTCTGGGAAGGGCTAATGAAGCGAGGCATGTCAAAAGACTTCACCGTGGGA 2458  
QY 537 ProCysArg 539  
DB 2459 CCATGCCGC 2467

RESULT 3  
AAV29756



Db	1261	AAAGGCATTGATCTCATTTCAACTTATCATACCGAGTCTCATGCGGGAAGATGTTCAATTT	1320
Qy	397	ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle	416
Db	1321	GTCAATGTTGGACTGCTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATC	1380
Qy	417	PhelyAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr	436
Db	1381	TTCAAGGATAAATTTCTGTCGATGGTGGATTTAGTGTCTCCAGTTTCCCAACCGAATAACT	1440
Qy	437	AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu	456
Db	1441	GCCGGCTGCCGATATATTGTTAATGCCATCCAGATTCCGAACCTTGTGGTCTCAATCAGCTA	1500
Qy	457	TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr	476
Db	1501	TATGCTATGAGTATGGACAGTCTCTGTTGTCCATGCAACTGGGGGCCCTTAGAGATACC	1560
Qy	477	ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAla	496
Db	1561	GTGGAGAACTTCAACCCCTTTCGGTGAAGATGGAGAGCAGGGTACAGGGTGGGCATTCGCA	1620
Qy	497	ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly	516
Db	1621	CCCTTACCCACAGAAAACATGTTTCTGGACATTTGCCAACTTGCAAATATCTACATACAGGA	1680
Qy	517	ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValIysArgLeuHisValGly	536
Db	1681	ACACAGTCTCTCTGGGAGGGCTAATGAAGCAGGCGTGTCAAAAGACTTTCAGTGGGA	1740
Qy	537	ProCysArg 539	
Db	1741	CCATGCCGC 1749	
RESULT 4			
AAV70960			
ID AAV70960 standard; DNA; 1749 BP.			
XX	AAV70960;		
XX	23-AUG-1999 (first entry)		
XX	DNA encoding maize starch soluble synthase I-2.		
XX	Non-glycogen-like polysaccharide production; fermentation;		
XX	starch synthetase enzyme; glycogen-synthetase enzyme; glycogen synthesis;		
XX	non-starch branching gene; amylopectin; amylose; plant-like starch;		
XX	maize starch soluble synthase I-2; ss.		
OS	Zea mays.		
XX	WO9844780-A1.		
XX	15-OCT-1998.		
XX	03-APR-1998; 98WO-US006660.		
XX	04-APR-1997; 97US-0042939P.		
XX	(EXSE-) EXSEED GENETICS LLC.		
XX	Guan H, Keeling PL;		
XX	WPI; 1998-568285/48.		
XX	P-PSDB; AAV70894.		
XX	Producing non-glycogen-like polysaccharides in bacteria, fungi or plants		
XX	- transformed with genes for enzymes involved in starch or glycogen		
XX	synthesis allows fermentative production of starches with engineered		
XX	properties.		
XX	Disclosure; Fig 52; 150pp; English.		



Db 721 GCCAGTCTAGTGCAGTCTCTTCTGCTGCAAAATATAGACCATATGTTGTTTAAAGAC 780  
 Qy 217 SerArgSerLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
 Db 781 TCCGACAGCATCTCTGTAATACATAATTTAGCACATCAGAGGTGTAGAGCCTGCAAGCACA 840  
 Qy 237 TyrProAspLeuGlyLeuProGluTyrProGluTyrGlyAlaLeuGluTyrValPheProGlu 256  
 Db 841 TATCCTGACCTTGGTGTGACCTGAAATGATATGAGCTCTGGAGTGGGTATTCCTCGAA 900  
 Qy 257 TrpAlaArgArgHisAlaLeuAspLeuGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
 Db 901 TGGGCGAGGAGCATGCCCTTGACAGGGTGAGGAGTAAATTTTGAAGGTGCGAGTT 960  
 Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
 Db 961 GTGACAGCAGATCGAATCGTGACTGTCTAGTAAGGTTATTCGTGGAGGTCACAACTGCT 1020  
 Qy 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316  
 Db 1021 GAAGGTGGAAGGCGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAGCGGAAT 1080  
 Qy 317 ValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHis 336  
 Db 1081 GTAAATGGAATTGACATTAATGATTGGAACCTGCCACACAAATGTATCCCTGTGCAT 1140  
 Qy 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
 Db 1141 TATTCCTGATGACCTCTCTGGAAGGCCAAATGTAAGGTGCATTCAGAGGAGCTG 1200  
 Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
 Db 1201 GGTATACCTATTAAGGCTGATGTCTCTCTGATGGCTTTATTCGAAGGTGGAATATCAG 1260  
 Qy 377 LysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPhe 396  
 Db 1261 AAAGGCATGATCTCAATTCACATATACACAGATCTCATGCGGAAGATGTTCAATTT 1320  
 Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416  
 Db 1321 GTCATGCTTGGATCTGTCAGCCAGAGCTTGAAGATTGGATGAGATCTACAGATCGATC 1380  
 Qy 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436  
 Db 1381 TTCAAGGATAAAATTTTCGTGATGGGTGGATTTAGTGTTCAGTTCCTCCACCGAATAACT 1440  
 Qy 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456  
 Db 1441 GCCGGCTGGATATATGTTAATGCTATCCAGATTCGAACTTGTGTGCTCAATCAGCTA 1500  
 Qy 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
 Db 1501 TATGCTATGAGTATGTCAGATGTCAGTCTGTTGTCATGCAACTGGGGGCTTAGAGATACC 1560  
 Qy 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAla 496  
 Db 1561 GTGGAGAACTTCAACCTTTTCGTGAGAAATGGAGACAGGGTACAGGGTGGGCATTCGCA 1620  
 Qy 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
 Db 1621 CCCTTAACACAGAAACATGTTTGTGGACATTCGCAATTCGCAATATCTACATACAGGA 1680  
 Qy 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536  
 Db 1681 ACACAGTCTCTCTGGGAGGGCTATGTAAGCGAGGAGCATGTCAAAAGACTTCACTGTGGA 1740  
 Qy 537 ProCysArg 539  
 Db 1741 CCATGCCGC 1749

RESULT 5  
 AAZ50643

ID AAZ50643 standard; cDNA; 2008 BP.  
 AC AAZ50643;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX  
 DE Corn soluble starch synthase gene fragment inserted in pSS65-C11.  
 XX  
 KW Soluble starch synthase; starch fine structure; corn; transgenic plant;  
 KW amylose; amylopectin; amylose polymerisation;  
 KW non-granule bound starch synthase; non-GBSSI; altered starch; food;  
 KW paper; plastic; adhesive; ss.  
 XX  
 OS Zea mays.  
 XX  
 PN WO200006755-A2.  
 XX  
 PD 10-FEB-2000.  
 XX  
 PF 26-JUL-1999; 99WO-US016296.  
 XX  
 PR 28-JUL-1998; 98US-0094436P.  
 XX  
 XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
 PA Broglie KB, Lightner JE;  
 PI WPI; 2000-195311/17.  
 XX  
 DR Producing transgenic cereal crops with altered starch structure useful  
 PT for preparing foodstuff, paper, plastic or adhesives, comprises  
 PT transforming crops with chimeric sense or antisense gene construct  
 PT encoding starch synthase.  
 XX  
 PS Claim 5; Page 53; 56pp; English.  
 XX  
 CC The present sequence is the corn soluble starch synthase (SSI) DNA  
 CC sequence comprising the entire SSI coding region and a 3' UTR fragment  
 CC inserted into plasmid pSS65-C11. The chimeric gene containing the zein  
 CC promoter followed by the 3'UTR is used as a sense construct for  
 CC preparation of transgenic corn expressing altered starch structure. The  
 CC starch fine structure derived from a grain of the cereal crop can be  
 CC altered in the transformed cereal crop by changes in amylose to  
 CC amylopectin ratio, amylopectin fine structure, increased abundance of  
 CC very short amylopectin chains and in the degree of polymerisation of  
 CC amylose. These modifications can be created by controlling the expression  
 CC of non-GBSSI (non-granule bound starch synthase) in transgenic plants.  
 CC Altered starches are useful in foods, paper, plastics or adhesives  
 XX  
 SQ Sequence 2008 BP; 486 A; 463 C; 543 G; 516 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 9.3e-290 Length: 2008  
 Score: 2832.00 Matches: 538  
 Percent Similarity: 92.3% Conservative: 0  
 Best Local Similarity: 92.3% Mismatches: 1  
 Query Match: 97.9% Indels: 45  
 DB: 3 Gaps: 1

US-10-628-525A-21 (1-539) x AAZ50643 (1-2008)  
 Qy 1 CysValAlaGluLeuSerArgGlu----- 8  
 Db 119 TCGTTCGGAGCTGAGCAGGAGGGGGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTG 178  
 Qy 8 ----- 8  
 Db 179 GCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 238  
 Qy 9 -----AspLeuGlyLeuGluP-ogluGly 16  
 Db 239 TCGACGCCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 298



CC The present sequence is the corn soluble starch synthase (SSI) composite-  
 CC gene. This was used in the construction of plasmid pSS31 for the  
 CC generation of an antisense construct for suppression of SSI expression in  
 CC corn. The starch fine structure derived from a grain of the cereal crop  
 CC can be altered in the transformed cereal crop by changes in amylose to  
 CC amylopectin ratio, amylopectin fine structure, increased abundance of  
 CC very short amylopectin chains and in the degree of polymerisation of  
 CC amylose. These modifications can be created by controlling the expression  
 CC of non-GBSSI (non-granule bound starch synthase) in transgenic plants.  
 CC Altered starches are useful in foods, paper, plastics or adhesives  
 XX

SQ Sequence 2491 BP; 597 A; 610 C; 657 G; 627 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1,27e-289 Length: 2491  
 Score: 2832.00 Matches: 538  
 Percent Similarity: 92.3% Conservative: 0  
 Best Local Similarity: 92.3% Mismatches: 1  
 Query Match: 97.9% Indels: 45  
 DB: 3 Gaps: 1

US-10-628-525A-21 (1-539) x AAZ50636 (1-2491)

QY 1 CysValAlaGluLeuSerArgGlu-----8  
 DB 262 TGGCTCGCGAGCTGAGCAGGAGGGGCGCGCGCGCGCTGCGCACCGCGCTGCTG 321  
 QY 8 -----8  
 DB 322 GCGCCCCCGCTGCTGCGCGCTTCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCA 381  
 QY 9 -----AspLeuGlyLeuGluProGluGly 16  
 DB 382 TCGACGCGCGCGCGCGCTGCGCGCGCGCGCGCGCTGCGCGCGCTGCGAACCTGGAAGG 441  
 QY 17 IleAlaGluGlySerIleAspAanThrValValAlaSerGluGlnAspSerGluIle 36  
 DB 442 ATTGCTGAAGGTTCCATCGATACACAGTAGTTGTGGCAAGTGAAGCAAGATTCTGAGATT 501  
 QY 37 ValValGlyGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
 DB 502 GTGGTTGGAAGGAGGAGCTCGAGCTAAGTAACCAAGCAATGTCTTTGTAAACCGGC 561  
 QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
 DB 562 GAAGCTTCTCCTTATGCMAAGTCTGGGGGTCTAGGAGATGTTTGTGTTTCATTGCCAGTT 621  
 QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAanGlyThr 96  
 DB 622 GCTCTTTGCTGCTGCTGGTCAACGCTGATGTTGTAATGCCAGATATTAAATGGTACC 681  
 QY 97 SerAspLysAanTyrAlaAanAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
 DB 682 TCCGATAAGAAATATGCAATGCAATTTTACACAGAAATAACACATTCGGATTCCATGCTTT 741  
 QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136  
 DB 742 GCGCGGTGAACATGAAGTTACCTTCTCCATGATATAGATATGAGATTCAGTTGCGGTGTTT 801  
 QY 137 ValAspHisProSerTyrHisArgProGlyAanLeuTyrGlyAspLysPheGlyAlaPhe 156  
 DB 802 GTTGATCATCCCTCATATACAGACCTGGAAATTTATATGGAGATTAAGTTTGGTGTCTTT 861  
 QY 157 GlyAspAanGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
 DB 862 GGTGATAATCAGTTCAGATACACACTCTCTTGTGATGCTGCTGATGAGGCTCTTTGATC 921  
 QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAanCysMetPheValValAanAspTrpHis 196  
 DB 922 CTTGAATTGGGAGGATATATTTATGACAGAAATTGCAATGTTGTTGTTGTTGTTGTTGTT 981  
 QY 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216

#### RESULT 7

AAT95785

ID AAT95785 standard; cDNA to mRNA; 2383 BP.

DB 982 GCCAGTCTAGTGCAGCTCTTCTTCTGCTCAAAATATAGACCATATGCTGTTTATAAGAC 1041  
 QY 217 SerArgSerIleLeuValIleHisAanLeuAlaHisGlnGlyValGluProAlaSerThr 236  
 DB 1042 TCCGCGAGCAATCTTGTAAATACATAATTTAGCACATCAGGGTGTAGAGCCCTGCAGGACA 1101  
 QY 237 TyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256  
 DB 1102 TATCTCGACCTGGGTGGCCACCTGAATGCTATGGAGCTCTGGAGTGGTATTCCCTGAA 1161  
 QY 257 TTPAlaArgHisAlaLeuAspLysGlyGluAlaValAanPheLeuLysGlyAlaVal 276  
 DB 1162 TGGCGGAGGAGGCGATGCCCTTGCAAGGGGTGAGCGAGTTAAATTTTGAAGGTGCGAGTT 1221  
 QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
 DB 1222 GTGACAGCAGATCGATCGTACTGTTCAGTAAGGGTTATTTCGTGGGAGGTTCACAACTGCT 1281  
 QY 297 GluGlyGlyGlnGlyLeuAanGluLeuLeuSerSerArgLysSerValLeuAanGlyIle 316  
 DB 1282 GAAGGTGGACAGGGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACGGAATT 1341  
 QY 317 ValAanGlyIleAspIleAanAspTrpAanProAlaThrAspLysCysIleProCysHis 336  
 DB 1342 GTAAATGGAAATTGACATAATGATTGGAACCCCTGCCACAGACAAATGTATCCCTGTGAT 1401  
 QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
 DB 1402 TATTCGTGTAGTACCTCTCTGGAAGGCCAATGTAAAGTGCATTCGAAAGGAGCTG 1461  
 QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
 DB 1462 GGTTTACCTATAAGGCTGATGTTCTCTGATTGGCTTTATTGGAAGTTGGATTATCAG 1521  
 QY 377 LysGlyIleAspLeuIleGlnIleIleProAspLeuMetArgGluAspValGlnPhe 396  
 DB 1522 AAAGGCATTGATCTCAATCACTTATATACCAAGATCTCATGCGGGAAGATGTTCAATTT 1581  
 QY 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416  
 DB 1582 GTCATGCTTGGATCTGGTGACCCAGAGCTTGAAGATTGGATGGAGTCTACAGAGTCGATC 1641  
 QY 417 PheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr 436  
 DB 1642 TTCAAGGATAAATTTCTGGATGGGTGGATTAGTGTTCAGTTCCTCCCAACCGAATAACT 1701  
 QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAanGlnLeu 456  
 DB 1702 GCGGGCTGCGATATATTGTTAATGCCATCCAGATTCGAAACCTTTGTGGTCTCAATCAGCTA 1761  
 QY 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
 DB 1762 TATGCTATCGATATGGCACAGTTCTGTTGTCATGCAACTGGGGGCCCTTAGAGATACC 1821  
 QY 477 ValGluAanPheAanProPheGlyGluAanGlyGluGlnGlyThrGlyTrpAlaPheAla 496  
 DB 1822 GTGGAGAACTTCAACCTTTCTGGTGAAGATGGAGAGCAGGGTACAGGGTGGCGCATTCGCA 1881  
 QY 497 ProLeuThrThrGluAanMetPheValAspIleAlaAanCysAanIleTyrIleGlnGly 516  
 DB 1882 CCCCTAACACAGAAACATGTTTGTGGACATTTGCGCACTGCAATATCTACATACAGGGA 1940  
 QY 517 ThrGlnValLeuLeuGlyArgAlaAanGluAlaArgHisValLysArgLeuHisValGly 536  
 DB 1941 ACACAGTCTCTCTGGGAAGGGCTAATGAAGCGAGGCTGTCAAAAGACTTTCACGTTGGA 2000  
 QY 537 ProCysArg 539  
 DB 2001 CCATGCCGC 2009

XX AAT95785;  
 XX AC  
 XX 22-MAY-1998 (first entry)  
 XX DT  
 XX Maize starch synthase type I cDNA.  
 XX DE  
 XX Maize; starch synthase type I; starch; ds.  
 XX KW  
 XX Maize; starch synthase type I; starch; ds.  
 XX OS  
 XX Zea mays.  
 XX FH  
 XX Key Location/Qualifiers  
 XX FT CDS 2..1951  
 XX FT /\*tag= a  
 XX FT /product= "starch\_synthase\_type\_I"  
 XX FT  
 XX DE19619918-A1.  
 XX PN  
 XX 20-NOV-1997.  
 XX PD  
 XX 17-MAY-1996; 96DE-01019918.  
 XX PF  
 XX 17-MAY-1996; 96DE-01019918.  
 XX PR  
 XX (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.  
 XX PA  
 XX Kossmann J, Frohberg C;  
 XX PI  
 XX WPI; 1998-000821/01.  
 XX DR P-PSDB; AAW38218.  
 XX DR  
 XX DNA encoding maize starch synthase type I protein - for producing  
 XX PT transgenic plants.  
 XX PT  
 XX Claim 1; Page 16-20; 23pp; German.  
 XX PS  
 XX The present sequence encodes maize starch synthase type I, useful in the  
 XX CC production of starch. Starch can be used in various conventional starch  
 XX CC applications, e.g. starch hydrolyzate products, foods, papermaking,  
 XX CC adhesives, textiles, building materials, soil stabilisation,  
 XX CC agrochemicals, pharmaceuticals, cosmetics, coal briquettes, ore and coal  
 XX CC slurries, foundry casting, rubber, leather and synthetic polymers. The  
 XX CC enzyme produces a starch stated to have different physicochemical  
 XX CC properties, especially viscosity and gelling properties, from wild type  
 XX CC starch  
 XX CC  
 XX SQ Sequence 2383 BP; 582 A; 546 C; 633 G; 622 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 3 65e-288 Length: 2383  
 Score: 2818.00 Matches: 534  
 Percent Similarity: 92.1% Conservative: 3  
 Best Local Similarity: 91.6% Mismatches: 2  
 Query Match: 97.4% Indels: 45  
 DB: 2 Gaps: 1  
 US-10-628-525A-21 (1-539) x AAT95785 (1-2383)  
 QY 1 CysValAlaGluLeuSerArgGluAep----- 9  
 Db 146 TCGGTCCGGAGCTGAGCAGGAGGCGCCCGCGCGCGCGATGCCACCCGCGTGTG 205  
 QY 9 ----- 9  
 Db 206 GCGCCCGCGCTCGTCCCGGCTTCCTCGCGCGCGCGCGAGCCACCGGGTGAGCCGCA 265  
 QY 10 -----LeuGlyLeuGluProGluGly 16  
 Db 266 TTGACGCCCGCCCGTGCAGCGCGGCTGGGGGGTCTCGGTGTCGAACCTGAAGG 325  
 QY 17 lleAlaGluGlySerIleAspAenThrValValAlaSerGluGlnAspSerGluIle 36  
 Db 326 ATTGTGAAGGTTCATCGATAACACAGTAGTTGTGGCAAGTGAGCAAGATTCTGAGATT 385

QY 37 ValValGlyIysGluGlnAlaArgAlaIysValThrGlnSerIleValPheValThrGly 56  
 Db 386 GTGGTTGGAAAGGAGCAAGCTCGAGCTAAAGTAAACACAAACATTGTCTTTGTAACGGC 445  
 QY 57 GluAlaSerProTyrAlaIysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
 Db 446 GAAGCTTCCTTATGCAAAAGTCTGGGGTCTAGGAGATGTTTGGTTCATTCGCAATT 505  
 QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAenGlyThr 96  
 Db 506 GCTCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 565  
 QY 97 SerAspIysAenTyrAlaAenAlaPheTyrThrGluIysHisIleArgIleProCysPhe 116  
 Db 566 TCCGATAAGATTATGCAAAATGCAATTTTACACAGAAAAACACATTCCGATTCATGCTTT 625  
 QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136  
 Db 626 GCGGGTGAACATGAAGTTACCTTCTTCATGAGTATAGAGATTCAGTTGACCTGGGTGTT 685  
 QY 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspIysPheGlyAlaPhe 156  
 Db 686 GTTGATCATCCCTCATATCACAGACTGGAATTTATATGGAGATAAGTTTGGTGTCTTT 745  
 QY 157 GlyAspAenGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
 Db 746 GGTGATAATCAGTTGAGATACACATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 805  
 QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAenCysMetPheValValAenAspTrpHis 196  
 Db 806 CTTGAATTGGGAGGATATATTATGACAGAGATTGCATGTTGTTGTCATGATTGGCAT 865  
 QY 197 AlaSerLeuValProValLeuLeuAlaIysTyrArgProTyrGlyValTyrIysAsp 216  
 Db 866 GCGAGTCTAGTCCAGTCTCTTCTGCTGCAAAATATAGACCATATGCTGTTTATAAAGAC 925  
 QY 217 SerArgSerIleLeuValIleHisLeuAlaHisGlnGlyValGluProIleAspThr 236  
 Db 926 TCCCGCAGCATTTCTGTAATACATAATTTAGCACATCAGGGGTAGAGCTCAGAGCACA 985  
 QY 237 TyrProAspLeuGlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGlu 256  
 Db 986 TATCTTGACCTTGGGTGGCCACTGAAATGATGATGAGCTCTGGAGTGGGTATTCCTGAA 1045  
 QY 257 TrpAlaArgArgHisAlaLeuAspIysGlyGluAlaValAenPheLeuIysGlyAlaVal 276  
 Db 1046 TGGCGCAGGAGGATGCCCTTGACAAGGCTGAGGAGTTAAATTTTGAAGGTGCAGTT 1105  
 QY 277 ValThrAlaAspArgIleValThrValSerIysGlyTyrSerTrpGluValThrAla 296  
 Db 1106 GTGACAGCAGATCGAATCGTGAATCGTGAATGAGGTATTTATGAGAGTCAACTGCT 1165  
 QY 297 GluGlyGlyGlnGlyLeuAenGluLeuSerArgLysSerValLeuAenGlyIle 316  
 Db 1166 GAAGGTGGACAGGGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACGGAAT 1225  
 QY 317 ValAenGlyIleAspIleAenAspTrpAenProAlaThrAspIysCysIleProCysHis 336  
 Db 1226 GTAAATGGAATTTGACATTAATGATTGGAACCTCGCCACAGACAAATGTATCCCTGTCAT 1285  
 QY 337 TyrSerValAspAspLeuSerGlyIysAlaIysCysIysGlyValAenGlnIysGluLeu 356  
 Db 1286 TATTCGTGTGATGACTCTCTGGAAGGCCAAATGTAAGGTGCATTCGAGAGGAGCTG 1345  
 QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
 Db 1346 GGTTTTACCTATAAGCCCTGATGTTCTCTGATTGCTTTATTGGAAGATTGATATATCAG 1405  
 QY 377 LysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPhe 396  
 Db 1406 AAAGGCATTGATCTCATTTCACTTATACAGATCTCATCGGGAAGATGTTCAATTT 1465

QY 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416  
Db 1466 GTCATGCTTGGATCTGGTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATC 1525  
QY 417 PheLysAspLysPheArgGlyTropValGlyPheSerValProValSerHisArgIleThr 436  
Db 1526 TTCAGAGTAATTTCTGGATGGTTGGATTAGTTTCCAGTTTCCACCCGAATAACT 1585  
QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456  
Db 1586 GCCGGCTCGCATATATTGTTAATGTCATCCAGATTCGAACCTTGTGGTCTCAATCAGCTA 1645  
QY 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
Db 1646 TAGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1705  
QY 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTropAlaPheAla 496  
Db 1706 GTGGAGNACTTCAACCTTTGGTGAGATGGAGAGCGAGGTACAGGGTGGGCAATTGCA 1765  
QY 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
Db 1766 CCCTTAACACACAGAAACATGTT-GTGGACATTGGCAACTGCAATATCTACATACAGGA 1824  
QY 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536  
Db 1825 ACAAGTCTCTCTGGAGAGGCTAATGAAGCGAGGCGATGTCAAAAGACTTCAAGTGGGA 1884  
QY 537 ProCysArg 539  
Db 1885 CCATGCCG 1893  
RESULT 8  
AAV66832  
ID AAV66832 standard; DNA; 2990 BP.  
XX  
AC AAV66832;  
XX  
DT 05-JAN-1999 (first entry)  
XX  
DE Zea mays soluble starch synthase gene SSS1052 and SSS64.  
XX  
XX Zea mays; US yellow-dent corn line; maize; soluble starch synthase; SSS;  
KW glycogen biosynthetic pathway; branching enzyme; ss.  
XX  
XX Zea mays.  
XX  
XX US5824790-A.  
XX  
XX 20-OCT-1998.  
XX  
XX 15-DEC-1995; 95US-00572951.  
XX  
XX 21-JUN-1994; 94US-00263921.  
XX  
XX 29-NOV-1994; 94US-00346602.  
XX  
XX (ZENE ) ZENECA LTD.  
XX  
XX Guan H, Keeling PL, Knight ME;  
XX  
XX WPI; 1998-582626/49.  
XX  
XX Isolated nucleic acid molecule, used to produce transgenic plants -  
PT comprises nucleotide sequence encoding polypeptide having soluble starch  
PT synthase activity, where polypeptide is encoded by maize gene.  
XX  
XX Claim 1; Col 25-28; 29pp; English.  
XX  
XX The present sequence represents an isolated nucleic acid molecule which  
CC has been isolated and comprises a nucleotide sequence encoding a  
CC polypeptide having soluble starch synthase (SSS) activity, where the  
CC polypeptide is encoded by a maize gene. The isolated nucleic acid  
CC molecule can be used to produce transgenic plants with altered starch

CC production. The transgenic plants produced using the nucleic acid  
CC molecule have an enhanced ability to produce structurally-altered starch  
XX  
SQ Sequence 2990 BP; 758 A; 655 C; 801 G; 776 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1.51e-281 Length: 2990  
Score: 2757.00 Matches: 523  
Percent Similarity: 90.9% Conservative: 8  
Best Local Similarity: 89.6% Mismatches: 8  
Query Match: 95.3% Indels: 45  
DB: 2 Gaps: 1  
US-10-628-525A-21 (1-539) x AAV66832 (1-2990)  
QY 1 CysValAlaGluLeuSerArgGlu-----8  
Db 718 TGGTTCGGAGCTGAGCAGGGAGGGGGCCGCCGCCGCCGCTGCGACCCCGCTGCGACCCCGCTGCTG 777  
QY 8 -----8  
Db 778 GCGCCCCCGCTCGTGGCCCGCTTCTCGCGCCGCCGCCGCCGCGCGCTGAGCGCCGCA 837  
QY 9 -----AspLeuGlyLeuGluProGluGly 16  
Db 838 TCGACGCCGCCGCCCGCTGGCCGCGCGCTGGGGGACCTCGGTCTCGAACCTGAAGGG 897  
QY 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36  
Db 898 ATTGCTGAAGGTTCCATCATCAACAGTAGTTGTGGCAAGTGAGCAAGATTCTGAGATT 957  
QY 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
Db 958 GTGGTTGGAAGGAGGAGCAAGCTCGAGCTAAGTAACACAAAGCATTTCTTTGTAAACCGC 1017  
QY 57 GluAlaSerPro-TyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVa 76  
Db 1018 GAAGCTTCTCTTAATCGAAAGTCTGGGGTCTAGGAGATGTTTGTGTTCATTGCGAGT 1077  
QY 76 LalAlaLeuAlaArgGlyHisArgValMetValMetProArgTyrLeuAsnGlyTh 96  
Db 1078 TGTCTCTGTCTGCGCGGTACCGTGTGATGTTGTAATGCCAGACATTTAAATGGTAC 1137  
QY 96 rSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPh 116  
Db 1138 CTCGGATAGAATTATGCAATGCAATTTACTCAGAAACAAACATTCGGATTCATTCTT 1197  
QY 116 eGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPh 136  
Db 1198 TGGCGGTGAACATGAAGTTACCTTCTTCATGATATAGAGATTTCAGTTGACTGGGTGTT 1257  
QY 136 eValAspHisProSerTyrHisArgProGlyValAsnLeuTyrGlyAspLysPheGlyAlaPh 156  
Db 1258 TGTGTGATCATCCTCATATACAGACCTCGAAATTTATATAGAGATAAGTTGCTGCTTT 1317  
QY 156 eGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuI 176  
Db 1318 TGGTGATAATCAGTTCAGATACACACTCCTTTGCTATGCTGCAATGTGAGGCTCCTTTGGT 1377  
QY 176 eLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHi 196  
Db 1378 CCTTGAATGGGAGGATATATTATGACAGAAATTCATGTTGTTGTTGTTCAATGATTGGCA 1437  
QY 196 eAlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAs 216  
Db 1438 TGGCAGTCTAGAGCCAGTCTCTTCTGTCGCAAAATATAGACCATATATGTTGTTTATAGA 1497  
QY 216 pSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerTh 236  
Db 1498 CTCGCCGACATCTCTGTATATACATAATTTAGACATCAGGGGTAGAGCCTGCAAGCAC 1557  
QY 236 rTyrProAspLeuGlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGl 256  
|||||

Db 1558 ATATCTCGACCTTGGGTGCCACCTGAATGGTATGGAGCTCTGGAGTGGGTATTCCTCTGA 1617  
Qy 256 uTrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVala 276  
Db 1618 ATGGCGAGGAGCATGCCCTTGACAAAGGCTGAGGCAGTAAATTTTGTGAAGGTGCAGT 1677  
Qy 276 lValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAl 296  
Db 1678 TGTGACAGCAGATCGAATCGTACTGTCTAGTAAGGGTTATTCATGGAGGTCACAACTGC 1737  
Qy 296 adluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyI 316  
Db 1738 TGAAGGTGCACAGGGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACGGAT 1797  
Qy 316 eValaenGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHi 336  
Db 1798 TGTAAATGGAAATTGACATTAATGATTGGAACCTTGCCACAGACAAATGATCCCTGTCA 1857  
Qy 336 sTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLe 356  
Db 1858 TTATTCGTGTGATGACCTCTCTTGAAGGCTAAATGTAAGGTGCATTCAGAGGAGCT 1917  
Qy 356 uGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGl 376  
Db 1918 GGGTTTACCTATAAGGCTGATGTTCTCTGATTGGCTTTATTGGAAGATTGGATTATCA 1977  
Qy 376 nLysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPh 396  
Db 1978 GAAAGCATGTGATCAATTCATCTATCATACAGATCTCATGCGGAAGAAATGTTCAAT 2037  
Qy 396 eValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerI 416  
Db 2038 TGTCTATGCTTGATCTGCTGGTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGATCGAT 2097  
Qy 416 ePheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleTh 436  
Db 2098 CTTCAAGGATAAAATTTCTGTGGATGGGTTCGATTAGTTTCCAGTTTCCACCGCAATAC 2157  
Qy 436 rAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLe 456  
Db 2158 TCGCGGTGGGATATATTGTTAATGCCATCCAGATTCGAACCTTGTTGGTCTCAATCAGCT 2217  
Qy 456 uTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspTh 476  
Db 2218 ATATGCTATGATGATGGCACAGTCTCTGTTGTCATGCAACTGGGGGCTTAGAGATAC 2277  
Qy 476 rValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAl 496  
Db 2278 CGTGGAGAACTTCAACCCCTTTCGGTGAGAAATGGAGAGCAGGGTACAGGGTGGGCATTCGC 2337  
Qy 496 aProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGl 516  
Db 2338 ACCCTTAACCAAGAAACATGTTTGTGGACATTCGGAATGCAATATCTCATACAGGG 2397  
Qy 516 YThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGl 536  
Db 2398 AACACAGTAATAATGGAGAGGCTAATGAAGCCAGGCATGTCAAAAGAGTTCACGTGGG 2457  
Qy 536 YProCysArg 539  
Db 2458 ACCATGCCGC 2467

RESULT 9  
AAT67285  
ID AAT67285 standard; cDNA; 2992 BP.  
XX  
AC  
XX  
XX  
DT 17-OCT-2003 (revised)  
DT 11-SEP-1997 (first entry)  
XX  
DE Soluble starch synthase cDNA clone SSS10.52.  
XX

KW Soluble starch synthase; SSS10.52; transgenic plant; cereal; maize; ss.  
XX  
OS Zea mays; inbred line W64A.  
XX  
FN WO9720936-A1.  
XX  
PD 12-JUN-1997.  
XX  
PF 04-DEC-1996; 96WO-CB002990.  
XX  
PR 06-DEC-1995; 95GB-00024938.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Keeling PL, Knight ME;  
XX  
XX WPI; 1997-319782/29.  
XX  
XX cDNA encoding soluble starch synthase - used to produce transgenic plants  
PT with increased capacity for producing and storing starch.  
XX  
XX Claim 5; Page 17-20; 44pp; English.  
XX  
XX cDNA clones SSS10.52, SSS6.31 and SSS56 (AAT67285-87) code for maize  
CC soluble starch synthase (SSS). They were isolated from a maize inbred  
CC line W64A library by screening with a probe (AAT67288) based on pea SSS,  
CC rice SSS and maize GSSS. The cDNAs can be used to produce plants with an  
CC increased capacity for producing starch, or a capacity to produce starch  
CC with an altered fine structure. They can also be used to isolate the  
CC corresponding genomic sequences from crop plants, to determine the  
CC contribution of the SSS gene to the net regulation of starch  
CC biosynthesis, and to modify the levels of starch produced by the plant.  
CC Transgenic plants (esp. maize) can be used to produce hybrid plants which  
CC have higher rates of starch synthesis at temperatures above the normal  
CC optimum. (Updated on 17-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 2992 BP; 758 A; 655 C; 801 G; 776 T; 0 U; 2 Other;  
Alignment Scores:  
Pred. No.: 1.51e-281 Length: 2992  
Score: 2757.00 Matches: 523  
Percent Similarity: 90.9% Conservative: 8  
Best Local Similarity: 89.6% Mismatches: 8  
Query Match: 95.3% Indels: 45  
DB: 2 Gaps: 1  
US-10-628-525A-21 (1-539) x AAT67285 (1-2992)  
Qy 1 CysValAlaGluLeuSerArgGlu-----8  
Db 719 TCGTTCGGAGCTGAGCAGGAGGGGGCGCGCGCGCGCGCGCGCGCGCGCTGCCACCGCGCTGCTG 778  
Qy 8 -----8  
Db 779 GCGCCCCGCTCGTCCCGGCTTCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 838  
Qy 9 -----AspLeuGlyLeuCluProGluGly 16  
Db 839 TCGACGCGCGCGCGCTGCCCCGACGCGCGCTCGGGGACCTCGGTCTCGAACTCGAAGGG 898  
Qy 17 lIleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36  
Db 899 ATTGCTGAAGTTCCATCGATTAACACAGTAGTTGTGGCAAGTAGCAGCAGATTTCTGAGATT 958  
Qy 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
Db 959 GTGGTTGGAAGGAGCAAGCTCAGCTAAAGTAAACACAAAGCATTTCTTTCTTAACCGGC 1018  
Qy 57 GluAlaSerPro-TyrAlaLysSerGlyLeuGlyAspValCysGlySerLeuProVa 76  
Db 1019 GAAGCTTCTCCCTTAATCGAAAGTCTAGGGGCTCTAGAGATGTTTGTGGTTCATTGCCAGT 1078  
Qy 76 lAlaLeuAlaAlaArgGlyHisArgValMetValMetProArgTyrLeuAsnGlyTh 96



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1079 TGCTCTTGTCTGCTGCGGTACCGTGTGATGTTGTAATGCCAGACATTTAAATGGTAC 1138
Qy rSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIlePProCysP 116
1139 CTCGATAAGAAATATGCAAAATGCAATTTACTCAGAAAAACACATTCGGATTCATCTT 1198
Qy eGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPh 136
1199 TGGCGGTGAACATGAAGTCTACCTTCTCCATGATGATAGAGATTCACTGACTGGGTGTT 1258
Qy eValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPh 156
1259 TGTGATCATCCCTCATATACAGACCTGGAAATTTATATGGAGATAAGTTTGGTCTTT 1318
Qy eGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuII 176
1319 TGGTGATAATCAGTTTCAGATACACACTCCTTTGCTATGCTGCTGATGGAGCTCTTTGGT 1378
Qy eLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrP 196
1379 CCTTGAATGGGAGGATATATTTATGACAGAAATTCATGTTGTTGCTCAATGATGGCA 1438
Qy sAlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAs 216
1439 TGCAGTCTAGACCGAGTCTCTTCTGCTGCAAAATATAGACCATATGTTGTTGTTATAAGA 1498
Qy pSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerTh 236
1499 CTCCCGCAGCATCTTGTATATACATAATTTAGCACATCAGGGGTGTAGAGCTCGAAGCAC 1558
Qy rTyrProAspLeuGlyLeuProGluTyrPProGlyAlaLeuGluTyrPValPheProGl 256
1559 ATATCTCGACTTGGGTGGTCCACTGAAATGTTATGGAGCTCTGGAGTGGGTATTCCTGA 1618
Qy uTPrAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVa 276
1619 ATGGGCGAGGAGCGATGCCCTTGACAGGGGTGAGGCAGTTAATTTTGAAGGTGAGT 1678
Qy lValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrGluValThrAl 296
1679 TGTGACAGCAGATCGAATCGTGTGATGTCAGTAAGGTTTATTCATGGAGGTCACACTGC 1738
Qy aGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyI 316
1739 TGAAGGTGACAGGGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACGGAAT 1798
Qy eValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHi 336
1799 TGTAAATGGAATTGACATTAATGATTGGAAACCTGCCACAGACAAATGATATCCCTGTCA 1858
Qy sTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyValAlaLeuGlnLysGluLe 356
1859 TTATTCGTGTGATGACTCTCTTGAAGGCTAAATGTAAAGGTGCATTCGAGAGAGGCT 1918
Qy uGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGl 376
1919 GGGTTTACCTATAAGGCTGATGTTCTCTGATTGGCTTTATTTGGAAGATTGGATTATCA 1978
Qy nLysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPh 396
1979 GAAAGCATGTGATCTCATTCACCTTATCATACAGATCTCATCGGAAAGAAATGTTCAAT 2038
Qy eValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerI 416
2039 TGTGATGCTTGGATCTGGTGACCCAGAGCTTGAGATTGGATGAGATCTACAGAGTCGAT 2098
Qy ePheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleTh 436
2099 CTTCAAGGATAAATTTCTGGATGGGTGGATTAGTGTTCAGTTTCCACCGCAATAAC 2158
Qy rAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLe 456

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Db 2159 TGGCGGTGGCGATATATTTGTAATGCCATCCAGATTCGAACCTTGTGGTCTCAATCAGCT 2218
Qy uTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspTh 476
Db 2219 ATATGCTATGCAGTATGGCACAGTCTCTGTTGTCATGCAACTGGGGGCCCTTAGGATAC 2278
Qy rValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAl 496
Db 2279 CGTGGAGAACTTCAACCCCTTTCGGTGAGAAATGGAGAGCAGGGTACAGGGTGGGCATTTCGC 2338
Qy aProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGl 516
Db 2339 ACCCTTAACACAGAAACATGTTGTGGACATTTGGCACTTGGCAATATCTACATACAGGG 2398
Qy yThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGl 536
Db 2399 AACACAGTAATTAATGGGAAGGCTAATGAGGAGGCTATGAGGAGGCTTCAAGAGTTTACGTTGGG 2458
Qy yProCysArg 539
Db 2459 ACCATGCCGC 2468

RESULT 10
AAZ50637/c
ID AAZ50637 standard; cDNA; 1528 BP.
XX
AC AAZ50637;
XX
DT 23-MAY-2000 (first entry)
XX
DE Corn soluble starch synthase gene fragment inserted in pSS42.
XX
KW Soluble starch synthase; starch fine structure; corn; transgenic plant;
KW amylose; amylopectin; amylose polymerisation;
KW non-granule bound starch synthase; non-GBSSI; altered starch; food;
KW paper; plastic; adhesive; ss.
XX
OS Zea mays.
XX
PN WO200006755-A2.
XX
PD 10-FEB-2000.
XX
PF 26-JUL-1999; 99WO-US016296.
XX
PR 28-JUL-1998; 98US-0094436P.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Broglie KE, Lightner JE;
XX
PS WPI; 2000-195311/17.
XX
DR Producing transgenic cereal crops with altered starch structure useful
XX for preparing foodstuff, paper, plastic or adhesives, comprises
XX transforming crops with chimeric sense or antisense gene construct
XX encoding starch synthase.
XX
PS Claim 5; Page 51-52; 56pp; English.
XX
CC The present sequence is the corn soluble starch synthase (SSI) DNA
CC sequence inserted into plasmid pSS42. Chimeric gene of pSS42 was cloned
CC into the vector pKS17 for the generation of an antisense construct for
CC suppression of SSI expression in corn. The starch fine structure derived
CC from a grain of the cereal crop can be altered in the transformed cereal
CC crop by changes in amylose to amylopectin ratio, amylopectin fine
CC structure, increased abundance of very short amylopectin chains and in
CC the degree of polymerisation of amylose. These modifications can be
CC created by controlling the expression of non-GBSSI (non-granule bound
CC starch synthase) in transgenic plants. Altered starches are useful in
CC foods, paper, plastics or adhesives
XX
SQ Sequence 1528 BP; 440 A; 383 C; 300 G; 405 T; 0 U; 0 Other;

```

Alignment Scores:			
Pred. No.:	3.76e-271	Length:	1528
Score:	2655.00	Matches:	495
Percent Similarity:	99.8%	Conservative:	0
Best Local Similarity:	99.8%	Mismatches:	1
Query Match:	91.8%	Indels:	1
DB:	3	Gaps:	0
US-10-628-525A-21 (1-539) x AAZ50637 (1-1528)			
QY	44	AtqAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAlaLys	63
Db	1527	CGAGCTAAAGTAACACAAAGCATTTGCTTTGPAACGGCGAAGCTCTCTCTATGCAAG	1468
QY	64	SerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHis	83
Db	1467	TCTGGGGGTCTAGGAGATGTTTGTGGTTCATTTGCCAGTTGCTCTTGTCTGCTGGTGCAC	1408
QY	84	ArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsn	103
Db	1407	CTGTGATGGTTGTAATGCCCGAGATATTAAATGGTACTCTCCGATAGAAGATTATGCAAA	1348
QY	104	AlaPheTyrThrGlnLysHisIleArgIleProCysPheGlyGlyGluHisGluValThr	123
Db	1347	GCATTTTACACAGAAAAACACATTCGATTCCATGCTTTGGCGGTGAACATGAAGTTACC	1288
QY	124	PhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSerTyrHis	143
Db	1287	TTCTTCCATGAGTATAGATATTCAGTTGACTGGGTGTTTGTGATCATCCCTCATATCAC	1228
QY	144	ArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyr	163
Db	1227	AGACCTGGAATTTATATGAGATAGTTTGTGCTTTTGGTGAATAATCAGTTTCAGATAC	1168
QY	164	ThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIle	183
Db	1167	ACACTCTTTGCTATGCTGCATGTGAGGCTCTCTTTGATCCTTGAATTTGGAGGATATATT	1108
QY	184	TyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeu	203
Db	1107	TATGGACAGAAATGCAATGTTGTGTCAATGATGGCATGCCAGTCTAGTGGCAGTCTTT	1048
QY	204	LeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIle	223
Db	1047	CTTGCTGCAAAATATAGACCATATGTTGTTTATAAGACTCCCGCAGCAATCTTGTAAATA	988
QY	224	HisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuPro	243
Db	987	CATAATTTAGCACATCAGGGGTGAGAGCTGCAAGCACATATCCTGACCTTGGGTGGCA	928
QY	244	ProGluTyrTyrGlyAlaLeuGlnTrpValPheProGluTyrAlaArgHisAlaLeu	263
Db	927	CCTGAATGTTATGGAGCTCTGGAGTGGGTATTCCTCGAATGGCGGAGGAGCATGCCCTT	868
QY	264	AspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleVal	283
Db	867	GACAGGGTGAGCGAGTTAAATTTTGAAGGTGCAGTTGTGACAGCAGATCGAATCGTG	808
QY	284	ThrValSerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsn	303
Db	807	ACTGTCTAGTAAGGTTATTTCGTGGGAGGTCAACAATGCTGTAAGGTGGACAGGCGCTCAAT	748
QY	304	GluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsn	323
Db	747	GAGCTCTTAAGCTCCAGAAAGATGTTATTAACCGGAATTTGTAATGGAATTCACATTAAT	688
QY	324	AspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSer	343
Db	687	GAATGGAACTTCCACACAGCAAAATGATTCCTCTGTCATATTTCTGTTGATGACCTCTCT	628
QY	344	GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp	363

(CAOY/) CAO Y.

XX PA  
XX PI Liu J, Zhou Y, Kovalic DK, Screen SG, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
XX  
XX New recombinant DNA construct, useful for improving plant tolerance to  
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
XX pests, for conferring increased resistance to plant disease, or for  
XX improving yield.  
XX  
XX Claim 1; SEQ ID NO 19497; 15pp; English.  
XX  
XX The invention describes a recombinant DNA construct comprising a  
XX polynucleotide consisting of a sequence encoding an amino acid sequence  
XX available in electronic form from the US patent office at  
XX ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
XX of the invention are also useful in physical arrays of molecules and as  
XX plant breeding markers. The recombinant DNA construct is useful for  
XX improving plant tolerance to cold, heat, drought, herbicides, extreme  
XX osmotic conditions, pathogens or pests, for manipulating growth rate in  
XX plant cells by modification of the cell cycle pathway, for conferring  
XX increased resistance to plant disease, for producing galactomannan,  
XX lignin or plant growth regulators, for increasing the rate of homologous  
XX recombination in plants, for improving yield by modification of  
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
XX or by providing improved plant growth and development under at least one  
XX stress condition or for modifying seed oil or protein yield and/or  
XX content. This sequence represents a plant full length insert  
XX polynucleotide that can be used in the recombinant DNA construct of the  
XX invention.  
XX  
XX SQ Sequence 1855 BP; 492 A; 371 C; 461 G; 531 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1-29e-258	Length:	1855
Score:	2538.00	Matches:	471
Percent Similarity:	99.8%	Conservative:	0
Best Local Similarity:	99.8%	Mismatches:	1
Query Match:	87.7%	Indels:	1
DB:	13	Gaps:	0

US-10-628-525A-21 (1-539) x ADX36677 (1-1855)

QY 68 GlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetVal 87  
DB 1 GGAGATGTTTGTGTTCAATGGCCAGTTGCTTCTGCTCGTGTCCACCGTGTGATGTT 60  
QY 88 ValMetProArgTyrLeuAsnGlyThrSerAspHisAsnTyrAlaAsnAlaPheTyrThr 107  
DB 61 GTAAATGCCAGATATTTAAATGGTGTACCTCCGATAAGAAATATGCAATGCAATTTTACACA 120  
QY 108 GluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlu 127  
DB 121 GAAACACACATTCCGATTCATGCTTTGGCGGTGACATGAGTTACCTTCTCCATGAG 180  
QY 128 TyrArgAspSerValAspTyrValPheValAspHisProSerTyrHisArgProGlyAsn 147  
DB 181 TATAGAGATTCACTGAGTGGGTGTTTGTGATCATCCCTCATATCACACACCTGGAAAT 240  
QY 148 LeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCys 167  
DB 241 TTATATGGAGATAGTTTGTGCTTTTGGTGATAAATCAGTTTCAGATACACACTCTTTC 300  
QY 168 TyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsn 187  
DB 301 TATGCTGCATGTGAGGCTCTTTGATCCTTGAATGGAGATATATTTATGACAGAAAT 360  
QY 188 CysMetPheValValAsnAspTyrHisAlaSerLeuValProValLeuLeuAlaAlaLys 207  
DB 361 TGCATGTTTGTGTAATGATGGCATGCCAGTCTAGTCCAGTCTCTTCTTGTGCAAAA 420  
QY 208 TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla 227

Db 421 TATAGACCATATGCTGTTTATAAAGACTCCCGCAGCATTCCTGTATAACATAATTTAGCA 480  
QY 228 HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProProGluTyrTyr 247  
DB 481 CATCAGGCTGTAGAGCCTGCAAGCACATATCTGACCTTGGGTTGCCACCTGAAATGGTAT 540  
QY 248 GlyAlaLeuGluTyrValPheProGluTyrAlaArgHisAlaLeuAspLysGlyGlu 267  
DB 541 GGAGCTCTGGAGTGGGTATTCCTGTAATGGCGAGGAGGCATGCCCTTGACAGGGTGAG 600  
QY 268 AlaValAsnPheLeuLysGlyAlaValThrAlaAspArgIleValThrValSerLys 287  
DB 601 GCAGTTAAATTTTGAAGGTGCAGTTGTGACAGCAGATCGAATCGTACTGTTCAGTAAG 660  
QY 288 GlyTyrSerTyrGluValThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSer 307  
DB 661 GGTATTTCTGGGAGGTCAACATGCTGTAAGGTGGACAGGGCCTCAATGAGCTCTTAAGC 720  
QY 308 SerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTyrAsnPro 327  
DB 721 TCCAGAAAGAGTGTATTAACCGGAATTTGTAATGGAATTCACATTAATGATTGGAACCT 780  
QY 328 AlaThrAspLysCysIleProCysHisTyrSerValAspLeuSerGlyLysAlaLys 347  
DB 781 GCCACAGACAAATGTATCCCTGTCTCATTTCTGTGATGACCTCTCTGGAAAGGCCAAA 840  
QY 348 CysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIle 367  
DB 841 TGTAAAGTGCATTCGCAAGAGGAGTGGGTTTACCTATAAGGCTGTATGTTCTCTGATT 900  
QY 368 GlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIlePro 387  
DB 901 GGCTTTATTCGAAAGTGTGATTTATCAGAAAGCATTTGATCTCTCACTTATCATACCA 960  
QY 388 AspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGlu 407  
DB 961 GATCTCATGCGGGAAGATGTTCAATTTGTCTGCTGATCTGCTGACCCAGAGCTTGAA 1020  
QY 408 AspTyrMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPhe 427  
DB 1021 GATTGGATGAGATCTCAGAGTGCATCTTCAAGGATAAATTTCTGTGATGGTGGATTT 1080  
QY 428 SerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArg 447  
DB 1081 AGTGTTCAGTTTCCACCGAATAACTGCCGCTGCGATATATTTGTAATGCCATCCAGA 1140  
QY 448 PheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValVal 467  
DB 1141 TTCGAACCTTGTGGTCTCAATCAGCTATATGCTATGCAAGTATGTCACAGTTCTCTGTGTC 1200  
QY 468 HisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGly 487  
DB 1201 CATGCAACTGGGGGCTTTAGAGATACCGTGAGAACTTCAACCTTTCCGTGAGAAATGGA 1260  
QY 488 GluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPheValAspIle 507  
DB 1261 GAGCAGGTTACAGGGTGGGCAATTCGCACCCCTTAACCCACAGAAACATGTTTGTGGACATT 1319  
QY 508 AlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAla 527  
DB 1320 GCGAACTGCAATATCTACATACAGGGAACACAAAGTCTCTCTCGGAAGGGCTAATGAAGCG 1379  
QY 528 ArgHisValLysArgLeuHisValGlyProCysArg 539  
DB 1380 AGCATGTCAAAGACTTCACGTGGGACCATGCGCG 1415

RESULT 12  
ADQ37148  
ID ADQ37148 standard; DNA; 1881 BP.  
XX  
AC ADQ37148;  
XX

DT 07-OCT-2004 (first entry)

XX Cell proliferation-related nucleic acid sequence #154.

DE cell proliferation related polypeptide; cell proliferation; senescence;

XX differentiation; stress response; ds.

KW Oryza sativa.

OS WO2004061122-A2.

XX 22-JUL-2004.

XX 23-DEC-2003; 2003WO-US041200.

PF 26-DEC-2002; 2002US-043656P.

PR (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX Cooper B;

PI WPI; 2004-534388/51.

XX New nucleic acid molecule encoding a cell proliferation-related

PT polypeptide, useful for modulating cell proliferation, senescence,

PT differentiation, development, and stress response in plants, and for

PT producing enhanced food crops.

XX Claim 57; SEQ ID NO 307; 408pp; English.

XX The present invention relates to an isolated nucleic acid molecule

CC encoding a cell proliferation-related polypeptide. The nucleic acid

CC molecule and the encoded polypeptide, and methods are useful for

CC modulating cell proliferation, senescence, differentiation, development,

CC and stress response in plants, and for producing enhanced food crops. The

CC present sequence represents a cell proliferation-related nucleic acid

CC sequence. The present sequence is published separately from the main body

CC of the specification as EPO data.

XX SQ Sequence 1881 BP; 454 A; 398 C; 548 G; 481 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,79e-257	Length:	1881
Score:	2525.50	Matches:	475
Percent Similarity:	85.8%	Conservative:	31
Best Local Similarity:	80.5%	Mismatches:	33
Query Match:	87.3%	Indels:	51
DB:	12	Gaps:	3

US-10-628-525A-21 (1-539) x ADQ37148 (1-1881)

QY 1 CysValAlaGluLeuSerArgGlu----- 8

DB 100 TCGGTGGCGGAGCTGAGCAGGACGGTGGGTGGCGGACGCCCGCTGGCACCGCGCGC 159

QY 8 ----- 8

DB 160 CTGGTGAACGACCGGTCTGCCGACCTTCCTCGTGGCGGACGCTGACGCCACCGCGGCC 219

QY 9 -----AspLeuGly----- 11

DB 220 ACGCAGTCGCGCGCGCGCGGACCCCGCGCGCGGTTCGCGGACTCCGCGCTGGGGAG 279

QY 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAsnThrValValAla 29

DB 280 ATCGAGCCCGATCTAGAAGGTCTCAGAGAAGATTCACAGAAACAAATTTTGTGGCT 339

QY 30 SerGluGlnAspSerGluIleValValGlyLysGluGlnAlaArgAlaLysValThrGln 49

DB 340 AGTGACGAGATCTGAGATCAAGATGTGAAGAGCAAGCTCAAGCTAAAGTAACAGC 399

QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAsp 69

DB 400 AGCGTTGTCTTTGTAACCGGTGAAGCTTCTCTTATGCAAGTCAGGTGAGCTAGGAGAT 459

QY 70 ValCysGlySerLeuProValAlaLeuAlaAaArgGlyHisArgValMetValMet 89

DB 460 GTTGTGGTTCACCTGCCAATTCCTTGTCTTCGTGGTGCATCGTGTGATGGTGAATG 519

QY 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109

DB 520 CCAGATACATGACGGCCCTTGAACAAATTTTGCACGCAATTTTACACTGAGAAG 579

QY 110 HisIleArgIleProCysPheGlyGluHisGluValThrPhePheHisGluTyrArg 129

DB 580 CACATTAAGATTCCATGCTTTGGCGGAGAACATGAAGTTTACTTTTTTCCAGGATAGG 639

QY 130 AspSerValAspTyrPheValAspHisProSerTyrHisArgProGlyAsnLeuTyr 149

DB 640 GATTCGTGGATTGGGTGTTTGTTCATCATCTCATATCATAGACCTCGAAATTTGTAT 699

QY 150 GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla 169

DB 700 GGAGATAATTTTGGTGTCTTTGGCGATATCATGTTCCAGATACACACTCTCTGTCTATGCG 759

QY 170 AlaCysGluAlaProLeuIleLeuGlyGlyTyrIleTyrGlyGlnAsnCysMet 189

DB 760 GCGTGTGAAGCCCCCATTAATCTTGAACCTGGGAGGATATATCTATGGACAGAAATGCATG 819

QY 190 PheValValAsnAspTyrPheHisAlaSerLeuValProValLeuLeuAlaLysTyrArg 209

DB 820 TTTGTGTGAATGATTGGCATGCCAGTCTTGTGCCAGTCTTCTTGTCTCAAAATATAGA 879

QY 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGln 229

DB 880 CCATATGTGTGTACAGGAGCCCGCAGTGTCTTGTCTATACATATATCTAGACATCAG 939

QY 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAla 249

DB 940 GGTGTGGAGCTTCCAGTACATATCTGACCTGGGATGGCCACCTGAATGGTATGGAGCA 999

QY 250 LeuGluTyrPheProGluTyrPheAlaArgArgHisAlaLeuAspLysGlyGluAlaVal 269

DB 1000 TTAGAATGGGTGTTTCCAGAGTGGCAGGGCGCATGCCCTTGACAAAGGCTGAGGCAGTC 1059

QY 270 AsnPheLeuLysGlyAlaValThrAlaAspArgIleValThrValSerLysGlyTyr 289

DB 1060 AATTTTTTAAAGGCGCAGTGTGTGACAGCATCAATTTGTGACTGTGACGACAGGGTAT 1119

QY 290 SerTyrGluValThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArg 309

DB 1120 TCATGGGAGGTCACAACTGCTGAAGGTGGGCAAGGCCTCAATGAGCTCTTAAGCTCCCGG 1179

QY 310 LysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTyrAsnProAlaThr 329

DB 1180 AAGAGTGTATTGAATGGAAATTTGTAATGGAATTGACATTAATGATGGAAACCCATCCACA 1239

QY 330 AspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLys 349

DB 1240 GACAAATTTCTCCCTATCATTTATCTGTTGATGACCTGTCCGGAAGGCCAAGGTGATA 1299

QY 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe 369

DB 1300 GCTGAATTCAGAAAGGAGCTGGGTTTACTATAAGGCCCGCATGTGCTCTGATTGGCTTT 1359

QY 370 IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeu 389

DB 1360 ATTGGAAGATTGGACTATCAAAAGCGATTGATCTAATAAACTTGGCAATTCAGATCTC 1419

QY 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyr 409

DB 1420 ATGCGGGACATATTAATTCATGCTGATGTTGATCTGTTGACCCAGGTCTTGAAGATCG 1479

QY 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPheSerVal 429

DB 1480 ATGAGATCCACAGAAATCAGGGTACAGGGATAAATTTTCGTGGATGGGTTGGATTTAGTGT 1539

QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuMetProSerArgPheGlu 449  
Db |||||  
1540 CCAGTTTCCACCGAATAACTGCAGGTTGCGATATATTGTTGATGCCATCCAGATTGGAA 1599  
QY 450 ProCysGlyLeuAenGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469  
Db |||||  
1600 CCTGTGGCTCAATCAGCTATATGCTATGCAATATGCTACAGTGCTGTGTTTCATGGA 1659  
QY 470 ThrGlyGlyLeuArgAspThrValGluAenPheAenProPheGlyGluAenGlyGluGln 489  
Db |||||  
1660 ACTGGAGGCTCAGAGATACAGTGCAGAAATTTTAAACCGTTTGTCTGAGAAAGGAGACAG 1719  
QY 490 GlyThrGlyTyrAlaPheAlaProLeuThrThrGluAenMetPheValAspIleAlaAen 509  
Db |||||  
1720 GGTACAGGGTGGGCAATCTCGCCACTAACCATTTGAAAAAAATGCTGTGGGCATTTGCCGAT 1779  
QY 510 CysAenIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAenGluAlaAenHis 529  
Db |||||  
1780 GGCATTTCCACATACAGGGAACAAGTCTCTTGGGAGGGTCTAATGAAGCGAGGCAT 1839  
QY 530 ValIysArgLeuHisValGlyProCysArg 539  
Db |||||  
1840 GTCAAGCGACTTACATGGGACCATGCGC 1869

## RESULT 13

ADQ15732

ID ADQ15732 standard; DNA; 1881 BP.

XX AC ADQ15732;

XX XX

DT 07-OCT-2004 (first entry)

XX XX

DE Rice stress-related protein coding sequence #71.

XX KW

KW rice; stress-related protein; plant maturation; plant development;

KW KW

KW plant proliferation; plant senescence; plant disease-resistance;

KW KW

KW plant stress response; transgenic plant; pest tolerance;

KW KW

KW herbicide tolerance; biotic stress tolerance; abiotic stress tolerance;

KW KW

KW improved nutritional value; increased yield; increased proliferation;

KW KW

OS gene; ds.

XX XX

OS Oryza sativa.

XX XX

XX WO2004061080-A2.

PN XX

XX 22-JUL-2004.

XX XX

XX 23-DEC-2003; 2003WO-US041098.

XX XX

XX 26-DEC-2002; 2002US-0436564P.

PR XX

XX (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX XX

XX Cooper B;

XX XX

XX WPI; 2004-S34374/51.

DR XX

XX P-PSDB; ADQ15733.

XX XX

XX New isolated nucleic acids and proteins, useful for producing transgenic

PT PT

PT plants having improved properties, e.g. tolerance to pests, herbicides,

PT PT

PT or biotic or abiotic stresses, improved nutritional value, or increased

PT PT

PT yield or proliferation.

XX XX

XX Claim 45; SEQ ID NO 141; 551pp; English.

PS XX

XX The invention comprises the amino acid and coding sequences of rice

CC CC

CC or proliferation, or improved structure causing less loss from lodging or  
CC shattering. The present DNA sequence encodes a rice stress-related  
CC protein of the invention.

XX Sequence 1881 BP; 454 A; 398 C; 548 G; 481 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 2,79e-257 Length: 1881  
Score: 2525.50 Matches: 475  
Percent Similarity: 85.8% Conservative: 31  
Best Local Similarity: 80.5% Mismatches: 33  
Query Match: 87.3% Indels: 51  
DB: 12 Gaps: 3

US-10-628-525A-21 (1-539) x ADQ15732 (1-1881)

QY 1 CysValAlaGluLeuSerArgGlu-----8

Db |||||

100 TCGTGGCGGAGCTGACAGGAGCGTGGTGGCGCAGCGCCGCTGGCACCGCGCCG 159

QY 8 -----8

Db 160 CTGGTGAAGCAGCGGCTCTGCGCAGCCTTCTGTCGCGAGCTGCGACCCGCGCC 219

QY 9 -----AspLeuGly-----11

Db 220 ACGCAGTGGCGCGCGCGCGCGACCCCGCGCGCTGTCGCGAGCTCCGGCGGGGAG 279

QY 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAenThrValValAla 29

Db |||||

280 ATCGAGCCCGATCTAGAAGGTCTCACAGAAGATTCTCATCGACAAAACAATTTTGTGGCT 339

QY 30 SerGluGlnAspSerGluIleValValGlyLyseGluGlnAlaArgAlaLysValThrGln 49

Db |||||

340 AGTGACGAGGAGCTCAGATCATGGATGCAAGAGCAGCTCAAGCTAAGTAACACGC 399

QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69

Db |||||

400 AGCGTTGTCTTGTAAACCGGTGAAGCTTCTCTTATGCAAGTCAGGTGACCTAGGAGAT 459

QY 70 ValCysGlySerLeuProValAlaLeuAlaArgGlyHisArgValMetValMet 89

Db |||||

460 GTTGTGGTTCATGCGCAATTCCTTGTCTTCTGTCGTCATCTGTGTGTTGTAATG 519

QY 90 ProArgTyrLeuAenGlyThrSerAspLysAenTyrAlaAenAlaPheTyrThrGluLys 109

Db |||||

520 CCGAGATACATGACGGGCGCTTGAACAAAATTTTGCAACCATTTTACCTAGAGAG 579

QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129

Db |||||

580 CACATTAAGATTCATGCTTGGCGGAGAACATGAAGTTACTTTTTTTCACGAGTAGG 639

QY 130 AspSerValAspTyrValPheValAspHisProSerTyrHisArgProGlyAenLeuTyr 149

Db |||||

640 GATTCGTGTGATGGGTGTGTTGATCATCCCTCATATCATAGACTCTCTGCTATGCG 699

QY 150 GlyAspLysPheGlyAlaPheGlyAspAenGlnPheArgTyrThrLeuLeuCysTyrAla 169

Db |||||

700 GGAGATAATTTTGGTGTCTTTGGGATATCAGTTGATACACACTCTCTGCTATGCG 759

QY 170 AlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAenCysMet 189

Db |||||

760 GCGTGTGAAGCCCATTAATTTCTTGAACCTGGGAGGATATATCTATGACAGAAATGCATG 819

QY 190 PheValValAsnAspTyrPheIleAspLeuValProValLeuLeuAlaLysTyrArg 209

Db |||||

820 TTTGTTGTAATGATGGCATGCCAGTCTTGTGCCAGTCTCTTCTGCTCAAAATATAGA 879

QY 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAenLeuAlaHisGln 229

Db |||||

880 CCATATGGTGTACAGGATGCCCGCAGTGTCTTGTATACATATCTAGCACATCAG 939

QY 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAla 249

Db 940 GGTGTGGAGCTCCAGTACATATCTGACCTGGGATTCACCTGAATGGTATGGAGCA 999  
QY 250 LeuGluTrpValPheProGluTrpAlaArgHisAlaLeuAspLysGlyGluAlaVal 269  
Db 1000 TTAGAATGGGTGTTTCCAGAGTGGGCAAGCGGCATGCCCTTCACAAAGGTCGAGGCAGTC 1059  
QY 270 AsnPheLeuLysGlyAlaValThrAlaAspArgIleValThrValSerLysGlyTyr 289  
Db 1060 AATTTTTTAAAGCGCCAGTGTGTGACAGAGATCGAAATTTGTGACTGTCCAGCAGGGGTAT 1119  
QY 290 SerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArg 309  
Db 1120 TCATGGGAGGTCACAACTGCTGAGGTGGCAAGGCTCAATGAGCTCTTAAGCTCCCG 1179  
QY 310 LysSerValLeuAsnGlyIleValLeuGlyIleAspIleAsnAspTrpAsnProAlaThr 329  
Db 1180 AAGAGTGTATTGAATGGAATTTGAAATGGAATTTGACATTAATGATTTGGAACCCATCCACA 1239  
QY 330 AspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLys 349  
Db 1240 GACAGATTCTCCCTTATCATTTATCTGTGTGATGACCTGTCCGGAAGGCCAAGTGTAAA 1299  
QY 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe 369  
Db 1300 GCTGAATTCAGAGGAGCTGGGTTTACCTATAAGGCCCGATGCTGCTCTGATTCGCTTT 1359  
QY 370 IleGlyArgLeuAspTrpGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeu 389  
Db 1360 ATTGGAAGATTGGACTATCAAAAGGCATTTGATCTAAATTAATTAATTCGCAATTCAGATCTC 1419  
QY 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrp 409  
Db 1420 ATGCGGGAACAATTAATTCGTGCTGCTGTGATCTGTGACCGCCAGTTTGAAGATGG 1479  
QY 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerVal 429  
Db 1480 ATGAGATCCAGATNATCAGGTACAGGATTAATTTCTGTGGATGGTTGGATTTAGTGT 1539  
QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449  
Db 1540 CCAGTTTCCACCGAATAACTGCAGGTTCCGATATATTGTTGATGCCATCCAGATTCGAA 1599  
QY 450 ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469  
Db 1600 CTTGTGGCTCAATCAGCTATATGCTATGCAATATGTTACAGTGCCTGTTGTCATGGA 1659  
QY 470 ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln 489  
Db 1660 ACTGGAGGCTCAGAGATACAGTGGAGATTTTAACCGCTTGTCTGAGAAAGAGAGCAG 1719  
QY 490 GlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsn 509  
Db 1720 GGTACAGGTGGGCATTTCTCGCACTTAACCATTTGAAATAAATGCTGTGGGCATTCGGAT 1779  
QY 510 CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529  
Db 1780 GGCAATTCGACATACAGGGAACACAAATGCTCTTGGGGAGGTCTAATGAAGCAGGCAT 1839  
QY 530 ValLysArgLeuHisValGlyProCysArg 539  
Db 1840 GTCAGGCACTTACATGGGACCATGCCGC 1869

## RESULT 14

ID ADR04094  
XX ADR04094 standard; DNA; 1881 BP.  
XX AC ADR04094;  
XX DT 21-OCT-2004 (first entry)  
XX DE Rice starch synthase 3 coding sequence.  
XX

transgenic; plant; ds; gene; starch synthase 3; targeted expression;  
starch-containing tissue; feed; pathogen resistance; nutritional quality;  
SS3; rice.

Oryza sativa.

Key Location/Qualifiers  
CDS 1..1881  
/\*tag= a  
/product= "starch synthase 3"

WO2004065537-A2.  
05-AUG-2004.  
15-JAN-2004; 2004WO-EP000241.  
20-JAN-2003; 2003DE-01002324.  
(SUNG-) SUNGENE GNEH & CO KGAA.  
Heim U, Herbers K, Sonnewald U, Glickmann E;  
WPI; 2004-562151/54.  
P-PSDB; ADR04095.

Targeted transgenic expression in starch-containing plant tissue, useful  
e.g. for imparting pathogen resistance, comprises placing nucleic acid  
under the control of a promoter from a starch synthase 3 gene.

Claim 3; SEQ ID NO 9; 158pp; German.

The present invention relates to a method for the targeted transgenic  
expression of a nucleic acid in a starch-containing tissue of a plant,  
which comprises transforming plant cells and regenerating the cells to  
produce plants. The nucleic acid is contained on an expression cassette  
comprising at least one promoter of a gene encoding starch synthase 3  
(SS3) functionally linked to the nucleic acid. Transgenic organisms, or  
their products, that express the nucleic acid in their starch-containing  
tissues are useful for preparation of foods, animal feeds, seeds,  
pharmaceuticals and fine chemicals, e.g. enzymes, vitamins, amino acids,  
antibodies, tocopherols and carotenoids; also they may have improved  
resistance to pathogens and abiotic stress, improved nutritional quality,  
better germination and storage properties, and better growth rate or  
harvest yield. The present sequence is an SS3 coding sequence.

Sequence 1881 BP; 454 A; 398 C; 548 G; 481 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2,79e-257 Length: 1881  
Score: 2525.50 Matches: 475  
Percent Similarity: 85.8% Conservative: 31  
Best Local Similarity: 80.5% Mismatches: 33  
Query Match: 87.3% Indels: 51  
DB: 13 Gaps: 3

US-10-628-525A-21 (1-539) x ADR04094 (1-1881)

QY 1 CysValAlaGluLeuSerArgGlu----- 8  
Db 100 TCGTGGCGGAGCTGAGCAGGACGCTGGTGGTGGCGCAGCGCGCTGCGCGCG 159  
QY 8 ----- 8  
Db 160 CTGGTGAAGCAGCGCTCTGCGGACCTTCTCTGTCGACGTCGACGCCACCGCGGCC 219  
QY 9 -----AspLeuGly----- 11  
Db 220 AGCAGTCCCGCGCGCGCGCGCGCGCGCGCGCGCTGTCGCGGACTCCGCGCTGGGGAG 279  
QY 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAsnThrValValAla 29  
Db 280 ATCGAGCCGATCTAGAGGTTCTCAGAAAGATTCCATCGAAGAAATTTTGTGGCT 339



QY 30 SerGluGlnAspSerGluIleValValGlyLysGluGlnAlaAArgAlaLysValThrGln 49  
 DB 340 AGTGAAGAGGAGTCTGAGATCATGGATGTGAAGGAGCAAGCTCAAGCTAAAGTAACACGC 399  
 QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69  
 DB 400 AGCGTGTCTTGTAAACGGGTGAAGCTTCTCTTATGCAAGGTCAAGGTGGACTAGGAGAT 459  
 QY 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValValMet 89  
 DB 460 GTTAGTGGTTCACATGCAATGTCTCTTGTCTCTTGTGTCTCATCTGTGTGTGTGTATG 519  
 QY 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109  
 DB 520 CCGAGATACATGAACGGGGCTTGAACAAATAATTTTGCACCAACGATTTTACACTGAGAG 579  
 QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129  
 DB 580 CACATTAAGATTCCATGCTTGGCGGAGACATGAGTTACTTTTTTTCACGAGTATAGG 639  
 QY 130 AsnSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyr 149  
 DB 640 GATTCTGTGATTGGGTGTGTGTGATCATCCCTCATATCATAGACCTGGAAATTTGTAT 699  
 QY 150 GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla 169  
 DB 700 GAGAGATAAATTTTGGTGTCTTGGCGGATTAATCAGTTTCAGATACACACTCTCTGTGCTATGCG 759  
 QY 170 AlaCysGluAlaProLeuIleLeuGluGlyGlyTyrIleTyrGlyGlnAsnCysMet 189  
 DB 760 GCCTGTGAGACCCCATTAATCTTGAACCTGGAGGATATATCTATGGACAAATGCGATG 819  
 QY 190 PheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaLysTyrArg 209  
 DB 820 TTATGTTGTAATGATTGGCATGCCAGTCTTGTGCGAGTCTCTTGTGTCGCAAAATATAGA 879  
 QY 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGln 229  
 DB 880 CCATATGGTGTGTTACAGGGATGCCCGCAGTGTCTTGTGCATACATAATCTAGCACATCAG 939  
 QY 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAla 249  
 DB 940 GGTGTGAGGCTCCAGTACATATCTGTGACCTGGGATTCGCACTGAATGGTATGAGCA 999  
 QY 250 LeuGluTrpValPheProGluTrpAlaAArgArgHisAlaLeuAspLysGlyGluAlaVal 269  
 DB 1000 TTAGAATGGTGTGTTCCAGAGTGGCAAGGCGCATGCCCTTGACCAAGGCTGAGGCAGTC 1059  
 QY 270 AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr 289  
 DB 1060 AATTTTTTAAAGCGCGAGTGTGACAGCAGATCGAATTTGTGACTGTGACCCAGGGGTAT 1119  
 QY 290 SerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGlnLeuLeuSerSerArg 309  
 DB 1120 TCATGGAGGTCAACTGCTGAAGTGGCGAAGGCTCAATGAGCTCTTAAGCTCCCGG 1179  
 QY 310 LysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThr 329  
 DB 1180 AAGAGTGTATTGAATGGAATGTAAATGGAATTTGACATTAATGATTTGGAACCCATCCACA 1239  
 QY 330 AspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLys 349  
 DB 1240 GACAGTTTCTCCCTTATCATTAATCTGTGTGATGACCTGTCCGGAAGGCGCAAGTGTAA 1299  
 QY 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe 369  
 DB 1300 GCTGAATTCAGAGGAGCTGGGTGTACCTATTAAGCCCGCATGTGCTCTGATTTGCTTT 1359  
 QY 370 IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeu 389  
 DB 1360 ATTGGAAGATTGGACTATCAAAAGGCAATGATCTAATTAACCTTCCATTCGAGATCTC 1419

QY 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrp 409  
 DB 1420 ATCGGAGCAATATTCATTCGTCATGCTTGGATCTGTCACCCAGGTTTTGAAGGATGG 1479  
 QY 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerVal 429  
 DB 1480 ATGAGATCCACAGATCAGGGTACAGGGATAAAATTTCTGTGATGGGTGGATTTAGTGTT 1539  
 QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449  
 DB 1540 CCAGTTTCCACCGAATAACTCAGGTTGCGATATATTTGTTGATGCCATCCAGATTCGAA 1599  
 QY 450 ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469  
 DB 1600 CCTTGTGGCTCAATCAGCTATATGCTATGCAATATGCTACAGTGCCTGTTGTTTCATGGA 1659  
 QY 470 ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln 489  
 DB 1660 ACTGGAGGCTTCAGAGATACAGTGGAGAATTTTAAACCCGTTTGTGAGAAGGAGAGCAG 1719  
 QY 490 GlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsn 509  
 DB 1720 GGTACAGGTGGGCATTTCTCGCCACTAACCATTTGAAAAAAATGCTGTGGCATTTGCCGAT 1779  
 QY 510 CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529  
 DB 1780 GGCAATTTTCACATACAGGGAACACAAAGTCTCTTGGAGGGTCTAATGAAGCAGGCAT 1839  
 QY 530 ValLysArgLeuHisValGlyProCysArg 539  
 DB 1840 GTCAGGACTTTACATGAGGCATGCCGC 1869  
 RESULT 15  
 AAQ45183  
 ID AAQ45183 standard; cDNA to mRNA; 2533 BP.  
 XX AAQ45183;  
 DT 16-NOV-1994 (first entry)  
 XX Soluble rice starch synthetic enzyme.  
 DE Rice; starch synthetic enzyme; transit peptide; amyloplast; transition;  
 KW protoplast; expression; ss.  
 XX Oryza sativa.  
 OS  
 PH Key Location/Qualifiers  
 FT 5'UTR 1..113  
 FT /\*tag= a  
 FT CDS 114..1994  
 FT /\*tag= b  
 FT sig\_peptide 114..452  
 FT /\*tag= c  
 FT mat\_peptide 453..1991  
 FT /\*tag= d  
 FT 3'UTR 1992..2533  
 FT /\*tag= e  
 XX JP06070779-A.  
 XX 15-MAR-1994.  
 XX 07-JUL-1992; 92JP-00179947.  
 XX 07-JUL-1992; 92JP-00179947.  
 XX (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.  
 XX WPI; 1994-128678/16.  
 XX P-PSDB; AAR51231.  
 XX Soluble rice starch synthetic enzyme gene and transit peptide - for the

efficient transport of heterologous proteins to amyloplast.

Claim 1; Page 15-17; 18pp; Japanese.

The soluble rice starch synthetic enzyme gene has, at the N-terminal, the transit peptide that is required for the transition of this enzyme to the amyloplast. Introduction of this gene into the rice protoplast augments the expression of soluble rice starch synthetic enzyme. The transit peptide coding sequence can be used for the efficient transition of any protein into amyloplasts

Sequence 2533 BP; 630 A; 550 C; 701 G; 652 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 4,31e-257 Length: 2533  
Score: 2525.50 Matches: 475  
Percent Similarity: 85.8% Conservative: 31  
Best Local Similarity: 80.5% Mismatches: 33  
Query Match: 87.3% Indels: 51  
DB: 2 Gaps: 3

US-10-628-525A-21 (1-539) x AAQ45183 (1-2533)

QY	1	CysValAlaGluLeuSerArgGlu	-----8
DB	213	TGCGTGGCGGAGCTGAGCAGGACGGTGGTGGCGCCACGGCCGCGCGCG 272	
QY	8	-----8	
DB	273	CTGGTGAAGCAGCGGCTCTGCGGACCTTCTGTCGCGCAGCTCGACGCCACCGCGGCC 332	
QY	9	-----AspLeuGly-----11	
DB	333	ACGAGTCCGCGCGCGCGCGCGACCCCGCGCGCGCTTCCGCGACTCCCGCGGGAG 392	
QY	12	LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAsnThrValValAla 29	
DB	393	ATCGAGCCGAGTCTAGAGGTCTCAGAGAAGATTCCATCGACAAACAATTTTGTGGCT 452	
QY	30	SerGluAlaAspSerGluIleValValGlyLysGluGluAlaArgAlaLysValThrGln 49	
DB	453	AGTGACGAGGAGTCTGAGATCATGGATGTGAAGGAGCAAGCTCAAGCTAAAGTAAACACGC 512	
QY	50	SerIleValPheValThrGlyLysAlaSerProTyrAlaLysSerGlyLysGlyAsp 69	
DB	513	AGGTTGTCTTGTAAACCGGTGAAGCTTCTCTTATGCAAGTCAAGTGGACTAGAGAT 572	
QY	70	ValCysGlySerLeuProValAlaAlaLeuAlaAlaArgGlyHisArgValMetValMet 89	
DB	573	GTITGTGGTTCACGTGCAATGCTCTTGTCTTCTGTCGTCATCGTGTGATGTTGTAATG 632	
QY	90	ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109	
DB	633	CCGAGATACATGAACGGGCGCTTGAACAAAAATTTTGAACGCAATTTTACACTGAGAAG 692	
QY	110	HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlyTyrArg 129	
DB	693	CACATTAAAGATTCCATGCTTGGCGGAGAACATGAAGTTACTTTTTTCCAGAGTATAGG 752	
QY	130	AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyr 149	
DB	753	GATTCGTGTGATGGGTGTTGTGTGATCATCCCTCATATACATAGACCTCGAATTTGTAT 812	
QY	150	GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla 169	
DB	813	GGAGATAAATTTGGTCTTTTGGCGATAATCATGATTCAGATACACACTCTGCTGCTATGCG 872	
QY	170	AlaCysGluAlaProLeuIleLeuGluLeuGlyLysGlyTyrIleTyrGlyGlnAsnCysMet 189	
DB	873	GGGTGGAAGCCCAATTAATTTTGAACCTGGGAGGATATATCATGGACAGAAATCCATG 932	
QY	190	PheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaLysTyrArg 209	

DB	933	TTTGTGTGATGATTTGGCATGCCAGTCTGTGTGCCAGTCTCTTCTTCTGCTGCAAAATATAGA 992	
QY	210	ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGln 229	
DB	993	CCATATGGTGTTTACAGGAGTCCCGCAGTGTCTTGTCTATACATAATCTAGCACATCAG 1052	
QY	230	GlyValGluProAlaSerThrTyrProAspLeuGlyLysLeuProProGluTrpTyrGlyAla 249	
DB	1053	GGTGTGGAGCTCCAGATACATATCTGACCTGGGATTCACCTGAATGTTATGGAGCA 1112	
QY	250	LeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGlyGluAlaVal 269	
DB	1113	TTAGAATGGTCTTTCCAGTGGCGCAAGCGCGCATGCCCTTGACAAGGTGAGGCAGTC 1172	
QY	270	AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr 289	
DB	1173	AAATTTTAAAAAGCGCAGTGTGTGACAGCAGATCGAATTTGCTGCTCAGCCAGGGGTAT 1232	
QY	290	SerTrpGluValThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArg 309	
DB	1233	TCATGGAGGTCAAACTGCTGAAGTGGCGAAGGCTCATAGGCTCTTAAGCTCCCG 1292	
QY	310	LysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThr 329	
DB	1293	AAGAGTGTATTGAATGGAATTCATAATGGAAATTGACATTAATGATTGGAACCCATCCACA 1352	
QY	330	AspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLys 349	
DB	1353	GACAAAGTTTCTCCCTTATCATTTATCTGTGTGATGACCTGTCGCGAAAGCCCAAGTGTA 1412	
QY	350	GlyAlaLeuGluLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe 369	
DB	1413	GCTGAATTCAGAGAGAGCTGGGTTTACCTATAGGCCCGATGTGCTCTGATTGGCTTT 1472	
QY	370	IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeu 389	
DB	1473	ATTGGAAGATTGGACTATCAAAAAGGCAATGATTAATTAACCTTGCCATTCAGATCTC 1532	
QY	390	MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrp 409	
DB	1533	ATGCGCGCAATTAATCAATTCGTCTGATGCTGTGATCTGTTGAGCCAGGTTTGAAGGATGG 1592	
QY	410	MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPheSerVal 429	
DB	1593	ATGAGATCCACAGATCAGGTTACAGGATAAATTTCTGTGGATGGTGTGATTTAGTGT 1652	
QY	430	ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449	
DB	1653	CCAGTTTCCACCCGAATTAACCTGCGATATATTGTTGATGCCATCCAGATTCGAA 1712	
QY	450	ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469	
DB	1713	CCTTGTGGCTCAATCAGCTATATGCTATGCAATATGGTACAGTGCCTGTGTTCATGGA 1772	
QY	470	ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln 489	
DB	1773	ACTGAGGCTCAGATACAGTGGAGATTTTAACCCCTTTGCTGAGAAAGGAGAGCAG 1832	
QY	490	GlyThrGlyTrpAlaPheAlaProLeuThrGluAsnMetPheValAspIleAlaAsn 509	
DB	1833	GGTACAGGTGGGCTTCTCGCCACTTAACCAATGAAAAAATGCTGTGGCGCATTCGGAT 1892	
QY	510	CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529	
DB	1893	GGCAATTTTCGACATACAGGGAACACAAGTCTCTTGGGGAGGCTTAATGAAGCGAGCAT 1952	
QY	530	ValLysArgLeuHisValGlyProCysArg 539	
DB	1953	GTCAAGGACTTATCATGGACCATGCGCG 1982	

RESULT 16  
ADA70523  
ID ADA70523 standard; DNA; 1926 BP.



Db 1420 ATGGGGCAATATTCAATTCGTCATGCTTGGATCTGGTGACCCAGGTTTGAAGATGG 1479  
Qy 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerVal 429  
Db 1480 ATGAGATCCACAGAATCAGGTACAGGATATAATTTTCGTGGATGGGTTGGATTTAGTGT 1539  
Qy 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449  
Db 1540 CCAGTTTCCACCGAATACTGAGGTTGCGATATATTGTTGATGCCATCCAGATTCGAA 1599  
Qy 450 ProCysGlyLeuAsnGlnLeuTyzAlaMetGlnTyzGlyThrValProValValHisAla 469  
Db 1600 CCTTGGGCTCAATCAGCTATATGCTATGCAATATGTTACATGCTCTGTTCATGGA 1659  
Qy 470 ThrGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln 489  
Db 1660 ACTGGAGGCTCAGAGATACAGTGGAGAAATTTTAACCCGTTTCTGAGAAAGGAGAGCAG 1719  
Qy 490 GlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsn 509  
Db 1720 GGTACAGGTGGGCTATCTCGCCTACCTAACCTTGAAAAATGCT-GTGGCATTCGGAT 1778  
Qy 510 CysAsnIleTyzIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529  
Db 1779 GGCATTTTCGACATACAGGGAACACAAAGTCTCTTGGGAGGTCTTAATGAAGGAGGCAT 1838  
Qy 530 ValLysArgLeuHisValGlyProCysArg 539  
Db 1839 GTCAAGCGACTTTACATGGGACCATGCCGC 1868

RESULT 17  
ADT20132  
ID ADT20132 standard; cDNA; 2747 BP.  
XX  
AC ADT20132;  
XX  
DT 13-JAN-2005 (first entry)  
XX  
DE Plant cDNA, Seq ID 5458.  
XX  
KW Plant; ss; gene; transgenic; cold tolerance; growth rate;  
KW drought tolerance; disease resistance; galactomannan production;  
KW plant growth regulator; heat tolerance; herbicide tolerance;  
KW lignin production; extreme osmotic condition tolerance;  
KW pathogens resistance; pest resistance; yield improvement; seed oil yield;  
KW seed protein yield.  
XX  
OS Viridiplantae.  
XX  
PN US2004216190-A1.  
XX  
PD 28-OCT-2004.  
XX  
PF 18-DEC-2003; 2003US-00739930.  
XX  
PR 28-APR-2003; 2003US-00424599.  
XX  
PR 28-APR-2003; 2003US-00425115.  
XX  
PA (KOVA/) KOVALIC D K.  
XX  
PI Kovalic DK;  
XX  
DR WPI; 2004-757369/74.  
XX  
PT New recombinant DNA constructs useful in the field of biochemistry and  
PT genetics, and in particular for producing transgenic plants with improved  
PT biological characteristics.  
XX  
PS Claim 1; SEQ ID NO 5458; 14pp; English.  
XX  
CC The invention relates a recombinant DNA construct comprising a  
CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:

CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences  
CC (SEQ ID NO: 5545-11098). The cDNAs and proteins are from corn, soybean,  
CC Arabidopsis, wheat and rape but the specification does not indicate which  
CC sequences is derived from which organism. Also included is a method of  
CC producing a plant having an improved property, comprising transforming a  
CC plant with a recombinant DNA construct comprising a promoter region  
CC functional in a plant cell operably joined to a polynucleotide encoding a  
CC polypeptide associated with the property, and growing the transform encoded a  
CC plant. The property is selected from improving plant cold tolerance, for  
CC manipulating growth rate in plant cells by modification of the cell cycle  
CC pathway, for improving plant drought tolerance, for providing increased  
CC resistance to plant disease, for galactomannan production, for production  
CC of plant growth regulators, for improving plant heat tolerance, for  
CC improving plant tolerance to herbicides, for increasing the rate of  
CC homologous recombination in plants, for lignin production, for improving  
CC plant tolerance to extreme osmotic conditions, for improving plant  
CC tolerance to pathogens or pests, for yield improvement by modification of  
CC photosynthesis, for modifying seed oil yield and/or content, for  
CC modifying seed protein yield and/or content, for yield improvement by  
CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake  
CC and for yield improvement by providing improved plant growth and  
CC development under at least one stress condition. The polynucleotide may  
CC also encode a plant transcription factor. The methods and compositions of  
CC the present invention are useful in the field of biochemistry and  
CC genetics, in particular for producing transgenic plants with improved  
CC biological characteristics such as increased yield, improved nitrogen  
CC flow, increasing plant tolerance to cold or heat, improving plant  
CC tolerance to extreme osmotic and drought conditions, and improving plant  
CC tolerance to plant pests or pathogens. They can also be used in physical  
CC arrays of molecules, plant breeding markers, computer-based storage and  
CC analysis systems. The present sequence is one of the 5544 plant cDNA  
CC sequences of the invention. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20040216190.  
XX  
SQ Sequence 2747 BP; 661 A; 688 C; 759 G; 639 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 3.32e-251 Length: 2747  
Score: 2470.50 Matches: 465  
Percent Similarity: 91.8% Conservative: 29  
Best Local Similarity: 86.4% Mismatches: 41  
Query Match: 85.4% Indels: 4  
DB: 13 Gaps: 2

US-10-628-525A-21 (1-539) x ADT20132 (1-2747)

Qy 2 ValAlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGlySer 21  
Db 538 GTGGGGGAACCTCGCG---CCCGACCTCTCTGCTC-----GAAGGGATTCTGAGGATTCC 598  
Qy 22 IleAspAsnThrValValAlaSerGluGlnAspSerGluIleValValGlyLysGlu 41  
Db 589 ATCGACAGCATAAATTGTGGCTGCAAGTGACGAGGATTCGTGAGATCATGATCGAATGAG 648  
Qy 42 GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61  
Db 649 CAACCTCAAGCTAAAGTTACACGTAGCATCGTGTGTTGTGACTGGTGGTGAAGCTCTTAT 708  
Qy 62 AlaLysSerGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaArg 81  
Db 709 GCANAAGTCAGGGGGCTGGAGATGTTTGTGTTCTGTACCAATTGCTCTTGTCTCGT 768  
Qy 82 GlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr 101  
Db 769 GGTCCCGCTGTGATGGTTGTAATGCCAGATACCTTGAATGGGTCTCTGTATAAACTAT 828  
Qy 102 AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGluHisGlu 121  
Db 829 GCAAAAGGCATTATACACTGGGAAGACATTAATGATTCATGCTTTGGGGGATCACAATGA 898  
Qy 122 ValThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSer 141



Query Match:	85.3%	Indels:	4
DB:	2	Gaps:	2
US-10-628-525A-21 (1-539) x AAX34651 (1-2662)			
QY	2	ValAlaGluLeuSerArgGluLeuGlyLeuGluProGluGlyLeuAlaGluGlySer	21
DB	539	GTGGGGAACTCCGCG--CCCGACCTCCCTGCTC-----GAGGGATTGCTGAGGATTCC	589
QY	22	IleAspAsnThrValValValAlaSerGluGlnAspSerGluIleValValGlyLeuGlu	41
DB	590	ATCGACAGCATTAATTTGGCTGCGCAAGTGAGCAGGATTCTGAGATCATGGATCGCAATGAG	649
QY	42	GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr	61
DB	650	CAACCTCAAGCTAAAGTTACAGTAGCATCGTGTGTGTGACCTGGTGAAGCTGCTCTTAT	709
QY	62	AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaArg	81
DB	710	GCAAACTCAGGGGGCTGGGAGATGTTTGTGGTTCGTTACCAATTGCTCTTGTGCTCGT	769
QY	82	GlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr	101
DB	770	GGTCAACGCTGATGGTTGTAATGCCAGATACCTGAATGGGTCCTCTCATAAACTAT	829
QY	102	AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu	121
DB	830	GCAAGGCATTAATACCTGGGAAGCACAATTAGATTCCATGCTTTGGGGGATCACAATGA	889
QY	122	ValThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSer	141
DB	890	GTGACCTTTTTCATGAGTATAGACAACGTCGATTGGGTGTTGTCGATCATCGTCA	949
QY	142	TyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe	161
DB	950	TATCATAGACCAAGGAATTTATATGAGATAATTTTGGTCTTTGGTGTATATCATGTTTC	1009
QY	162	ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluGlyGly	181
DB	1010	AGATACACACTCTTTGCTATGCTGATCGATGGAGGCCCACTAATCTTGAAATGGGAGA	1069
QY	182	TyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHisAlaSerLeuValPro	201
DB	1070	TATATTTATGGACAGAAATTCATGTTTGTGTGAACGATTGGCATGCCAGCCTTGTGCCA	1129
QY	202	ValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeu	221
DB	1130	GTCCCTTCTTGTGCAAAATATAGACCATACGGTGTGTTACAGAGATTTCCCGCAGCACCCCTT	1189
QY	222	ValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGly	241
DB	1190	GTTATACATAATTTAGCACATCAGGCTCTGGAGCTCGAAGTACATATCTGATCTGGGA	1249
QY	242	LeuProProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHis	261
DB	1250	TTGGCAACCTGAATGGTATGAGCTTTAGAAATGGGTATTTCCAGAAATGGGAGGAGCAT	1309
QY	262	AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArg	281
DB	1310	GCCCTTGAACAGGGGTGAGCAGTTAACTTTTGAAGAGGAGCAGTGTGACAGCATGCA	1369
QY	282	IleValThrValSerLysGlyTyrSerTyrGluValThrThrAlaGluGlyGlyGlnGly	301
DB	1370	ATTGTGACCGTCAGTCAGGCTTATTCATGGAGGTACACACTGCTGAAAGGTGGACAGGCG	1429
QY	302	LeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp	321
DB	1430	CTCAATGAGCTCTTAAGCTCCCGAAAGAGTATTGAATGGAATTTGAATGGAATTTGAC	1489
QY	322	IleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp	341
DB	1490	ATTAATGATTGAACCCCAACCAAGAGTGTCTCCCTCATCATTAATTTCTGTGATGAC	1549
QY	342	LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg	361
DB	1550	CTCTCTGGAAGGCCCAATGTAAGCTGAATTCGAGAAGAGCTGGTTTACCTGTAAAG	1609
QY	362	ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu	381
DB	1610	GAGGATGTTTCTCTGATTGGCTTTATTGGAAGACTGGATTACAGAAAGGCATTGATCTC	1669
QY	382	IleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer	401
DB	1670	ATTAAATGGCCATTTCCAGAGCTCATGAGGAGGAGCTGAGTTTGTGATGCTTGGATCT	1729
QY	402	GlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPhe	421
DB	1730	GGGGATCCAATTTTGAAGGCTGGATGAGATCTACCGACTCGAGTTACAGGATAAATTC	1789
QY	422	ArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle	441
DB	1790	CGTGGATGGTGGATTTAGTGTTCAGTTTCCAGATTTCCACAGAAATACTGCAGGTTGCCATATA	1849
QY	442	LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr	461
DB	1850	TTGTTAATGCCATCCAGGTTTGAACCTGTGTCTTAAATCAGCTATATGCTATGCAATAT	1909
QY	462	GlyThrValProValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsn	481
DB	1910	GGTACAGTTCTCTGATGTTTCATGGAACCTGGGGCTCCGAGACACAGTCGAGACCTTCAAC	1969
QY	482	ProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGlu	501
DB	1970	CCTTTTGTGCAAAAGGAGGAGGAGGTACAGGGTGGCGCTTCTCACCGCTAACCCGTGGAC	2029
QY	502	AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu	521
DB	2030	AGATGTTTGTGGCATTCGGAACCGGATGTCGACATTCAGGGAGCACCAAGCCGTCCTG	2088
QY	522	GlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg	539
DB	2089	GGAGGGCTCATGAAGCGGAGCATGACGAAGACCATACATGTTGGGACCATGCCGC	2142
RESULT 19			
ID	AAV01527	standard; cDNA to mRNA; 2239 BP.	
XX	AAV01527;		
XX	27-AUG-2003 (revised)		
XX	21-MAY-1998 (first entry)		
XX	Wheat soluble starch synthase partial cDNA sequence.		
XX	Starch synthase; wheat; transgenic plant; ss.		
XX	Triticum aestivum.		
XX	Key Location/Qualifiers		
XX	CDS 3-2018		
XX	/*tag= a		
XX	WO9745545-A1.		
XX	04-DEC-1997.		
XX	28-MAY-1997; 97WO-EP002793.		
XX	29-MAY-1996; 96DS-01021588.		
XX	11-SEP-1996; 96DE-01036917.		
XX	(AGRE ) HOECHST-SCHERING AGREVO GMBH.		
XX	Block M, Loerz H, Luetticke S, Walter L, Froberg C, Kossmann J;		
XX	WPI; 1998-032652/03.		







Db 1607 CTCTCTGGAAGGCCAAATGTAAAGCTGAATTGACAGAGGAGTTGGGTTTACCTGTAAAGG 1666  
Qy 362 ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381  
Db 1667 GAGGATGTTCTCTGATGGCTTTATTGGAAGACTGGATTACCAAGAAAGGCAATTGATCTC 1726  
Qy 382 IleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer 401  
Db 1727 ATTAAATGGCATTCAGAGCTCATGAGGAGACGTGCAATTTGTTCATGCTTGGATCT 1786  
Qy 402 GlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPhe 421  
Db 1787 GGGGATCCATTTTGAAGCTGGATGAGATCTACCGAGTCGAGTTACAGGATTAATTC 1846  
Qy 422 ArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle 441  
Db 1847 CGTGGATGGGTGGATTTAGTTTCCAGTTTCCACAGAATAACTGCAGGTTCGATATA 1906  
Qy 442 LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461  
Db 1907 TTGTTAATGCATCGAGATTGAACCTTGGCGGTCTTAATCAGCTATATGCTATGCAATAT 1966  
Qy 462 GlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsn 481  
Db 1967 GGTACAGTTCCTGTAGTTTCATGGACTGGGGGCTCCGAGACACATCGAGACCTTCAC 2026  
Qy 482 ProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGlu 501  
Db 2027 CCTTTTGGTCAAAAGGAGAGGAGGTACAGGGTGGGCGTTCTCACCGCTAACCGTGGAC 2086  
Qy 502 AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu 521  
Db 2087 AAGATGTT-GTGGGCATTCGGAACCGCGATGTGCACATTCAGGGAGCACAAAGCCGCTCTG 2145  
Qy 522 GlyArgAlaAsnGluAlaArgHisValLysValLeuHisValGlyProCys 538  
Db 2146 GGAGGGCTCATGAGCGAGGCGATGACGAAGACCATACGTGGGACCACTGC 2196

RESULT 21  
AAZ50642  
ID AAZ50642 standard; cDNA; 1415 BP.  
AC AAZ50642;  
XX  
XX 23-MAY-2000 (first entry)  
XX  
XX Corn soluble starch synthase gene fragment inserted in pSS64-C5.  
DE  
XX Soluble starch synthase; starch fine structure; corn; transgenic plant;  
KW amylose; amylopectin; amylose polymerisation;  
KW non-granule bound starch synthase; non-GBSSI; altered starch; food;  
KW paper; plastic; adhesive; ss.  
XX  
OS Zea mays.  
XX  
XX WO200006755-A2.  
PN  
XX 10-FEB-2000.  
PD  
XX 26-JUL-1999; 99WO-US016296.  
PF  
XX 28-JUL-1998; 98US-0094436P.  
PR  
XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
PA  
XX Broglie KB, Lightner JE;  
PI  
XX WPI; 2000-195311/17.  
DR  
XX Producing transgenic cereal crops with altered starch structure useful  
PT for preparing foodstuff, paper, plastic or adhesives, comprises  
PT transforming crops with chimeric sense or antisense gene construct  
PT encoding starch synthase.

XX Claim 5; Page 52-53; 56pp; English.  
PS  
CC The present sequence is the corn soluble starch synthase (SSI) DNA  
CC sequence comprising the SSI coding region of amino acids 1-494 inserted  
CC into plasmid pSS64-C5. The chimeric gene containing the zein promoter  
CC followed by the SSI gene fragment is used as a sense construct for  
CC preparation of transgenic corn expressing altered starch structure. The  
CC starch fine structure derived from a grain of the cereal crop can be  
CC altered in the transformed cereal crop by changes in amylose to  
CC amylopectin ratio, amylopectin fine structure, increased abundance of  
CC very short amylopectin chains and in the degree of polymerisation of  
CC amylose. These modifications can be created by controlling the expression  
CC of non-GBSSI (non-granule bound starch synthase) in transgenic plants.  
CC Altered starches are useful in foods, paper, plastics or adhesives  
XX  
SQ Sequence 1415 BP; 317 A; 335 C; 397 G; 366 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 2,87e-206 Length: 1415  
Score: 2043.00 Matches: 388  
Percent Similarity: 89.8% Conservative: 0  
Best Local Similarity: 89.8% Mismatches: 0  
Query Match: 70.6% Indels: 44  
DB: 3 Gaps: 1  
  
US-10-628-525A-21 (1-539) x AAZ50642 (1-1415)  
  
Qy 1 CysValAlaGluLeuSerArgGlu----- 8  
Db 119 TGGCTCGCGAGCTGAGCAGGGAGGGCGCGCGCGCTGCCACCCGCGCTGCTG 178  
Qy 8 ----- 8  
Db 179 GCGCCCCCGCTCGTGGCCCGCTTCCTCGCGCGCGCGCGCGCGCGGTGAGCCGGCA 238  
Qy 9 -----AspLeuGlyLeuGluProGluGly 16  
Db 239 TCGACGCCCGCGCCGCTGCGCGACCGCGCTGGGGGACCTCGGTCTCGAACCTGAAGGG 298  
Qy 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36  
Db 299 ATTGCTGAAGGTTCCATCGATAACACAGTAGTTGTGGCAAGTGAGCAAGATTCTGAGATT 358  
Qy 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
Db 359 GTGGTTGGAAAGAGGACGACCTGAGCTAAGTAACAAGCAATGTCTTTGTAAACCGGC 418  
Qy 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
Db 419 GAAGCTTCTCTTATGCAAAAGTCTGGGGGTCTAGGAGATGTTTGTGTTTCATTGCCAGTT 478  
Qy 77 AlaLeuAlaAlaArgGlyHisArgValMetValMetValMetProArgTyrLeuAsnGlyThr 96  
Db 479 GCTCTTGTGCTCGTGGGTCAACGCTGATGGTTGTAATCCACAGATATTAAATGTTGATCC 538  
Qy 97 SerAspLysAsnTyrAlaAlaAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
Db 539 TCCGATAGAATTTGCAATTCATTTTACACAGAAACACACATTCGGATTCCATGCTTTT 598  
Qy 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPhe 136  
Db 599 GCGGGTGAACATGAAGTTACCTTCTCCATGATAGATATAGAGATTTCAGTTCAGCTGGGTGTT 658  
Qy 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
Db 659 GTTGATCATCCCTCATATCACAGACCTGGAAATTTATATGGAGATAAGTTTGGTGTCTTT 718  
Qy 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
Db 719 GTTGATATATCAGTTTCAGATACACATCTCTTGTGATGCTGATGAGGCTCTCTTTGATC 778  
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrPhe 196



PR	19-JUL-1999;	99US-0144333P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159330P.
PR	20-JUL-1999;	99US-0144332P.	PR	14-OCT-1999;	99US-0159331P.
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159637P.
PR	21-JUL-1999;	99US-0144884P.	PR	14-OCT-1999;	99US-0159638P.
PR	21-JUL-1999;	99US-0144814P.	PR	18-OCT-1999;	99US-0159584P.
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160741P.
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160767P.
PR	22-JUL-1999;	99US-0145085P.	PR	21-OCT-1999;	99US-0160770P.
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160770P.
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160814P.
PR	22-JUL-1999;	99US-0145132P.	PR	21-OCT-1999;	99US-0160815P.
PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160980P.
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160981P.
PR	23-JUL-1999;	99US-0145224P.	PR	22-OCT-1999;	99US-0160989P.
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161404P.
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161405P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161406P.
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161359P.
PR	02-AUG-1999;	99US-0146386P.	PR	26-OCT-1999;	99US-0161360P.
PR	02-AUG-1999;	99US-0146388P.	PR	26-OCT-1999;	99US-0161361P.
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161320P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161992P.
PR	04-AUG-1999;	99US-0147204P.	PR	28-OCT-1999;	99US-0161993P.
PR	04-AUG-1999;	99US-0147302P.	PR	29-OCT-1999;	99US-0162142P.
PR	05-AUG-1999;	99US-0147192P.	Alignment Scores:		
PR	06-AUG-1999;	99US-0147303P.	Pred. No.:		
PR	06-AUG-1999;	99US-0147416P.	Score:		
PR	08-AUG-1999;	99US-0147493P.	Percent Similarity:		
PR	08-AUG-1999;	99US-0147935P.	Best Local Similarity:		
PR	10-AUG-1999;	99US-0148171P.	Query Match:		
PR	11-AUG-1999;	99US-0148319P.	DB:		
PR	12-AUG-1999;	99US-0148341P.	US-10-628-525A-21 (1-539) x AAC46797 (1-1984)		
PR	13-AUG-1999;	99US-0148565P.	Length:		
PR	13-AUG-1999;	99US-0148684P.	Matches:		
PR	16-AUG-1999;	99US-0149368P.	Conservative:		
PR	17-AUG-1999;	99US-0149175P.	Mismatch:		
PR	18-AUG-1999;	99US-0149426P.	Indels:		
PR	20-AUG-1999;	99US-0149723P.	Gaps:		
PR	20-AUG-1999;	99US-0149723P.	5.36e-172		
PR	20-AUG-1999;	99US-0149929P.	1722.00		
PR	23-AUG-1999;	99US-0149902P.	76.4%		
PR	23-AUG-1999;	99US-0149930P.	64.8%		
PR	25-AUG-1999;	99US-0150566P.	59.5%		
PR	26-AUG-1999;	99US-0150884P.	3		
PR	27-AUG-1999;	99US-0151065P.	3		
PR	27-AUG-1999;	99US-0151066P.	3		
PR	27-AUG-1999;	99US-0151080P.	3		
PR	30-AUG-1999;	99US-0151303P.	3		
PR	31-AUG-1999;	99US-0151438P.	3		
PR	01-SEP-1999;	99US-0151930P.	3		
PR	01-SEP-1999;	99US-0152363P.	3		
PR	10-SEP-1999;	99US-0153070P.	3		
PR	13-SEP-1999;	99US-0153758P.	3		
PR	15-SEP-1999;	99US-0154018P.	3		
PR	16-SEP-1999;	99US-0154039P.	3		
PR	20-SEP-1999;	99US-0154779P.	3		
PR	22-SEP-1999;	99US-0155139P.	3		
PR	23-SEP-1999;	99US-0155486P.	3		
PR	24-SEP-1999;	99US-0155659P.	3		
PR	28-SEP-1999;	99US-0156458P.	3		
PR	29-SEP-1999;	99US-0156596P.	3		
PR	04-OCT-1999;	99US-0157117P.	3		
PR	05-OCT-1999;	99US-0157753P.	3		
PR	06-OCT-1999;	99US-0157865P.	3		
PR	07-OCT-1999;	99US-0158029P.	3		
PR	08-OCT-1999;	99US-0158232P.	3		
PR	12-OCT-1999;	99US-0158369P.	3		
PR	13-OCT-1999;	99US-0159293P.	3		
PR	13-OCT-1999;	99US-0159294P.	3		
QY	38 ValGlyLeuGluGlnAlaArgAlaValThrGlnSerIleValPheValThrGlyGlu	57	QY	38 ValGlyLeuGluGlnAlaArgAlaValThrGlnSerIleValPheValThrGlyGlu	57
DB	506 GTTGGGATTCGAGTGGAAAGCTGAAGTTGTCAATAACCTGTTTCGTTACATCCGAG	565	DB	506 GTTGGGATTCGAGTGGAAAGCTGAAGTTGTCAATAACCTGTTTCGTTACATCCGAG	565
QY	58 AlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAla	77	QY	58 AlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAla	77
DB	566 GCGGCTCCTTACTCGAAACAGGAGGATTAGGAGATGTTTGTGGTCTCTTTGCCGATAGCT	625	DB	566 GCGGCTCCTTACTCGAAACAGGAGGATTAGGAGATGTTTGTGGTCTCTTTGCCGATAGCT	625
QY	78 LeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr---	96	QY	78 LeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr---	96
DB	626 TTAGCTGGTCGTGGGCATCGTGTATGGTCATTTCTCTCGGTACTTAATGAAGTCTGCT	685	DB	626 TTAGCTGGTCGTGGGCATCGTGTATGGTCATTTCTCTCGGTACTTAATGAAGTCTGCT	685
QY	97 SerAspLysAsnTyrAlaAlaAlaPheTyrThrGluLysHisIleArgIleProCysPhe	116	QY	97 SerAspLysAsnTyrAlaAlaAlaPheTyrThrGluLysHisIleArgIleProCysPhe	116
DB	686 GCAGACAAGACTATGCCCGGGCTAGGATTGGGGATACGTACAGTAAGTAATTCCTTT	745	DB	686 GCAGACAAGACTATGCCCGGGCTAGGATTGGGGATACGTACAGTAAGTAATTCCTTT	745
QY	117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe	136	QY	117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe	136
DB	746 GGTGGTTCTCAAGAAGCTTCTCTATCATGATAGATAGATGCTGCTGCTGGTCTTTT	805	DB	746 GGTGGTTCTCAAGAAGCTTCTCTATCATGATAGATAGATGCTGCTGCTGGTCTTTT	805
QY	137 ValAsnHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe	156	QY	137 ValAsnHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe	156
DB	806 GTTGATCAAAATCCTACCATGACCTGTAATCCTACGGAGATAGTAAGAGGACCTTT	865	DB	806 GTTGATCAAAATCCTACCATGACCTGTAATCCTACGGAGATAGTAAGAGGACCTTT	865
QY	157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle	176	QY	157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle	176
DB	866 GGTGACAAATCAGGTA-----	886	DB	866 GGTGACAAATCAGGTA-----	886
QY	177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHis	196	QY	177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHis	196
DB	887 TTGACATTG-----	895	DB	887 TTGACATTG-----	895
QY	197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp	216	QY	197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp	216
DB	896 TCCAAAGAAAGACTTTTGACTTTTGGCCCAAGATATCGCCCATATGAGATTATATAGGAT	955	DB	896 TCCAAAGAAAGACTTTTGACTTTTGGCCCAAGATATCGCCCATATGAGATTATATAGGAT	955

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QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProHisThr 236
DB 956 GCAGAGAGCATCTCAATATCCATAACCTCGCTCATCAGGGGTGAGCCAGCATCA 1015
QY 237 TyrProAspLeuGlyLeuProGluTyrGlyValAlaLeuGluTrpValPheProGlu 256
DB 1016 TACACCAACTTGGGATTCCTCGGAATGGTATGGAGCAGTCGGGTGGTATTTCCAACG 1075
QY 257 TrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276
DB 1076 TGGGCAAGAACTCATCCCTTGACACCGGTGAGCGTTAATGTTCTCAAGGGTGTATT 1135
QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296
DB 1136 GTGACCTCTGACCGTATCAATTAATCTGTGAGCCAGGGCTATGCAATGGGAAATCACTACTGTT 1195
QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316
DB 1196 GAAGGTGGTTATGGTCTTCAAGATTGGCTTTCTAGTCGGAAGTGTATATAATGGGATC 1255
QY 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336
DB 1256 ACAATATGGAATTAATGTTGATGAATGGAATCCATCCACGGATGAACACATTCCTTTCCAT 1315
QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyValAlaLeuGlnLysGluLeu 356
DB 1316 TACTCTGTGTGATGTCTTCGGAAGATCAATGCAATGCGACTACAAAGGAAATG 1375
QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
DB 1376 GGTCTCCCATAGGCTGCAATGCTCTATGATGGTTTATAGGAAGACTTGATTACCA 1435
QY 377 LysGlyIleAspLeuGlnLeuIleProAspLeuMetArgGluAspValGlnPhe 396
DB 1436 AAGGGCAATGATCTGATCCAAACCGCTGCTGCTGATCTCATGTGGATGACATCAATTC 1495
QY 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416
DB 1496 GTCATGCTTGGTTCGGGTGACCCAAATATGAAGCTGGATGAGAAATGTTGGAGGAAACA 1555
QY 417 PheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr 436
DB 1556 TACAGAGCAAAATTCGGTGGTGGTGGTGGTTCATGTCCTCATCTCATCGAATCACA 1615
QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456
DB 1616 GCCGGCTGTGACATCTCTCATGCGTCGAGATTGAGCCCTGTGGTTTAAATCAGCTA 1675
QY 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476
DB 1676 TACGCATGAGATACGGAACCAATTCAGTTGTTTCATGGCAGCTGGAGGACTCAGAGTACG 1735
QY 477 ValGluAsnPheAsnProPheGlyGlyLeuAsnGlyGlu--GlnGlyThrGlyTrpAlaPhe 495
DB 1736 GTTGAGAAATTCACCCCTTATGCAGAAAGTGGAGCTGCTGCTGCTGCTGCTGCTGCT 1795
QY 496 AlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGln 515
DB 1796 ACTCCCTTGTGAAAGATGAGTATGGTCTCGGCTTTGAGGTTGGCTGCACAAAC-GTACAG 1854
QY 516 GlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisVal 535
DB 1855 AGAGTATAACAGTCAATGGAGAGGATGATGAGAGAGGAAATGACCCGAAACTACTCTTG 1914
QY 536 GlyPro--CysArg 539
DB 1915 GGAAGAACGCTGCCGT 1929
RESULT 23
AAT32325
ID AAT32325 standard; cDNA; 1758 BP.
XX
AC AAT32325;
```

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XX 31-OCT-1996 (first entry)
DT Soluble starch synthase (Isoform B) coding sequence.
DE Soluble starch synthase; transformation; transgenic plant; starch;
KW amylose; amylopectin; ss.
XX Solanum tuberosum.
XX Key Location/Qualifiers
FT 1. .1377
FT /*tag= a
FT /product= "Soluble starch synthase."
XX DE4441408-Al.
XX 15-MAY-1996.
XX 10-NOV-1994; 94DE-04441408.
XX 10-NOV-1994; 94DE-04441408.
XX (GENB-) INST GENBIOLOGISCHE FORSCHUNG.
XX Kossmann J, Springer F, Abel GJ;
XX WPI; 1996-240218/25.
XX P-PSDB; AAR99540.
PT DNA encoding soluble starch synthase of potato - used to produce
PT transgenic plants with increased prodn. of starch or able to produce
PT modified starches.
XX Claim 2; Page 20-22; 32pp; German.
XX DNA sequences from the potato encoding soluble starch synthase having the
CC 459 C-terminal amino acid sequence encoded by this sequence or the 677 C-
CC terminal amino acid sequence given in AAR99539 can be used to identify
CC and isolate homologous sequences encoding soluble starch synthase and
CC enzymes with similar activities from plants or other organisms; to
CC transform prokaryotic or eukaryotic cells; to produce transgenic plants
CC which synthesise starch of altered structure or in increased yield
XX SQ Sequence 1758 BP; 529 A; 328 C; 413 G; 488 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,88e-164 Length: 1758
Score: 1645.50 Matches: 304
Percent Similarity: 81.7% Conservative: 63
Best Local Similarity: 67.7% Mismatches: 70
Query Match: 56.9% Indels: 13
DB: 2 Gaps: 5
US-10-628-525A-21 (1-539) x AAT32325 (1-1758)
QY 95 GlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIlePro 114
DB 1 GGCACGAGC-----AATGCTGTGTACCTTGATGTGGCGGCCACTGTCCAT 45
QY 115 CysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrp 134
DB 46 TCGTTTGGTGATGCACAGGAAGTAGCCTTCTACCATGATACAGGCGAGGTGTTGATTGG 105
QY 135 ValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGly 154
DB 106 GTATTTGTGGACCACTCTCTTACCGCAGACCTCGAAGCCCATATGGTGATATTATGGT 165
QY 155 AlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaPro 174
DB 166 GCATTTGGTGATAATCAGTTTCGTTCTCATCTTTGCTTTCTCAGCAGCATGTGAAGCGCCA 225
QY 175 LeuIleLeuGluGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAsp 194
```





Score:	1496.00	Matches:	284
Percent Similarity:	99.6%	Conservative:	0
Best Local Similarity:	99.6%	Mismatches:	1
Query Match:	51.7%	Indels:	1
DB:	13	Gaps:	0
US-10-628-525A-21 (1-539) x ADX59939 (1-1294)			
QY	255	ProGluThrAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly	274
DB	2	CCTGAATGGCGAGGAGGATGCCCTTGACAGGGTGAGCGCATTAATTTTGAAGGT	61
QY	275	AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThr	294
DB	62	GCAGTTGTGACAGCAGATCGATCGTGACTGTCGTAAGGGTTATTTCATGGGAGGTCACA	121
QY	295	ThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsn	314
DB	122	ACTGCTGAAGGTGGACAGGGCCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAAC	181
QY	315	GlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIlePro	334
DB	182	GGAAATTTGTAATGGAATTGACATTAATGATTTGGAACCTGCCACACAAATGTATCCCC	241
QY	335	CysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLys	354
DB	242	TGTCATATTCTGTTGATGACCTCTCTGGAAGGCCAAATGTAAGAGTCATTGCGAAG	301
QY	355	GluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAsp	374
DB	302	GAGCTGGGTTTACCTATAAGGCTGATGTTCCCTGATTTGGCTTTATTGGAAGATTGGAT	361
QY	375	TyrGlnLysGlyIleAspIleGlnLeuIleIleProAspLeuMetArgGluAspVal	394
DB	362	TATCAAAAGGCGATTGATCTCATTTCAACTTATCATACCAGATCTCATGCGGAAGATGT	421
QY	395	GlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGlu	414
DB	422	CAATTTGTCATGCTTGATGATCTGTGACCCAGAGCTTGGAAGTTGGATGAGATCTACAG	481
QY	415	SerIlePheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArg	434
DB	482	TCGATCTTCAAGGATAAAATTTCTGATGGTGGTTGGATTTAGTGTTCAGTTCCACCGCA	541
QY	435	IleThrAlaGlyCysAspIleLeuMetProSerArgPheGluProCysGlyLeuAsn	454
DB	542	ATAACTGCCGGCTGGATATATTGTTAATGCCATCCAGATTCCGAACCTTTGGTCTCAAT	601
QY	455	GlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArg	474
DB	602	CAGCTATATGCTATGCAATGTCACAGTTCCTGTTGTCATGCAACTGGGGCCCTTAGA	661
QY	475	AspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAla	494
DB	662	GATACCGTGGAGAATCTCAACCTTTCCGTGAGATGGAGAGCAGGGTACAGGGTGGCA	721
QY	495	PheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIle	514
DB	722	TTTCGACCCCTTAACCAAGAAACATGTTT- GTGGACATTTGCGAACTGCAATATCTACATA	780
QY	515	GlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHis	534
DB	781	CAGGGNACACAGTCTCTCTGGAGGGGCTATGAGCGGCGATGTCAAAAGACTTTCAC	840
QY	535	ValGlyProCysArg	539
DB	841	GTGGGACCATGCCG	855
RESULT 25			
ADX08949			
XX	ID	ADX08949 standard; cDNA; 1300 BP.	
AC	ADX08949;		

XX	21-APR-2005	(first entry)
DT	Plant full length insert polynucleotide seqid 3524.	
XX	plant protectant; plant growth regulant; gene therapy; plant;	
XX	recombinant DNA construct; physical array; plant breeding marker;	
KW	cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;	
KW	extreme osmotic condition; pathogen tolerance; pest tolerance;	
KW	growth rate; cell cycle pathway; disease resistance;	
KW	galactomannan production; lignin production; plant growth regulator;	
KW	yield; plant growth; plant development; seed oil; protein yield;	
KW	protein content; gene; ss.	
XX	Unidentified.	
OS	US2004034888-A1.	
XX	19-FEB-2004.	
XX	28-APR-2003; 2003US-00425114.	
PF	06-MAY-1999; 99US-00304517.	
PR	05-NOV-2001; 2001US-00985678.	
XX	(LIUJ/) LIU J.	
PA	(ZHOU/) ZHOU Y.	
PA	(KOVA/) KOVALIC D K.	
PA	(SCRE/) SCREEN S E.	
PA	(TABA/) TABASKA J E.	
PA	(CAOY/) CAO Y.	
XX	Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;	
PI	WPI; 2004-180133/17.	
XX	New recombinant DNA construct, useful for improving plant tolerance to	
PT	cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or	
PT	pests, for conferring increased resistance to plant disease, or for	
PT	improving yield.	
XX	Claim 1; SEQ ID NO 3524; 15pp; English.	
PS	The invention describes a recombinant DNA construct comprising a	
CC	polynucleotide consisting of a sequence encoding an amino acid sequence	
CC	available in electronic form from the US patent office at	
CC	ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide	
CC	of the invention are also useful in physical arrays of molecules and as	
CC	plant breeding markers. The recombinant DNA construct is useful for	
CC	improving plant tolerance to cold, heat, drought, herbicides, extreme	
CC	osmotic conditions, pathogens or pests, for manipulating growth rate in	
CC	plant cells by modification of the cell cycle pathway, for conferring	
CC	increased resistance to plant disease, for producing galactomannan,	
CC	lignin or plant growth regulators, for increasing the rate of homologous	
CC	recombination in plants, for improving yield by modification of	
CC	photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake	
CC	or by providing improved plant growth and development under at least one	
CC	stress condition or for modifying seed oil or protein yield and/or	
CC	content. This sequence represents a plant full length insert	
CC	polynucleotide that can be used in the recombinant DNA construct of the	
CC	invention.	
XX	Sequence 1300 BP; 354 A; 268 C; 327 G; 351 T; 0 U; 0 Other;	
SQ	Alignment Scores:	
	Pred. No.:	Length:
	Score:	2.32e-144 1300
	Percent Similarity:	1459.00 Matches: 278
	Best Local Similarity:	99.6% Conservative: 0
	Query Match:	99.6% Mismatches: 1
	DB:	50.4% Indels: 1
		13 Gaps: 0
	US-10-628-525A-21 (1-539) x ADX08949 (1-1300)	

QY 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAsp 280  
 Db |||||  
 3 CATGCCCTTGCAAGGGTGAGCGAGTTAAATTTTGAAGGTGCGAGTTGTGCACAGCAGAT 62  
 QY 281 ArgIleValThrValSerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGln 300  
 Db |||||  
 63 CGAATCGTGACTGTCACTAAGGGTTATTTCATGGAGGTGCACACTGCTGAAGGTGGACAG 122  
 QY 301 GlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320  
 Db |||||  
 123 GGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACGGAATTGTAAATGGAAAT 182  
 QY 321 AspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340  
 Db |||||  
 183 GACATTAAATGATTGGAAACCTCGCCACAGACAAATGTATCCCTGTCATTATTCTGTGTAT 242  
 QY 341 AspLeuSerGlyLysAlaLysCysLysGlyValAlaLeuGlnLysGluLeuGlyLeuProIle 360  
 Db |||||  
 243 GACCTCTCTGGAAAGGCCAAATGTAAGGTGCATTGCGAAGGAGCTGGGTTTACCTATA 302  
 QY 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380  
 Db |||||  
 303 AGGCTGATGTTCTCTGATGGCTTTATTGGAGATTGGATTATCAGAAAGGCATTGAT 362  
 QY 381 LeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
 Db |||||  
 363 CTCATTCAACTTATCATACCAGATCTCATCGGGAAGATGTTCAATTTGTTCATGCTTGA 422  
 QY 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys 420  
 Db |||||  
 423 TCTGGTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATCTTCAAGGATAA 482  
 QY 421 PheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440  
 Db |||||  
 483 TTTTGGTGGATGGGTGGATTAGTTTCCAGTTTCCACCGAATACTGCGGCTGGAT 542  
 QY 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460  
 Db |||||  
 543 ATATTGTTAATGTCATCCAGATTCGAACCTTGTGTCTCAATCAGCTATATGCTATGCAG 602  
 QY 461 TyrGlyThrValProValValHisAlaThrGlyLeuArgAspThrValGluAsnPhe 480  
 Db |||||  
 603 TATGGCACAGTTCCTGTGTGTCATGCAACTGGGGGCTTAGAGATACCGTGGAGAACTTC 662  
 QY 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThr 500  
 Db |||||  
 663 AACCTTTTCGGTGGATGGAGAGCAGGGTACAGGGTGGGCATTTCGACCCCTAACCA 722  
 QY 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520  
 Db |||||  
 723 GAAACATGTT-GTGGACATTGGCAATGCAATATCTACATACAGGGAACACAAGTCTTC 781  
 QY 521 LeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
 Db |||||  
 782 CTGGGAAGGGCTAATGAGCGAGGCATGTCAAAGACTTCACGTGGGACCACATGCCCG 838  
 RESULT 26  
 AAX34652  
 ID AAX34652 standard; DNA; 10336 BP.  
 XX AC AAX34652;  
 XX AC AAX34652;  
 DT 17-OCT-2003 (revised)  
 DT 05-JUL-1999 (first entry)  
 DE Wheat starch soluble synthase I (SSS I) gene sequence.  
 XX Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS;  
 KW starch branching enzyme; starch soluble synthase; debranching enzyme;  
 KW endosperm; wheat; barley; granule-bound synthase; glutenin; starch;  
 KW grain softness protein I; bacterial isoamylase; glycogen synthase;  
 KW wSBE I-D4 gene; ds.

XX OS Aegilops tauschii.  
 FH Key Location/Qualifiers  
 CDS 1..9713  
 FT /\*tag= a  
 FT /product= "SSS I"  
 FT /note= "contains introns"  
 FT 1..316  
 FT /\*tag= b  
 FT /number= 1  
 FT 317..1471  
 FT /\*tag= c  
 FT /number= 1  
 FT 1472..1828  
 FT /\*tag= d  
 FT /number= 2  
 FT 1829..2765  
 FT /\*tag= e  
 FT /number= 2  
 FT 2766..2823  
 FT /\*tag= f  
 FT /number= 3  
 FT 2824..2905  
 FT /\*tag= g  
 FT /number= 3  
 FT 2906..3028  
 FT /\*tag= h  
 FT /number= 4  
 FT 3029..4112  
 FT /\*tag= i  
 FT /number= 4  
 FT 4113..4194  
 FT /\*tag= j  
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FT /number= 12  
FT 8916. .8991  
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FT /number= 12  
FT 8992. .9104  
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FT /number= 14  
FT 9200. .9497  
FT /tag= ac  
FT /number= 14  
FT 9498. .9713  
FT /tag= ad  
FT /number= 15

PN W09914314-A1.

PD 25-MAR-1999.

PF 11-SEP-1998; 98NO-AU000743.

PR 12-SEP-1997; 97AU-00009108.

PR 20-MAR-1998; 98AU-00002509.

XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.

PA (AUSU ) UNIV AUSTRALIAN NAT.

PA (GOOD-) GOODMAN FIELDER LTD.

PA (LINA-) GRP LIMAGRAIN PACIFIC PTY LTD.

XX Li Z, Morell M, Rahman S;

XX WPI; 1999-229525/19.

DR P-PSDB; AAY09004.

XX New isolated cereal plant enzyme genes used for, e.g. expression of

PT antisense sequences of granule bound synthase.

XX Claim 10; Page 87-94; 171pp; English.

XX The invention relates to a novel enzyme of starch biosynthetic pathway in  
CC a cereal plant, where the enzyme is selected from starch branching enzyme  
CC (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme  
CC (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of  
CC rice or maize. The methods and products can be used for targeting  
CC expression specifically to the endosperm of the seeds of cereal plants  
CC such as wheat or barley. They can be used for the expression of e.g.  
CC antisense sequences of granule-bound synthase (GBSS), SBE II, low mol.  
CC wt. glutenin, grain softness protein I, bacterial isomylase, bacterial  
CC glucogen synthase, and wheat high mol. wt. glutenin Bx17. They can be  
CC used for modifying the characteristics of starch produced by a plant. The  
CC present sequence represents the wheat SSS I gene sequence. (Updated on 17  
CC -OCT-2003 to standardise OS field)

SQ Sequence 10336 BP; 2733 A; 2055 C; 2625 G; 2921 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	4.68e-124	Length:	10336
Score:	1280.00	Matches:	346
Percent Similarity:	29.2%	Conservative:	19
Best Local Similarity:	27.7%	Mismatches:	20
Query Match:	44.2%	Indels:	864
DB:	2	Gaps:	9

US-10-628-525A-21 (1-539) x AAX34652 (1-10336)

QY	12	LeuGluProGluGlyIleAlaGluGlySerIleAspAsnThrValValValAlaSerGlu	31
DB	1463	TTGCAACCA---GGGATTCTGAGGATTCATCGACAGCATATATCTGGCTGCAAGTAG	1519
QY	32	GlnAspSerGluIleValValGlyLyysGluGlnAlaAraGAlaLyysValThrGlnSerIle	51
DB	1520	CAGGATTCAGATCATGGATGGAATGAGCAACCTCAAGCTAAAGTTACACGTAGCATC	1579
QY	52	ValPheValThrGlyGluAlaSerProTyrAlaLyysSerGlyGlyLeuGlyAspValCys	71
DB	1580	GTGTTTGTGACTGGTGAAGCTGCTCCTATGCAAAAGTCAGGGGGGCTGGAGATGTTGT	1639
QY	72	GlySerLeuProValAlaLeuAlaAraGlyHisGluValMetValValMetProAsnG	91
DB	1640	GGTTGTTTACCAATGCTCTGCTGCTGTCACCGTGTGATGTTGATGTTGATGCCAAGA	1699
QY	92	TyrLeuAsnGlyThrSerAspLyysAsnTyrAlaAsnAlaPheTyrThrGluLyHisIle	111
DB	1700	TACTTGAATGGGTCTCTGATTAATAACTATGCAAGGCATTTACACTGCGAAGCACATT	1759
QY	112	ArgIleProCysPheGlyGlyHisGluValThrPhePheHisGluTyrArgAspSer	131
DB	1760	AAGATTCCATGCTTTGGGGGATCACATGAAGTGACCTTTTTTCATGAGTATAGAGACAAC	1819
QY	132	ValAspTyr-----	134
DB	1820	GTGCAATGGGTGGGTACACAATCACCTTCTTATTCTCTGTTGAAATGTAGCAACTGTTTA	1879
QY	134	-----	134
DB	1880	TCCTTGTTTACACTTCTTTTAGCCCTGCAAGACATATGTGATTTCCATACTTTTTTGT	1939
QY	134	-----	134
DB	1940	ATTTCCCTTGTACTCTTGCTCATGAAGGTCAAAATATCATATATCCATGGAAGTCATGCA	1999
QY	134	-----	134
DB	2000	TGTGCTAGTATTTTGGTGTGGTGCCTTTAACTTTCAAGGATTAATACGTGGAATTTG	2059
QY	134	-----	134
DB	2060	ATAACTAAAGTTTATTTATTGAAAAAAATTTAGTGTGGTGAGCCACAGCCACGACGT	2119
QY	134	-----	134
DB	2120	GGCACCACTGCTTGCACATGATTTTGCAATTTCTGTTTGCACCGACATTCATGTGAATA	2179
QY	134	-----	134
DB	2180	AGGTGTAAATCATAAAGTACCATTTTATTCTGCCAATTTGCACCTTAAGAGTATATACAT	2239
QY	134	-----	134
DB	2240	TTATCTTGCCCTCAATCATGGGAGTACTGTGCAATTCAGTGCCACCATCATTTGTTCTAAGGA	2299
QY	134	-----	134
DB	2300	GAAAATGTGGGTGCAAGGAAGACACTTTTGTCCCTTAATAAAAGGAGGCACTCTGTTGT	2359
QY	134	-----	134
DB	2360	CATATAGTAGAAAGCAACAACACTTATTTCAAAGAGCTAACAAATGCAAAAGAACCAAA	2419
QY	134	-----	134
DB	2420	AAAGCATGCTAAGGGGTGCACACAAAGGTGAGGGGGGCTTTGTGACTGACAGCACCCCC	2479
QY	134	-----	134
DB	2480	AAACTATTGCCATTTGTTTACTTAATAATGAAGATCATTTTGAAGCTCTCAGGAACCTTCGAA	2539
QY	134	-----	134

Db 2540 AACAGTGGCTTTCCGTCCACAGATCGTCTGTAAATATTTTGTCCAGTGATACATTTTTTT 2599  
Qy 134 ----- 134  
Db 2600 GCTCCTTACAAGAGTGCTATGTTGACATATACATTGTTAAGTTGTTCAATAAGTTTACTT 2659  
Qy 134 ----- 134  
Db 2660 CTTATTCTAAACAGCAAGTGCTTAATGCTTGCAATTTATTGCTATTATTTTATTCT 2719  
Qy 135 ----- ValPheValAspHisProSerTyrHisArgProGlu 146  
Db 2720 CATTTCAATCAACTTTTGTGTCAGGTGTTGTGCGATCATCCGTCATATCATAGACCAGG 2779  
Qy 146 YAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsn----- 159  
Db 2780 AAGTTTATATGGAGATAATTTTGGTGCTTTTGGTGATAATCAGGTACACTACACTATACT 2839  
Qy 159 ----- 159  
Db 2840 AAGCTCCTAGTTGACTAAGTCGTAAAGTTGTACTCTCTCGCTGACCGGCTGCTATGTGC 2899  
Qy 160 --GlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuLeuGluL 179  
Db 2900 TGGAGGATATATTATGGACAGAAATTCATGTTTGTGTGACGAGGCCCACTAATCCTTGAAT 2959  
Qy 179 euGlyGlyTyrIleTyrGlyLysMetPheValValAsnAspTyrHisAlaSerL 199  
Db 2960 TGGAGGATATATTATGGACAGAAATTCATGTTTGTGTGACGAGGCCCACTAATCCTTGAAT 3019  
Qy 199 euValProVal----- 202  
Db 3020 TTGTGCCAGT-GTACGTTGTTTGGGATCTGAAAGTCCAATCCTTTATTCTCTCTGCT 3078  
Qy 202 ----- 202  
Db 3079 TTGCAGTGTCCCATGCTACATTTCTTTTATGCTTTTTCATGTCGTCTTATATGTC 3138  
Qy 202 ----- 202  
Db 3139 ATATATGCTTATGGAGTCTAAAGTTACCGAGGGGAATACTCTTAAGGATTTCTCTCAAT 3198  
Qy 202 ----- 202  
Db 3199 CAATTATCTTTAGCTTTAGTTAAATTTACTGTGTGGCAACATAATATGTTTTCAGATTTA 3258  
Qy 202 ----- 202  
Db 3259 CAAGTTCAGAGATTGCATTTCACTAGTTGCTAGCTAATCTGATGTTTTTCCCGAGAAAT 3318  
Qy 202 ----- 202  
Db 3319 GCCTAAAGCTTTGTGCTTGATGCAATGTATGAGAAAAGAGTTTATGTACACTCCCAAGA 3378  
Qy 202 ----- 202  
Db 3379 GGGGACCCAAAATTACAAACACACACCCCTGAGAACTAGGCGCTGCGGAAGAAGCGATG 3438  
Qy 202 ----- 202  
Db 3439 CAAGCCCCACTGCCCTTGCCTTATAGCTCAAAAGCCGGGCGTCAGCTTGATGTGTCAAGTAA 3498  
Qy 202 ----- 202  
Db 3499 GCTAGCAGTCTAGATTGCGCAAGTGCATTCGTCGAGATGACAGTGTGGCGCTGCTTC 3558  
Qy 202 ----- 202  
Db 3559 CAAATCCACCAACTATGAGCATGATCACTGGAGAGTACCTTTTCTCGGGGTGAGGGG 3618  
Qy 202 ----- 202

Db 3619 GTGGACTGGTGGTCTGCTGCTGCCAGTTTTTCAGATAATCTGAATAATGCAATGTTTTGATG 3678  
Qy 202 ----- 202  
Db 3679 ATTTTAGTATCTTGGCGGACCTGGGTACCACTAAGCTTTTCCACACAGTAATTTGCACTTA 3738  
Qy 202 ----- 202  
Db 3739 CACCTATAAAAGTAAACGGTCAATGATATGATGTTGTTGGGTAGATCATGGTGATGCAT 3798  
Qy 202 ----- 202  
Db 3799 TTTAGGAATTAGACATGCCAGAACCCAGTGAAGCTTANCGGGCAATTTCAATTTGTTCCAT 3858  
Qy 202 ----- 202  
Db 3859 TATACGAGTCATGAATATGGTTTCAGCATGTTTGGACGCTACTTGTGTTGGGGCAATTTTCAG 3918  
Qy 202 ----- 202  
Db 3919 ATGGTGAATTTAGTCTGCTTGATGTTGGCTAGCTGGCTTATTTTGTACAAATATCGATGT 3978  
Qy 202 ----- 202  
Db 3979 TAGATGCATATTTCCCTTTTGTCTTGTGCTGTTTGGCAATGTTGTAATTCCTTTCCTGTC 4038  
Qy 202 ----- 202  
Db 4039 GCCAGTGTTCATGTTAAATGGTTTTCATTACATAATCAACTTTGTTGCTGACATCAGT 4098  
Qy 203 ----- LeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerA 218  
Db 4099 CATTTTATTTACGCTTCTGCTGCAAAATATAGACATACGCGTGTTTACAGAGATTTCCC 4158  
Qy 218 rGSerIleLeuValIleHisAsnLeuAlaHisGln----- 229  
Db 4159 GCAGCACCCCTTTGTATACATAATTTAGCACATCAGGTTTGGGCTATCACCTTTTCATTAT 4218  
Qy 229 ----- 229  
Db 4219 CCGTACATGGCTTTGTAAGTCGGTTCCACAGTATCGTACATCTGTATGTTATTTTCAATGT 4278  
Qy 230 ----- GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyr 247  
Db 4279 CATTAGGGTGTGGAGCTGCAAGTACATATCTCTGATCTGGGATGTCACCTGTAATGTAAT 4338  
Qy 248 GlyAlaLeuGluTyrValPheProGluTyrAlaArgHisAlaLeuAspLysGlyGlu 267  
Db 4339 GGAGCTTTTGAATGGGTATTTCCAGAAATGGGCAAGGAGCATGCCCTTGCACAAAGGGTGAG 4398  
Qy 268 AlaValAsnPheLeuLysGlyAlaValThrAlaAspArgIleValThrValSerLys 287  
Db 4399 GCAGTTAACTTTTGAAGGAGCGATTTGTGACAGCAGATCGAATTTGACCGTCAGTCAG 4458  
Qy 287 ----- 287  
Db 4459 GTGAATACTCAATACTCTCTTTTCTTTGGGGATGTTCTTCAGTTCAATTTGCCCTG 4518  
Qy 288 ----- GlyTyrSerTyrGluVal 293  
Db 4519 TCTTTCCCAATTAAGAATGATTAATCTTTTGTGTTCTAGGGTTATTTCATGGGAGGTC 4578  
Qy 294 ThrThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeu 313  
Db 4579 ACNACTGCTGAAGTGGACAGGGCCTCAATGAGCTCTTAAGCTCCCGAAAAAGTGTATTG 4638  
Qy 314 Asn----- 314  
Db 4639 AATGGTAACTATATTTGAATCCACTTATCTTCTTGAAACATATTTTACAGAAATAGATG 4698  
Qy 315 ----- GlyIleValHisGlyIle 320  
Db 4699 GATGGGTTCAGAAATAAATTCAGTTTGTCTTTCGGTATGAAGGAATTTGTAATGGAAT 4758

QY 320 eAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTrpSerValAs 340  
 DB 4759 TGACATTATGATTGGAACCCACACACAGAGTGTCTCCCTCATCATATTTCTGCGA 4818  
 QY 340 pAspLeuSerGlyLys----- 345  
 DB 4819 TGACCTCTCTGGAAAGGTGTGGATAGTACCCTATATATAAATACATGTATATCTGATCTA 4878  
 QY 345 ----- 345  
 DB 4879 GTACTTTCTTTTCTTTGCTAGTTGCTTCCCATGATGTTCTCACTAAATCTCTATGT 4938  
 QY 346 -----AlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuPr 359  
 DB 4939 GGTGGTCATCTGTTCAGCCCAATGTAAAGCTGAATTCAGAGGAGCTGGTTTACC 4998  
 QY 359 oIleArgProAspValProLeu----- 366  
 DB 4999 TGTAAAGGAGGATGTTCTCTGTTAGATACAAACCCCTAAGATATATATTTTAAATC 5058  
 QY 367 -----IleGlyPheIleGlyAr 372  
 DB 5059 CTTAAAAAAACTTGCAGATCATCTCATTTAGCTTGATTCACAGATTGGCTTTATTGGAAG 5118  
 QY 372 gLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgG 392  
 DB 5119 ACTGGATTACCAAGAAAGGCAATGATCTCAATTAATGGCCATTCAGAGCTCATGAGGA 5178  
 QY 392 uAspValGlnPheVal 397  
 DB 5179 GGACGTGCAGTTGTA 5194  
 RESULT 27  
 ADX13652  
 ID ADX13652 standard; cDNA; 1860 BP.  
 XX  
 AC ADX13652;  
 DT 21-APR-2005 (first entry)  
 DE Plant full length insert polynucleotide seqid 8227.  
 KW plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomannan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 KW protein content; gene; ss.  
 XX  
 OS Unidentified.  
 XX  
 FN US2004034888-A1.  
 PD 19-FEB-2004.  
 PF 28-APR-2003; 2003US-00425114.  
 PR 06-MAY-1999; 99US-00304517.  
 PR 05-NOV-2001; 2001US-00985678.  
 XX (LIU//) LIU J.  
 PA (ZHOU//) ZHOU Y.  
 PA (KOVA//) KOVALIC D K.  
 PA (SCRE//) SCREEN S E.  
 PA (TAB//) TABASKA J E.  
 PA (CAO//) CAO Y.  
 XX  
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 DR WPI; 2004-180133/17.

XX  
 PT New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.  
 XX  
 PS Claim 1; SEQ ID NO 8227; 15pp; English.  
 XX  
 CC The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This sequence represents a plant full length insert  
 CC polynucleotide that can be used in the recombinant DNA construct of the  
 CC invention.  
 XX  
 SQ Sequence 1860 BP; 529 A; 337 C; 481 G; 513 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 7,51e-115 Length: 1860  
 Score: 1183.00 Matches: 264  
 Percent Similarity: 62.2% Conservative: 67  
 Best Local Similarity: 49.6% Mismatches: 167  
 Query Match: 40.9% Indels: 36  
 DB: 13 Gaps: 11  
 US-10-628-525A-21 (1-539) x ADX13652 (1-1860)  
 QY 15 GluGlyIleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSer 34  
 DB 31 GAAGCTTTGAGTGAATCAAGT-----ACAAAGGAGGTGTGTAATGAAGCCGACAA 81  
 QY 35 GluIleValValGlyLysGluGln-----AlaArgAlaLysValThrGlnSerIle 51  
 DB 82 GTGGAGAGTAAAGGTGAACACCCACCCTGGTGGTGGGCCCAATGTC---ATGATATGTC 138  
 QY 52 ValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLysGlyLeuGlyAspValCys 71  
 DB 139 ATATTGGTTGCAGCAGAAATGTCTCCCTCGTCAAAACAGAGTGTCTTGGAGATGTTGCT 198  
 QY 72 GlySerLeuProValAlaLeuAlaArgGlyHisArgValMetValValMetProArg 91  
 DB 199 GGATCATTTACCTAAGGCTTTGGCTAGCGGTGGACACAGAGTTATGGTTGTAGTACCTCGG 258  
 QY 92 TyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIle 111  
 DB 259 TAT-----AGTCATTATGCTGACGACAGATATAGGATATGGAAA 300  
 QY 112 ArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlyTyrArgAspSer 131  
 DB 301 CGATACAAAGTAGATGTCAGGACATGGAAGTAACATATTTCCACTCTTATATTGATGCT 360  
 QY 132 ValAspTrpValPheValAspHisProSerTyr---HisArgProGlyAsnLeuTyrGly 150  
 DB 361 GTTGACTTCGTTTTTATTGACAGATCTTAAACCCATGCTGCTGTTTGTGCAAGCAGCT 420  
 QY 151 AspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAla 170  
 DB 421 -----GGNAACCGAGAGGATATTCTAAACCCATGCTGCTGTTTGTGCAAGCAGCT 471  
 QY 171 CysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGln---AsnCysMet 189



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Db 472 GCTGAGGTTCTTGGCATGTTCTTGGTGGAGTTGCTATGAGATGGAAATTTGGCC 531
Qy 190 PheValValAenAspTrpHisAlaSerLeuValProValLeuLeuAlaLysTyArg 209
Db 532 TTTCATCGCAATGATGCGTACTGCTTGGTGGCAGTGTATCTGAAAGCATATATCGT 591
Qy 210 ProTyGlyValTyLysAspSerArgSerIleLeuValIleHisAenLeuAlaHisGln 229
Db 592 GACCATGGTTTAAATGAAGTACACAGATCTGTTCTTGGATTTACATACAGCACACAG 651
Qy 230 GlyValGluProAlaSerThrTyProAspLeuGlyLeuProGluTyProGlyAla 249
Db 652 GGACGGGGCCCATGATGATTTCCGCTACACAGATTTACTTGACACATACATAGACCTT 711
Qy 250 LeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGlyGluAlaVal 269
Db 712 TTCAATATATATGACCGGTT-----GGAGGTGAGCACTTC 747
Qy 270 AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTy 289
Db 748 AATATCTTTTGGCTGGTTTAAAGGCAGCTGACCGGATTTGCTGTGAGTCAATGATAT 807
Qy 290 SerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAenGluLeuLeuSerSerArg 309
Db 808 GCATGGGAGATTAACACTTCTGAAGTGGTGGGTTTGATGGGATCAATAATGAGAAAT 867
Qy 310 LysSerValLeuAenGlyIleValAsnGlyIleAspIleAenAspTrpAsnProAlaThr 329
Db 868 GACTGGAAATTTGAGAGAAATTTGAATGAATTGACACCAAGATTTGGAACCCCAAGATT 927
Qy 330 AspLysCysIlePro-----CysHisTySerValAspLeu----SerGly 344
Db 928 GATGTTCACTTGAATCAGATGATACACTAACTACACCTTGAGACCCCTGCAAGTGGC 987
Qy 345 LysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspVal 364
Db 988 AAGCTCAGTGCAAAGCGCTTGCMAAGAGAGCTCGTTGCTGTCCTGAGAGATT 1047
Qy 365 ProLeuIleGlyPheIleGlyArgLeuAspTyrgLysGlyIleAspLeuIleGlnLeu 384
Db 1048 CCGTTACTTGAATTCATGGAAGCTGATCAACAGAAAGGCATTGATCTCATAGCCGAA 1107
Qy 385 IleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspPro 404
Db 1108 GCAATTCCTTGGATAGTGGCCAGGATGTCACACTAGTCTATGTTGGAACTGGAAGCCG 1167
Qy 405 GluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrp 424
Db 1168 GACTTAGAGATATGCTTAGGCAGTTTGAATCCACACCGTGACAAAGTCAGAGGATGG 1227
Qy 425 ValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMet 444
Db 1228 GTTGGCTTTTCGCTCAAGATGCTCACCAGTAACAGCAGGTGCAGACATATTTGCTGATG 1287
Qy 445 ProSerArgPheGluProCysGlyLeuAenGlnLeuTyAlaMetGlnTyThrVal 464
Db 1288 CCATCAAGATTTGAGCCATGTTGAATGAATCAACTCTATGCCATGAATTACGGAACAATT 1347
Qy 465 ProValValHisAlaThrGlyGlyLeuArgAspThrValGluAenPheAenProPheGly 484
Db 1348 CCAATTTGATACATCTGCTGCTGATGATGAGGATACAGTGAAGCTTTTATCAATTGAA 1407
Qy 485 GluAenGlyGluGlnGlyThrGlyTyTrpAlaPheAlaProLeuThrThrGluAenMetPhe 504
Db 1408 GAGTCG-----GGCCTTGGTGGACATTTGACAGTGCAGAACTAACAAGTTAATA 1458
Qy 505 ValAspIleAlaAenCysAenIleTyIleGlnGlyThrGlnValLeuLeuGlyArgAla 524
Db 1459 AATGCATATAGGAACACTGCTT-GTTGACCTTCAGGCAGTATTAAGCAGAGCTGGGAGGCT 1517
Qy 525 AsnGluAlaArgHisValLysArgLeuHisValGly 536
Db 1518 CCNACCGCGAGGATGA-CGCAGGATCTTAGTTGGG 1552
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RESULT 28
AAV29755
ID AAV29755 standard; DNA; 2097 BP.
XX
XX
AC AAV29755;
XX
XX 11-SEP-1998 (first entry)
XX
XX Zea mays soluble starch synthase IIb gene.
XX
XX SSR; starch-encapsulating region; fusion vector;
XX soluble starch synthase IIb; glucosyl transferase; ss.
XX
XX Zea mays.
XX
XX Key Location/Qualifiers
XX CDS 1..2097
XX /tag= a
XX /product= "soluble starch synthase IIb"
XX
XX WO9814601-A1.
XX
XX 03-APR-1998.
XX
XX 30-SEP-1997; 97WO-US017555.
XX
XX 30-SEP-1996; 96US-0026855P.
XX
XX (EXSE-) EXSEED GENETICS LLC.
XX
XX Keeling P, Guan H;
XX
XX WPI; 1998-240100/21.
XX P-PSDB; AAW56487.
XX
XX Hybrid polypeptide comprising starch-encapsulating region and protein -
XX useful for, e.g. producing protein(s) resistant to degradation by stomach
XX acids.
XX
XX Example 2; Page 36-38; 156pp; English.
XX
XX The sequence is that of the soluble starch synthase IIb gene. It can be
XX used in the production of a hybrid polypeptide comprising a starch-
XX encapsulating region (SER) fused to a payload protein. The hybrid
XX polypeptide can be used to make modified starches comprising the payload
XX protein, selected from, e.g. hormones, growth factors, antibodies,
XX enzymes, dyes, immunoglobulins, etc. The modified starch can also be used
XX to provide grain feeds enriched in amino acids. By encapsulating the
XX payload protein in starch, it is more resistant to degradation by stomach
XX acids
XX
XX Sequence 2097 BP; 409 A; 575 C; 696 G; 417 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,32e-109 Length: 2097
Score: 1130.50 Matches: 254
Percent Similarity: 57.2% Conservative: 64
Best Local Similarity: 45.7% Mismatches: 159
Query Match: 39.1% Indels: 80
DB: 2 Gaps: 11

US-10-628-525A-21 (1-539) x AAV29755 (1-2097)
Qy 3 AlaGluLeuSerArgGluAspLeuGlyLeuProGluGlyIleAlaGluGlySerIle 22
Db 565 GCTCCTTATGACAGGAGGAT-----AATGAACCTGGCCCTTGGCTGGCCCTAATGTG 618
Qy 23 AspAenThrValValValAlaSerGluGlnAspSerGluIleValValGlyLysGluGln 42
Db 619 ATGACGCTGCTGCTGGTGGCTTCT----- 642
Qy 43 AlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyAla 62
```





XX Non-glycogen-like polysaccharide production; fermentation;  
 KW starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis;  
 KW non-starch branching gene; amylopectin; amylose; plant-like starch;  
 KW maize starch soluble synthase IIB; ss.  
 XX  
 OS Zea mays.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 1632  
 FT /tag= a  
 FT /note= "this base represents a nucleotide missing from  
 FT the sequence given in the specification. It is included  
 FT to maintain the nucleotide numbering given in the  
 FT specification for this sequence"  
 XX  
 PN W09844780-A1.  
 XX  
 PD 15-OCT-1998.  
 XX  
 PP 03-APR-1998; 98WO-US006660.  
 XX  
 PR 04-APR-1997; 97US-0042939P.  
 XX  
 PA (EXSE-) EXSEED GENETICS LLC.  
 XX  
 PI Guan H, Keeling PL;  
 XX  
 XX WPI; 1998-568285/48.  
 DR P-PSDB; AAW70892.  
 XX  
 PT Producing non-glycogen-like polysaccharides in bacteria, fungi or plants  
 PT -transformed with genes for enzymes involved in starch or glycogen  
 PT synthesis allows fermentative production of starches with engineered  
 PT properties.  
 XX  
 PS Disclosure; Fig 50; 150pp; English.  
 XX  
 CC The specification describes a method for the production of non-glycogen-  
 CC like polysaccharides in a host. The method comprises transforming a host,  
 CC suitable for fermentation, with genes encoding starch- or glycogen-  
 CC synthesis enzymes, and fermenting the transformants. The specification  
 CC also describes hosts transformed with a gene active in glycogen synthesis  
 CC and at least one non-starch branching gene, involved in production of  
 CC amylopectin or amylose in its original host. The method is used to  
 CC produce plant-like starches by fermentation and new starches in plants.  
 CC These starches are useful for all food and non-food applications of  
 CC starch. The present sequence is used in the course of the invention  
 XX  
 SQ Sequence 2423 BP; 466 A; 656 C; 804 G; 496 T; 0 U; 1 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 1.39e-108 Length: 2423  
 Score: 1125.50 Matches: 253  
 Percent Similarity: 57.0% Conservative: 64  
 Best Local Similarity: 45.5% Mismatches: 160  
 Query Match: 38.9% Indels: 80  
 DB: 2 Gaps: 11  
 US-10-628-525A-21 (1-539) x AAV70958 (1-2423)  
 QY 3 AlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyLeuAlaGluGlySerIle 22  
 DB 565 GCTCTTATGACAGGAGAT-----AATGAACCTGGCCCTTTGGCTGGGCTCATATG 618  
 QY 23 AspAsnThrValValAlaSerGluGlnAspSerGluIleValValGlyLeuGluGln 42  
 DB 619 ATGAAGCTGCTGCTGCTCTCT----- 642  
 QY 43 AlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAla 62  
 DB 643 -----GAATGTCCTCTTCTGC 660

63 LysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAaArgGly 82  
 DB 661 AAGACAGGTGGCTTGGAGATGTCTGGGTGCTTTTGCCTAAGCTCTGCGGAGGAGGA 720  
 QY 83 HisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAla 102  
 DB 721 CACCGTGTATGTCGTGATACCAAGATAT-----GGAGAGTATGCC 762  
 QY 103 AsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluVal 122  
 DB 763 GAAGCCCGGATTTAGGTGTAAGGAGACGTTACAAGGTAGCTGGACAGATTCAGAAGTT 822  
 QY 123 ThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSerTyr 142  
 DB 823 ACTTATTTTCACTCTTACATTGATGAGTTGATTTGATTCGTAGAACCCCTCCCTTC 882  
 QY 143 ---HisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161  
 DB 883 CGGCACCGGCACATAATATTATGG-----GGAGAAAGATTGGATATTTGAAG 933  
 QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluGlyGly 181  
 DB 934 CGCATGATTTTGTCTCAAGGCCGCTGTGTAGGTTCATCGTATGCTCCATGTGCGGT 993  
 QY 182 TyrIleTyrGlyGln---AsnCysMetPheValValAsnAspTyrPheHisAlaSerLeuVal 200  
 DB 994 ACTGTCATGTGTGATGGCACTTAGTTTCATGTCATGATGTCATACCGCACTTCG 1053  
 QY 201 ProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
 DB 1054 CTGTCTATCTAAAGCCCTATTACCGGACAAATGTTGATCGAGTATGCTCGTCTGTG 1113  
 QY 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240  
 DB 1114 CTTGTGATACACAACTTCTCATCAGGTCGTGGCCCTGTAGACACTTCGCAATTT 1173  
 QY 241 GlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArg 260  
 DB 1174 GACTTGCCT-----GAA 1185  
 QY 261 HisAlaLeuAspLys-----GlyGluAlaValAsnPheLeu 272  
 DB 1186 CACTACATCGACCACTCAAACGTATGACAACTTGGTGGGATCACAGCAACGTTTTT 1245  
 QY 273 LysGlyAlaValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGlu 292  
 DB 1246 GCTGCGGGCTGAAGACGCGAGACCGGTGTGACCGTTAGCAATGGCTACATGTGGAG 1305  
 QY 293 ValThrThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerVal 312  
 DB 1306 CTGAAGACTTCGAAGGGGGTGGGCTTCCACGACATCATTAACCAAGCAACACTGGAAG 1365  
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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 15:18:57 ; Search time 8692.03 Seconds  
(without alignments)  
2901.306 Million cell updates/sec

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Zgapop 6.0 , Zgapext 7.0  
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Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

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Result No.	Score	Query Match %	Length	ID	Description
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3	1558	53.9	877	6	CD435568
4	1424	49.2	815	7	CN147393
5	1266.5	43.8	933	6	CA252614
6	1264.5	43.7	835	7	CO457819
7	1235	42.7	769	7	CK123179
SUMMARIES					
1	1910	66.0	2287	4	CNS09YPE
2	1858	64.2	1530	4	AY104834
3	1558	53.9	877	6	CD435568
4	1424	49.2	815	7	CN147393
5	1266.5	43.8	933	6	CA252614
6	1264.5	43.7	835	7	CO457819
7	1235	42.7	769	7	CK123179

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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VERSION	BX832183.1	GI:42450507			
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REFERENCE	Castelli, V., Aury, J.M., Jallou, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, P., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.				
AUTHORS	Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation				
TITLE	Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
JOURNAL	The sequences are based on single pass reads.				
AUTHORS	Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G				
TITLE	Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jallou O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.				
JOURNAL	URG INRA : Clepet C., Caboche M.				
COMMENT	Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.				
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ORIGIN					
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Query Match:	66.0%	Indels:	6		
DB:	4	Gaps:	3		
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Db 1724 GCCGGCTGTGACATTTCTCTCATGCCGTCGAGATTCGAGCCCTGTGGTTTAAATCAGTCT 1783
Qy 456 uTyrAlaMetGlnTyrGlyThrValProValVal-HisAlaThrGlyGlyLeuArgAspT 476
Db 1784 ATAGCGAATAGATAGCAACCAATTCAGTTGTTCATGGCACTGGAGGACTCAGAGATA 1843
Qy 476 hrValGluAsnPheAsnProPheGlyGluAsnGlyGlu---GlnGlyThrGlyTyrAlaP 495
Db 1844 CGGTTGAGAATTTCAACCCCTTATCGAGAGGTGAGCTGGTACTGGTACAGSGTGGTCT 1903
Qy 495 heAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleG 515
Db 1904 TCATCTCCCTTGTGAAAGATAGCATGCTCTCGCCCTTGGAGTTGGCTGCAGCAAC-GTAC 1962
Qy 515 lncGlyThrGlnValLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisV 535
Db 1963 AGAGAGTATTAACAGTCATGGGAAGGATTCATGAGAAGAAATGACCCGAAACTACTCT 2022
Qy 535 alGlyPro---CysArg 539
Db 2023 TGGGAAACCGCTGCCGT 2039

RESULT 2
AY104834 1530 bp mRNA linear HTC 18-FEB-2005
DEFINITION Zea mays PC0152066 mRNA sequence.
ACCESSION AY104834
VERSION AY104834.1 GI:21207912
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
1 (bases 1 to 1530)
Gardiner, J., Schroeder, S., Polacco, M.L., Sanchez-Villeda, H.,
Fang, Z., Morgante, M., Landewe, T., Fongler, K., Ueche, F.,
Hanafey, M., Tingey, S., Chou, H., Wing, R., Soderlund, C. and Coe, E.H.
Jr.
TITLE Anchoring 9,371 maize expressed sequence tagged unigenes to the
bacterial artificial chromosome contig map by two-dimensional
overgo hybridization
JOURNAL Plant Physiol. 134 (4), 1317-1326 (2004)
PUBMED 15020742
REFERENCE 2 (bases 1 to 1530)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 3 (bases 1 to 1530)
Coe, E.H.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
FEATURES Location/Qualifiers
source 1. 1530
/mol_type="mRNA"
/db_xref="MaizeGDB:638880"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Corneaus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
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contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Alignment Scores:  
Pred. No.: 1,42e-202 Length: 1530  
Score: 1858.00 Matches: 350  
Percent Similarity: 99.7% Conservatives: 0  
Best Local Similarity: 99.7% Mismatches: 1  
Query Match: 64.2% Indels: 1  
DB: 4 Gaps: 0

US-10-628-525A-21 (1-539) x AY104834 (1-1530)

QY 189 MetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyr 208  
DB 41 ATGTTTGTGTCAATGATTGGCATGCCAGTCTAGTGCCAGTCTTCTTCTGTCGCAAAATAT 100  
QY 209 ArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHis 228  
DB 101 AGACCATATGGTGTATTAAGACTCCCGACGACATTTCTTGAATCATTAATTAGCAT 160  
QY 229 GlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGly 248  
DB 161 CAGGGGTAGAGCGCTGCAAGCACATATCTGACCTTGGGTGGCCACTGAATGATGCA 220  
QY 249 AlaLeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeuAspLysGlyGluAla 268  
DB 221 GCTCTGGAGTGGTATTCCTGAATGGCGAGGAGCATGCCCTTGACAAAGGTCGAGCA 280  
QY 269 ValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGly 288  
DB 281 GTTAATTTTGAAGGTGAGTTGTGACAGACATCGAATCGTACTGTCAAGTAAAGGT 340  
QY 289 TyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSer 308  
DB 341 TATTTCAGGAGGTGACAACTGCTGAAGGTGGACAGGGCTCAATGAGCTCTTAAGCTCC 400  
QY 309 ArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAla 328  
DB 401 AGAAAGAGTGTATTAACCGAATTTGAAATGGAATTGACATTAATGATGGAACCTGTC 460  
QY 329 ThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCys 348  
DB 461 ACAGACAAATGATATCCCTGTCTATTCTGTGTGACCTCTCTGGAAGGCCAAATGT 520  
QY 349 LysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGly 368  
DB 521 AAAGGTGCAATTCAGAGGAGCTGGGTTTACCTATAAGGCGCTGATGTTCTCTGATTGGC 580  
QY 369 PheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProAsp 388  
DB 581 TTTATTGGAAGATTGGATTATCAGAAAGCATTTGATCTCAATCACTTATCATCAGAT 640  
QY 389 LeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAsp 408  
DB 641 CTCATGCGGGAAGATGTTCAATTTGATCTGTGGATCTGGTGACCAAGCTTGAAGAT 700  
QY 409 TrpMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPheSer 428  
DB 701 TGGATGAGATCTACAGAGTCGATCTTCAAGGATAAATTTTCGTGGATGGGTTGATTTAGT 760  
QY 429 ValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPhe 448  
DB 761 GTTCCAGTTTCCACCGCAATAATCTCCGGTTCGATATATTTGATGCAATCCAGATTC 820  
QY 449 GluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHis 468  
DB 821 GAACCTTGGTCTCATCATGCTATATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 880  
QY 469 AlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGlu 488

DB 881 GCAACTGCTGGGGCTTAGAGATACCGTGGAGAACTTCAACCCCTTCGTTGAGATGAGAG 940  
QY 489 GlnGlyThrGlyTyrAlaPheAlaProLeuThrGluAsnMetPheValAspIleAla 508  
DB 941 CAGGGTACAGGGTGGGCATTTCCACCCCTTAACACAGAAAACATGTT-GTGGACATTGGC 999  
QY 509 AsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArg 528  
DB 1000 AACTGCATATCTATCATCAGGGAACACAAAGTCTCTCTGGGAAGGCTTAATGAAGCAGG 1059  
QY 529 HisValLysArgLeuHisValGlyProCysArg 539  
DB 1060 CATGTCNAAAGACTTTCAGTGGGACCATGCCGC 1092

RESULT 3  
LOCUS CD435568 877 bp mRNA linear EST 03-JUN-2003  
DEFINITION ELO1N0362G08.b Endosperm\_3 Zea mays cDNA, mRNA sequence.  
ACCESSION CD435568  
VERSION CD435568.1 GI:31351211  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE  
AUTHORS Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F., Larkin, B., Bera, P. and Messing, J.  
TITLE Characterization of the maize endosperm transcriptome and its comparison to the rice genome  
JOURNAL Genome Res. 14 (10), 1932-1937 (2004)  
PUBMED 15466231  
COMMENT Contact: Lai, Jinsheng  
Dr. Joachim Messing's Lab  
Wakman Institute, Rutgers University  
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA  
Tel: 732-445-3801  
Fax: 732-445-5735  
Email: jlai@waksman.rutgers.edu  
Seq primer: T3.  
Location/Qualifiers  
1. 877  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="W22"  
/db\_xref="taxon:4577"  
/tissue\_type="Endosperm of 7-23DAP"  
/clone\_lib="Endosperm 3"  
/note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN  
Alignment Scores:  
Pred. No.: 2,4e-168 Length: 877  
Score: 1558.00 Matches: 287  
Percent Similarity: 99.3% Conservatives: 1  
Best Local Similarity: 99.0% Mismatches: 1  
Query Match: 53.9% Indels: 1  
DB: 6 Gaps: 0

US-10-628-525A-21 (1-539) x CD435568 (1-877)

QY 101 TyrAlaAsnAlaPheTyrThrGluLysHisIleArgIle-ProCysPheGlyGlyGluHi 120  
DB 9 TATGCAAAATGCAATTTTACACAGAAAACACATTCGATCTCCATGCTTTGGCGGTGAACA 68  
QY 120 sGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisPr 140  
DB 69 TGAAGTTACCTTCTTCCATGAGTATAGAGATTCAAGTTCAGTGGGTGTTTGTGATCATCC 128  
QY 140 oSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGl 160

```

Db      129 CTCAATACAGAGACTGGAATTTATATGGAGATAAGTTGGTCTTTTGGTGATAATCA 188
Qy      160 nPheArgTyrThrLeuLeuCyStyTyrAlaAlaCysGluAlaProLeuLeuLeuGlu 180
Db      189 GTTCAGATACACACTCCCTTGTCTATGCTGTCATGTGAGGCTCCTTTGGTCTTGAATGGG 248
Qy      180 yGlyTyrIleTyrGlyGlnAanCysMetPheValValAlaAsnAspTrpHisAlaSerLeuVa 200
Db      249 AGGATATATTTATGGACAGAAATGTCATGTTTGTGTCAATGATGGCATGCCAGTCTAGT 308
Qy      200 lProValLeuLeuAlaAlaTyrArgProTyrGlyValTyrLysAspSerArgSerIl 220
Db      309 GCCAGTCTCTTCTGCAAAATATAGACCATATGGGTATTTATAAAGACTCCCGCAGCAT 369
Qy      220 eLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLe 240
Db      369 TCTTGTAATACATAATTTAGCACATCAGGGGTGAGAGCTGCAAGCACATATCTGACCT 428
Qy      240 uGlyLeuProProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgAr 260
Db      429 TGGGTTCGCCACCTCAATGGTATGAGCTCTGGAGTGGGTATTCCTCGAATGGCGAGGAG 488
Qy      260 qHisAlaLeuAspLysGlyGluAlaValAlaAsnPheLeuLysGlyAlaValThrAlaAs 280
Db      489 GCATGCCCTTGACAGGGTGAAGGCGATTAATTTTGAAGGTGCAATGTTGACAGCAGA 548
Qy      280 pArgIleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyG 300
Db      549 TCGAATCGTCACTGCTCAGTAAGGGTTATTATCGGAGGTGCACACTGCTGAGGTGACA 608
Qy      300 nGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIl 320
Db      609 GGGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACCGAATGTAATGGAAT 668
Qy      320 eAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAs 340
Db      669 TGACATTAATGATGGAACTCCGCACAGACAAATGATCCCTGTCAATATTCTGTGA 728
Qy      340 pAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIl 360
Db      729 TGACCTCTCTGGAAGAGCCAAATGTAAGGTGCAATGTCAGAGGAGCTGGGTTTACCTAT 788
Qy      360 eArgProAspValProLeuLeuGlyPheIleGlyArgLeuAspTyrGlnLysGlyLeAs 380
Db      789 AAGGGCTGATGTTCTCTGATGGCTTTATTTGAAGATTTGCATATCAGAAAGGCATTGA 848
Qy      380 pLeuIleGlnLeuIleProAspLeu 389
Db      849 TCTCATTAACCTTATCATACCATCTC 876

RESULT 4
LOCUS   CN147393
DEFINITION WOUND1_49 A11_g1_A002 Wounded leaves Sorghum bicolor cDNA clone
VERSION WOUND1_49 A11_A002 5', mRNA sequence.
KEYWORDS CN147393.1 GI:45987913
SOURCE EST.
ORGANISM Sorghum bicolor (sorghum)
Sorghum bicolor
Sorghum bicolor
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 815)
Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C.,
Sun, F., Sullivan, R., Brady, J., Eastman, A.A., Miller, V., Gonzalez, M.,
Anfuoso, C., Chhabra, D., Johnson, H., Kaman, D. and Pratt, L.H.
A Sorghum EST database: mechanically damaged and methyl
Jasmonate-treated leaves
Unpublished (2003)
Other ESTs: WOUND1_49 A11_b1_A002
Contact: Cordonnier-Pratt MM

```

Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1360  
Fax: 706 583 0210  
Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in  
the Human Genome Center, University of Tokyo Institute of Medical  
Science; plant material and RNA prepared at Texas A & M University;  
sequencing done in the Laboratory for Genomics and Bioinformatics,  
University of Georgia. Sequence ends have been trimmed to exclude  
vector and regions below Phred quality 16. Three-prime sequences  
are presented as their reverse complement and have been trimmed to  
exclude polyA.

Seq primer: Sug5 (CTTCTGCTCTAAAGCTGGC).

#### FEATURES

Location/Qualifiers  
1..815  
/organism="Sorghum bicolor"  
/mol\_type="mRNA"  
/cultiivar="BTx623"  
/db\_xref="taxon:4558"  
/clone="WOUND1\_49 A11\_A002"  
/lab\_host="DH10B-T1 phage-resistant E. coli"  
/clone\_lib="Wounded leaves"  
/notes="Organ: Leaf; Vector: pME18S-FL3; Site\_1: XhoI;  
Site\_2: XhoI; The library was prepared from polyA+ RNA  
harvested from 8-day-old hydroponically grown, BTx623  
sorghum seedlings. For some plants, one-half of the second  
leaf was crushed without damaging the midvein. For others,  
methyl jasmonate was added to the growth medium to a final  
concentration of 100 uM. Leaves were harvested 3 and 27 hr  
after treatment and pooled. Double-stranded cDNA was  
cloned unidirectionally into different DraIII sites of the  
pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG,  
3-prime DraIII site is CACCATGTG). XhoI excises the cDNA  
insert."

#### ORIGIN

Alignment Scores:  
Pred. No.: 6,17e-153 Length: 815  
Score: 1424.00 Matches: 266  
Percent Similarity: 98.9% Conservative: 2  
Best Local Similarity: 98.2% Mismatches: 3  
Query Match: 49.2% Indels: 0  
DB: 7 Gaps: 0

US-10-628-525A-21 (1-539) x CN147393 (1-815)

Qy 189 MetPheValValaAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyr 208  
Db 1 ATGTTTGTGTGAATGATTTGGCATGCCAGTCTAGTGCCAGTCTTCTTGTGCAAAATAT 60

Qy 209 ArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHis 228  
Db 61 AGACCATATGGGTGTTTATAAAGACTCCCGCAGCATTTCTTGTATAATATTTAGCACAT 120

Qy 229 GlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGly 248  
Db 121 CAGGGGTGAGAGCTGCTCAAGCACATATCTGACCTTGGGTGGCCACTGAATGGTATGGA 180

Qy 249 AlaLeuGluTyrValPheProGluTyrAlaArgHisAlaLeuAspLysGlyGluAla 268  
Db 181 GCTCTGGAGTGGGTATTCCTGAATGGGCAAGGAGCATGCCCTTGCAAGGCTGAGGCA 240

Qy 269 ValaAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGly 288  
Db 241 GTTAATTTTTCAGAAAGGTGCAATGTTGACAGCAGATCGAATTTGTGACTGCTAGTAAGGT 300

Qy 289 TyrSerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSer 308  
Db 301 TATTCAATGGAGGTCACTGCTGAGGTGACAGGGTCTCATGAGCTCTTAAGCTCC 360

Qy 309 ArgLysSerValLeuAsnGlyIleValaAsnGlyIleAspIleAsnAspTrpAsnProAla 328

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Db      CGAAGAGTGTATTAAACGAATTGTAATGGAATTGACATTAAATGATTGGAACCTGCG 420
Qy      ThrAspLysCysIleProCysHisTyrSerValAspLeuSerGlyLysAlaLysCys 348
Db      ACGGACAAATGATCCCTTGTCTATTATCTGTGATGACCTCTCTGGAAGGCCAAATGT 480
Qy      LysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGly 368
Db      AAAAGTGCATTCGAGAGAGCTGGGTTTACCTATAGGCGCTGAAGTTCTCTGATTGT 540
Qy      PheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleProAsp 388
Db      TTTATTGGAAGATTGGATTATCAGAAGGCAATTGATCTCAATCACTTATCACCACAT 600
Qy      LeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAsp 408
Db      CTCATCGCGGAGACGCTTCAATTTGTCATGCTGGATCTGGTGACCCAGAGCTCGAAGAC 660
Qy      TrpMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPheSer 428
Db      TGGATGAGATCTACAGATCGGACTTCAGAGGATAAATTTCTGGATGGGTTGGAATTAGT 720
Qy      ValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPhe 448
Db      GTTCCAGTTTCCACCGCAATACTGCGGCTGCGATATATTGTTAATGCCATCCAGATTTC 780
Qy      GluProCysGlyLeuAsnGlnLeuTyrAlaMet 459
Db      GAACCTTGTGGTCTCAATCAGCTATATGCTATG 813

CA252614      983 bp      mRNA      linear      EST 25-SEP-2003
LOCUS      SCVPFL1139H12.9 FL1 Saccharum officinarum cDNA clone SCVPFL1139H12
DEFINITION      5', mRNA sequence.
ACCESSION      CA252614
VERSION      CA252614.1 GI:35338653
KEYWORDS      EST.
SOURCE      Saccharum officinarum
ORGANISM      Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
1. (bases 1 to 983)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bccccenter.fcav.unesp.br
Plate: 139 row: H column: 12
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1. .983
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCVPFL1139H12"
/lab_host="DH10B"
/clone_lib="FL1"
(note="Organ: Inflorescence at beginning of development
(lcm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI;
An unidirectional cDNA library generated from
[inflorescence at beginning of development (lcm-long)]").

```

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ORIGIN
Alignment Scores:
Pred. No.:      1.23e-134      Length:      983
Score:          1266.50      Matches:      263
Percent Similarity: 85.5%      Conservative: 20
Best Local Similarity: 79.5%      Mismatches: 34
Query Match:      43.8%      Indels:      14
DB:              6          Gaps:        7

US-10-628-525A-21 (1-539) x CA252614 (1-983)
Qy      116 PheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTTPVal 135
Db      2 TTTGGCGGTGAACACGAAAGTTACCTTTTCCATGAGTACAGAGATTCACTGACTGGGTG 61
Qy      136 PheValaspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAla 155
Db      62 TTTGTTGATCATCCCTCATATCACAGACCTGGAATTTATATGGAGATAAGTTTGGTGCT 121
Qy      156 PheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeu 175
Db      122 TTTGGTGAATAATCAGTTTCAGATACACGCTCTCTTGTCTATGCTGCATGTGAGGCTCTCTTTG 181
Qy      176 IleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTTP 195
Db      182 GTCTTGTGAATTGGAGAGATATATTTATGGGAGAAATTGCATGTTTGTGTGAATGATGG 241
Qy      196 HisAlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLys 215
Db      242 CATGCCAGTCTAGTGCCAGTCTCTCTGTCGCAAAATATAGACCATATGTTGTTTATATAA 301
Qy      216 AspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSer 235
Db      302 GACTCCCCGAGCATTTCTGTGAATACATAATTTAGCACATCAGGGGTGAGAGCTTGAACG 361
Qy      236 ThrTyrProAspLeuGlyLeuProProGluTTPtyrGlyAlaLeuGluTyrValPhePro 255
Db      362 ACATATCTTGACCTTGGGTGGCCACTGAATGGTATGAGGCTCTCGAGTGGGTATTCCT 421
Qy      256 GluTPAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAla 275
Db      422 GAATGGGCAAGGAGGAGCATGCCCTTCACAAGGCTGAGGCAGTTTAATTTTGAAGGTGCA 481
Qy      276 ValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrGluValThrThr 295
Db      482 GTTGTGACAGCAGATCGAATCGTGTGATAGAGGGTTATTCATGGGAGGTCAACACT 541
Qy      296 AlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGly 315
Db      542 GCTTCAAGTGGACAGGGCTCAATGAGCTCTTAAAGCTTCAGAAAGAGTGTATTAAACGGA 601
Qy      316 IleValAsnGly-IleAspIleAsnAspTyrAsnProAlaThrAspLysCysIlePro-- 334
Db      602 ATGGTAATGGAAATGACATTAATGATTGGAACCTGCCACGGACAAATGATTATTCCTTT 661
Qy      335 -CysHisTyrSerValAspAspLeuSerGly-LysAlaLysCysLysGlyAlaLeu--G 353
Db      662 GGCATTATTTCTGGTGATGAACCTTTTGGAAAAAGCAAAATGTAAAAATTGCATTGGCA 721
Qy      353 LnyLysGluLeuGlyLeuPro--IleArgProAspValProLeu--IleGlyPheIleG 371
Db      722 AAAAGGAAGTGGGGTTTAACCTTTTAAGGCGCTAGAAATTCCTCTGAAATGGCTTTTGTG 781
Qy      371 ly-ArgLeuAspTyr-GlnLysGlyIle---AspLeuIleGlnLeuIleIleProAsp-- 388

```

cDNA was prepared from polyA+ mRNA using SuperScript plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucst.lad.ic.unicamp.br/public>





```

DB      828 GTTAATG 834
|||||
CK123179
LOCUS   769 bp mRNA linear EST 01-MAR-2004
DEFINITION Hordeum vulgare subsp. vulgare cDNA clone
ACCESSION CK123179
VERSION   CK123179.1 GI:44806181
KEYWORDS EST.
SOURCE   Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 769)
AUTHORS Kramer,A., Fellner,T., Possling,A., Radchuk,V., Weschke,W.,
          Buerkle,L. and Kersten,B.
TITLE Application of the protein microarray technology for the
          identification of expression library derived target proteins for
          barley protein kinase CK2
JOURNAL Unpublished (2003)
COMMENT Contact: Birgit Kersten* and Winfriede Weschke**
          *Plant Protein Chip Group, Department Lehrach, **Department
          Molecular Genetics, Gene Expression Group
          **Max-Planck-Institute for Molecular Genetics, **Institute of Plant
          Genetics and Crop Plant Research Gatersleben
          *Inhestr. 73, D-14195 Berlin, Germany, **Corrensstrasse 3, D-06466
          Gatersleben, Germany
          Tel: **49 (0)30/84131648, **449 (0)394825500
          Fax: **49 (0)30/84131128, **449 (0)394825237
          Email: *kersten@molgen.mpg.de, **weschke@ipk-gatersleben.de
          Insert Length: 765 Std Error: 0.00
          Plate: 2 row; F column: 21
          Seq primer: pQE565.
FEATURES
          Location/Qualifiers
            1..769
              /organism="Hordeum vulgare subsp. vulgare"
              /mol_type="mRNA"
              /cultivar="Barke"
              /sub_species="vulgare"
              /db_xref="GABI:942940"
              /db_xref="taxon:112509"
              /clone="WPMGP2010P212"
              /tissue_type="embryosac"
              /dev_stage="0-10 DAF (days after flowering)"
              /lab_host="E. coli, SCS-1/pSE111"
              /clone_lib="BES1824"
              /note="Vector: pQE30NST (AF074376); Site 1: SalI; Site 2:
              NotI; 0-10 DAF (days after flowering), cDNA synthesis
              using pBluescript II XR cDNA-library construction kit
              (Stratagen) with an oligo(dT)-primer containing NotI
              restriction site and a SalI adapter (Invitrogen). The main
              library of 21500 clones was rearrayed into the sublibrary
              BES 1824 containing 4100 putative expression clones. Note:
              Due to a cloning artefact caused by the kit, in most cases
              the SalI site is NOT present, as well as the SalI Adapter
              used for cloning. To excise the insert, restriction sites
              upstream SalI should be used (e.g. BamHI). Average insert
              size is 1 kb. Library generation and sequencing was
              granted in context of GABI; data are also accessible at
              https://gabi.rzpd.de"
ORIGIN
Alignment Scores:
Pred. No.: 3.59e-131 Length: 769
Score: 1235.00 Matches: 228
Percent Similarity: 93.0% Conservative: 10
Best Local Similarity: 89.1% Mismatches: 17
Query Match: 42.7% Indels: 1
DB: 7 Gaps: 0

```

---

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US-10-628-525A-21 (1-539) x CK123179 (1-769)
QY      15  GluGlyIleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSer 34
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DB      4  GAAGGAGTGTCTGAGGATTCCATCGACACCATAGTGTGTGCTCAAGTGAGCAGGATTCT 63
QY      35  GluIleValValGlyLysGluGlnAlaArgAlaValThrGlnSerIleValPheVal 54
         |||||
DB      64  GAGATCATGATGATGCCAACGACCACTCTAGCTAAAGTTACACGTAGCATCGTGTGTG 123
QY      55  ThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeu 74
         |||||
DB      124 ACTGTGTGAAGTCTCTCTTATGCAAGTCAGGGGGCTGGGAGATGTTTGTGTTGTTG 183
QY      75  ProValAlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsn 94
         |||||
DB      184 CCAATGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243
QY      95  GlyThrSerAspLysAsnTyrAlaAlaAsnAlaPheTyrThrGluLysHisIleArgIlePro 114
         |||||
DB      244 GGGACCTCTGATATAAAACCTATGCAAGGCATTTATACCCGGGAGCACATTAAGATTCCA 303
QY      115 CysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyr 134
         |||||
DB      304 TGCTTCGGGGGATCATGAGTCACCTTTTTCATGAGTATAGAGACAACGTCGATTGG 363
QY      135 ValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGly 154
         |||||
DB      364 GTGTTTGTGATCATCCATCATATATAGACCAAGAGTTTGTATGGAGATTAATTTTGT 423
QY      155 AlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaPro 174
         |||||
DB      424 GCTTTTGTGATATATCAGTTTCAGATACACATCTTTGCTATGCTGCTTGTGAGGCCCA 483
QY      175 LeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAsp 194
         |||||
DB      484 CTAATCCTTGAATGGGAGGATATATTTATGACAGAGTTGTCATGTTTGTGTAACGAT 543
QY      195 TrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyr 214
         |||||
DB      544 TGGCATGCCAGCCTTGTGCCAGTCTCTTCTGCTGCAAAAGTATAGACCATATCGAGTTAC 603
QY      215 LysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAla 234
         |||||
DB      604 AGAGATTCTCGCAGCAGCTCTTGTATATATATTTAGACATCAGGGTGTGGAGCTGCA 663
QY      235 SerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPhe 254
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DB      664 AGTACATATCTGATCTGGGATGTCACCTGAATGTTATGGAGCTTTAGATGGGTATTT 723
QY      255 ProGluTyrPalaArgArgHisAlaLeuAspLysGlyGluAlaVal 269
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DB      724 NCCANAATGGGCAAGAGGCATGCCNTGACAAGGGGAGGGCGTT 769
          CA199168 672 bp mRNA linear EST 25-SEP-2003
          SCRFL1010G05.g FL1 Saccharum officinarum cDNA clone SCRFL1010G05
          5', mRNA sequence.
          CA199168
          CA199168.1 GI:35231161
          EST.
          Saccharum officinarum
          Saccharum officinarum
          ORGANISM
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
          complex.
          1 (bases 1 to 672)
          Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
          The libraries that made SUCST
          Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
          Contact: Arruda P

```

Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089

Email: parruda@unicamp.br  
Clone distribution: clone distribution information can be found  
through the Brazilian Clone Collection Center (BCCC) at  
http://www.bcccenter.fcav.unesp.br  
Plate: 010 row: G column: 05  
Seq primer: T7 Promoter Primer.  
Location/Qualifiers

## FEATURES

source

1. 672  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clones="SCRLFL1010G05"  
/lab\_host="DH10B"  
/clone\_lib="FL1"

/notes="Organ: Inflorescence at beginning of development  
(1cm-long); Vector: pSport1; Site 1: Salt; Site 2: NotI;  
An unidirectional cDNA library generated from  
[Inflorescence at beginning of development (1cm-long)].  
cDNA was prepared from polyA+ mRNA using SuperScript  
Plasmid System kit (Invitrogen). The double-strand cDNAs  
were fractionated in a sepharose CL-2B 40cm-columns and  
fragments sizing between 0.8 and 1.5 Kb were  
directionally cloned into the vector. Details  
source of RNA and library construction can be obtained at  
http://sucest.lad.ic.unicamp.br/public"

## ORIGIN

Alignment Scores:  
Pred. No.: 1.85e-121 Length: 672  
Score: 1150.00 Matches: 217  
Percent Similarity: 97.3% Conservative: 2  
Best Local Similarity: 96.4% Mismatches: 6  
Query Match: 39.8% Indels: 3  
DB: 6 Gaps: 0

US-10-628-525A-21 (1-539) x CA1199168 (1-672)

QY 83 HisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAla 102  
DB 1 CACCGTGTGATGGTGTGAATGCCAGATATTAAATGGTACCTCTGATAGAAATTATGCA 60  
QY 103 AsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGluHisGluVal 122  
DB 61 AATGCATTTTACACAGAAAGCACATTCGGATTCATGCTTTGGCGGTGAACAGAGTT 120  
QY 123 ThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSerTyr 142  
DB 121 ACCTTTTCCATGAGTACAGAGATTTCAGTTGACTGGGTGTTTGTTCATCATCTCATAT 180  
QY 143 HisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArg 162  
DB 181 CACAGACCTCGAAATTTATATGAGATAGAAATGGTGGTCTTTGGTGATATATCAGTTT 240  
QY 163 TyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyr 182  
DB 241 TACACGCTCTCTTGGCTATGCTGATGATGAGGCTCTTTGGTCTCTGAAATGGGAGATAT 300  
QY 183 IleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProVal 202  
DB 301 ATTTATGGGCAGAAATTCATGTTTGTGTGAATGATTGGCATGCCAGTCTAGTCCAGTC 360  
QY 203 LeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuVal 222  
DB 361 CTTCTTCTGCGCAAAATATAGACCATATGGTGTATATAAGACTCCCGCAGCATTTCTTGA 420  
QY 223 IleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeu 242  
DB 421 ATACATATTTAGCACATCAGGGGTAGAGCCTTCGACGCATATCTGACCTTGGGTTG 480

QY 243 ProProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAla 262  
DB 481 CCACCTGAATGGTATGGAGCTCTGGATGGGTATTCCTCGAATGGGACGAGCATGCC 540  
QY 263 LeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIle 282  
DB 541 CTTTGACAAGGGTGGGCGAGTTAAATTTTTTGAAGAGTGCAGTTGTGACACGAGATCGAATC 600  
QY 283 ValThrValSerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeu 302  
DB 601 GTGAATTCAGTAAAGGTTATCA-TGGGAGGGCACCACTGCTGGAAGG-GGACAGGGCCT- 657  
QY 303 AsnGluLeuLeuSer 307  
DB 658 AATGAGCTTTTAGCT 672

## RESULT 9

CO442565

LOCUS

DEFINITION

M2CCL10045D02.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA

ACCESSION

CO442565

VERSION

CO442565.1

KEYWORDS

EST.

SOURCE

Zea mays

ORGANISM

Zea mays

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br.

Location/Qualifiers

1. 805

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="F-352 near isogenic line"

/db\_xref="taxon:4577"

/sex="hermaphrodite"

/tissue\_type="endosperm"

/dev\_stage="multiple stages (10 to 25 days after

pollination, see publication for more information)"

/lab\_host="E. coli DH10B"

/clone\_lib="Maize Endosperm cDNA Library"

/note="Organ: seed; vector: pSPORT1; Site 1: Salt; Site 2:

plants from inbred line F352 were used. Ears were

harvested at 10, 15, 20 and 25 days after pollination

(DAP), seeds were cut from the ear and the upper third of

the endosperms, containing only endosperm, aleurone and

pericarpal tissues, was removed, frozen in liquid nitrogen

and stored at -800 C. Frozen endosperms were pulverized in

liquid nitrogen and total RNA was isolated according the

method of Manning (9). Poly(A)+RNA was isolated using

Oligotex-dr. cDNA libraries were constructed using

SuperScript Plasmid System for cDNA Synthesis and Plasmid

Cloning Kit as described in Vettore, et al. (2001). The

libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs

ranging from 500 to 800 bp in size were assigned as short

libraries (S10, S15, S20), and cDNAs &gt;800 were assigned as

long libraries (L10, L15, L20, L25). Unamplified



167 CysTyrAlaAlaCysGluAlaProLeuLeuLeuLeuGlyTyrIleTyrGlycIn 186.  
1488 TGTAAAGCTGCTGTGAGGTTCTTGGCAGCTTCCATCGCGTGTGTGCCATATGGCGAT 1547  
187 ---AenCysMetPheValValAAsnAspTrpHisAlaSerLeuValProValLeuLeuAla 205  
1548 GGCACACTGGTGTCTTGCMAAGATGGCAGCTGCACCTCTGCTGTATATCTCAAG 1607  
206 AlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAAsn 225  
1608 GCATATTACAGAGACAATGGCATGATGCATACATCGCTCTGTCTGTGTATACATAAT 1667  
226 LeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGlu 245  
1668 ATGCTCTACAGAGGCGCTGCCCAAGTAGAATTCCTCCATGGAATTGCCG----- 1721  
246 TrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLys 265  
1722 -----GAGCACTACCTGGATCAC 1739  
266 -----GlyGluAlaValAAsnPheLeuLysGlyAlaValVal 277  
1740 TTCAAGCTGTACGACCCGCTCGCGGAGCAGCACCAACATCTTCGGCGCGGCTGAAG 1799  
278 ThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAlaGlu 297  
1800 ATGCGGACCGGGTGTGACCGTGGCCGGCTACCTCTGGAGCTGAAGACGACGAG 1859  
298 GlyGlyGlnGlyLeuAAsnGluLeuSerSerArgLysSerValLeuAAsnGlyIleVal 317  
1860 GCGCGCTGGGCGCTCCACGACATCATACGGGAGACGACTGGAGATGAACGGGATCGTG 1919  
318 AsnGlyIleAspIleAAsnAspTrpAAsnProAlaThrAspLysCysIlePro----- 334  
1920 AACGGCATCGACTACCGGAGTGAACCCGAGGTGGAGTGCACCTGCAGTCGACGCGC 1979  
335 ---CysHisTyrSerValAspLeu---SerGlyLysAlaLysCysLysGlyAlaLeu 352  
1980 TAGCCCAACTACACCGTGGCTCGCTGGACTCCAGCAAGCGCGGTGCAAGCGCGGCTG 2039  
353 GlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArg 372  
2040 CAGCGGAGCTGGGCTGGAGGTGGCGGACGATCGCGCTGTATCGGTTTCATCGGCGCG 2099  
373 LeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGlu 392  
2100 CTCGACGGCAGAAAGGTGGACATCATCGCGACGCGATGCGTGGATCGCGCGGACG 2159  
393 AspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSer 412  
2160 GACGTGCAGCTGTGTCTGGGCTCGCGCGCGGACCTCGAGGTGATGCTGCAGCGG 2219  
413 ThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerValProValSer 432  
2220 TTCAGGCGGCGAGCACAACAGCAGGTGCGGGTGGGTGGGTTCGCGTGAAGATGGCG 2279  
433 HisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGly 452  
2280 CACCGGATCAGCGGGGCGGAGGTGCTGTATCGCGTTCGGGTTCGAGCGCGTGGCGC 2339  
453 LeuAAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGly 472  
2340 CTCACACGACTTACGCCATGGCGTACGCGCACCGCTCCCGCTGTCACGCGCTCGCGCG 2399  
473 LeuArgAspThrValGluAAsnPheAAsnProPheGlyGluAAsnGlyGlnGlyThrGly 492  
2400 CTGAGGACACCATGTGCGGCTTCGACCGCTTCAGGACACC-----GCGCTCGCG 2450  
493 TrpAlaPheAlaProLeuThrThrGluAAsnMetPheValAspIleAlaAAsnGlyAsnIle 512  
2451 TGGACGTTTCGACCGCGCGGCGGACAGCTCATCGAGCGCTCGGCGCTCGGCTCGCTCGA 2509

QY 513 TyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAAsnGluAlaArgHisVal----- 530  
Db 2510 GACGTACCGCAAGTACAAAGAGAGAGTGGAGGGGCTCCAGGTGCGCGCATGTGCGCAGGA 2569  
QY 531 -----LysArgLeuHisValGlyProCysArg 539  
Db 2570 CCTCAGCTGGGACCAACCGCCGAGCTCTACGAGGAGTCTCTGTTCAA 2617  
RESULT 11  
BI953855  
LOCUS  
DEFINITION  
HvCDNA0014 (Blumeria infected) Hordeum vulgare subsp. vulgare cDNA  
clone HvSME0015A15f, mRNA sequence.  
ACCESSION  
VERSION  
BI953855  
BI953855.1 GI:16298873  
EST.  
SOURCE  
Hordeum vulgare subsp. vulgare  
ORGANISM  
Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.  
REFERENCE  
1 (bases 1 to 639)  
Wing, R., Close, T. J., Kleinhofs, A., Wise, R., Chin, A., Begum, D.,  
Frisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T.,  
Simmons, J., Oates, R. and Main, D.  
Development of a genetically and physically anchored EST resource  
for barley genomics: Blumeria infected Morex (compatible) seedling  
cDNA library  
Unpublished (2001)  
COMMENT  
Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Total hg bases = 472  
Seq primer: AATTAACCTCACTAAAGG  
High quality sequence stop: 600.  
FEATURES  
Location/Qualifiers  
source  
1..639  
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/mol\_type="mRNA"  
/cultivar="Morex"  
/sub\_species="vulgare"  
/db\_xref="taxon:112509"  
/clone="HvSME0015A15f"  
/tissue\_type="green seedling leaf"  
/lab\_host="TJCI21"  
/clone\_lib="Hordeum vulgare green seedling EST library  
HvCDNA0014 (Blumeria infected)"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; Morex (mia) plants were greenhouse grown in the R  
Wise lab at Iowa State University, Ames, IA; 7 day old  
green seedlings were infected with isolate 5874 of  
Blumeria graminis f. sp. hordei, and leaves were harvested  
24, 48 and 72 hr post-inoculation and snap frozen (Wise).  
In the TJ Close lab at the University of California,  
Riverside, total RNA was prepared from each sample pool,  
equal quantities of all three RNA pools were combined,  
poly(A) RNA was purified from the mixture, one primary  
unamplified cDNA library was made, and 1 million pfu were  
in vivo excised to give pBluescript SK(-) cDNA phagemids  
(Chin). Phagemids were plated and picked at the Clemson  
University Genomics Institute (CUGI) (Begum, Palmer,  
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA  
sequencing and sequence analysis were performed at CUGI  
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).  
The sequence has been trimmed to remove vector sequence  
and contains a minimum of 100 bases of phred value 20 or  
above. For more details on library preparation and  
sequence analysis see

<http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wang R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. *Barley Genetics Newsletter* 31:29-30. (<http://wheat.pw.usda.gov/qapaces/bam/31/cover.html>).



Db 411 CAGTTTGTGATGCTGGGATCCAAATTTTGAAGGCTGGATCAGATCTACCGAG 470

Qy 415 SerlePheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArg 434

Db 471 TCGAGTTTACAAGGATAAATTCGGTGGATGGCTTGGATTTAGTGTTCAGTTTCCACACAGA 530

Qy 435 IleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsn 454

Db 531 ATAACTGCAGGTTCCGATATATTGTAATGCCATCCAGGTTTGAACCTTGGTGTCTTAAT 590

Qy 455 GlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArg 474

Db 591 CAGCTATATGCTATGCAATATGTTACAGTCTCTGTAGTTCATGCAACTGGGGGCTCCGA 650

Qy 475 AspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAla 494

Db 651 GACACAGTCGAGACCTTCAACCTTTTGGTGCAAAAGGAGGAGGGGTACAGGGTGGGCG 710

Qy 495 PheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIle 514

Db 711 TTCTCACCGCTAACCGTGGACAGATGTT-GTGGGCATTGGCAACCGCATGTCCACATT 769

Qy 515 GlnGlyThrGlnValLeuLeuGlyIArg-AlaAsnGluAlaArgHisValLysArgLeuHi 534

Db 770 CAGGAGCACACAGCGCTCTGGGAGGGGCTCATGAAGCGAGGCGATCACAAGACATYA 829

Qy 534 sVal 535

Db 830 CGTG 833

RESULT 13

BM410663

LOCUS

DEFINITION

EST584990 tomato breaker fruit Lycopersicon esculentum cDNA clone

CL54M19 5' end, mRNA sequence.

BM410663

EST.

BM410663.1 GI:18262293

Source

Lycopersicon esculentum (Solanum lycopersicum)

ORGANISM

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 787)

Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A.,

Tsai, J., Bougri, O., Kirkness, E., Utterback, T., Van Aken, S.,

Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and

Giovannoni, J.

Generation of ESTs from tomato fruit tissue, breaker stage (2002)

Unpublished (2002)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

This clone is available through the Clemson University Genomics

Institute

Seq primer: T3.

Location/Qualifiers

1..787

/organism="Lycopersicon esculentum"

/mol\_type="mRNA"

/cultivar="TA496"

/db\_xref="taxon:4081"

/clone="CL54M19"

/tissue type="Pericarp"

/dev stage="breaker"

/lab\_host="SOLR"

/clone lib="tomato breaker fruit"

/note="Vector: pBluescriptSKmCuadapt; Site 1: EcoRI;

Site 2: XhoI; supplier: Boyce Thompson Institute;

sequencing: The Institute for Genomic Research. Fruit

were harvested at the breaker stage (first sign of

RESULT 14

BM111144

lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

ORIGIN

Alignment Scores:

Pred. No.: 1.07e-109 Length: 787

Score: 1049.00 Matches: 190

Percent Similarity: 86.6% Conservative: 36

Best Local Similarity: 72.8% Mismatches: 35

Query Match: 36.3% Indels: 1

DB: 3 Gaps: 0

US-10-628-525A-21 (1-539) x BM410663 (1-787)

Qy 161 PheArgTyrThrLeuLeuCysTyrAlaAaCysGluAlaProLeuIleLeuGluLeuGly 180

Db 1 TTTCCGCTTCACTTGTCTTCTCAGCGCAGCATGGAAGCGCATGGTTCCTCCACTGGGA 60

Qy 181 GlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuVal 200

Db 61 GGCTTCACCTTATGGAGAGAAGTGTCTTCTCGCTAATGATTTGGCATGCTTCCTCGTT 120

Qy 201 ProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220

Db 121 CCTTTACTTTTAGCAGCAAGTATCGTCTTATGGTGTTTTACAAGGATGCTCGTAGTATT 180

Qy 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240

Db 181 GTCGCAATACCAACATTCATCAGGAGTGGAGCTCGACCACTCACTAATAATTG 240

Qy 241 GlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArg 260

Db 241 GGATTCCTCTCAATGGTATGAGCATTGATGATATTTCCACATGGCGAAGGCC 300

Qy 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAsp 280

Db 301 CATGCCCTTGACACTGGTGAACAGTGAATGTTTGAAGGGGCAATCTCAGTTGCTGAT 360

Qy 281 ArgIleValThrValSerLysGlyTyrSerTrpGluValThrThrAlaGlyGlyGln 300

Db 361 CGATTAATGATGGAACCCGTCGACAGATGAGCATATTGCTTCGCATTAATCAAT 420

Qy 301 GlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320

Db 421 GGCTACATGAGCTGCTGAGCAGTACAGCAGTCTTCTTAATGGAATTACTAATGGAATA 480

Qy 321 AspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340

Db 481 GATGTTAATGATGGAACCCGTCGACAGATGAGCATATTGCTTCGCATTAATCAAT 540

Qy 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGlyLeuLeuProIle 360

Db 541 GACCTCTCGGAAGGCTCAGTGCAAGACTGATCTGCAAAAGGAACCTGGGCCCTTCCAATT 600

Qy 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380

Db 601 CGACCTGATTGCTCGCTGATGGATTATTTGGAAGGCTGGACTACCAAGAGGTGTGAC 660

Qy 381 LeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400

Db 661 ATAATCCTGTCAGCAATTCAGAACTTTTGCAGAAAGGATGTCCATTTGTAAATGCTTGA 720

Qy 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys 420

Db 721 TCTGGTGAGAAACATAT-GAAGACTGGATGAGACATACAGAGAAATCTTTTAAAGACAAAT 779

Qy 421 Phe 421

Db 780 TTC 782

LOCUS BM111144 782 bp mRNA linear EST 10-MAR-2003  
 DEFINITION EST58680 potato roots Solanum tuberosum cDNA clone cPRO10K18 5'  
 end, mRNA sequence.  
 ACCESSION BM111144  
 VERSION BM111144.1 GI:17073444  
 KEYWORDS EST.  
 SOURCE Solanum tuberosum (potato)  
 ORGANISM Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 asterids; lamids; Solanales; Solanaceae; Solanum.  
 1 (bases 1 to 782)  
 van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S.,  
 Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C.,  
 Tanksley, S. and Baker, B.  
 Generation of ESTs from potato roots  
 Unpublished (2001)  
 Contact: Robin Buell  
 The Institute for Genomic Research  
 9712 Medical Center Dr, Rockville, MD 20850, USA  
 Email: potato-array@tigr.org  
 This clone can be obtained from the University of Arizona Genomics  
 Institute. Orders can be made through URL:  
 http://genome.arizona.edu/orders/  
 Seq primer: T3.  
 FEATURES  
 Location/Qualifiers  
 1..782  
 /organism="Solanum tuberosum"  
 /mol\_type="mRNA"  
 /cultivar="Kennebec"  
 /db\_xref="taxon:4113"  
 /clone="cPRO10K18"  
 /tissue\_type="roots"  
 /dev\_stage="in vitro grown stem cuttings"  
 /lab\_host="SOLR"  
 /clone\_lib="potato roots"  
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:  
 XhoI; supplier: Cornell University, Tanksley lab;  
 sequencing: The Institute for Genomic Research. Roots were  
 isolated from in vitro grown stem cuttings on CM medium.  
 Roots were isolated two weeks after placing the stem  
 cuttings from in vitro grown plants on medium."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 3,998-109 Length: 782  
 Score: 1044.00 Matches: 186  
 Percent Similarity: 84.1% Conservative: 31  
 Best Local Similarity: 72.1% Mismatches: 41  
 Query Match: 36.1% Indels: 0  
 DB: 3 Gaps: 0  
 US-10-628-525A-21 (1-539) x BM111144 (1-782)  
 QY 115 CysPheGlyGlyGluHisGluThrPhePheHisGluTyrArgAspSerValAspTrp 134  
 Db 5 TGCTTTGGTGACAGGAGTAGCTTCTACCATGATACAGGCGAGGTGTGATGG 64  
 QY 135 ValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGly 154  
 Db 65 GTATTTGTGGACCACTCTTTACTGCGACACCGCCATATGATGATTTATGGT 124  
 QY 155 AlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 174  
 Db 125 GCATTTGGTGATGATAGTTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 184  
 QY 175 LeuLeuLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnGlyMetPheValValAsnAsp 194  
 Db 185 TTGGTTCTTCCATCGGAGGGTTTCACTATGATGAGAGAGAGTGTGTGTCTCGCTATGAT 244  
 QY 195 TrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyr 214  
 Db 245 TGGCATGTCGCCCTGGTTCCTTTACTTTTATGCGGCCAGTATCGTCTTATGTTGTTTAC 304

QY 215 LysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAla 234  
 Db 305 AAGGATGCTCGTAGTATTTCGCAATACACACATCGCATCAGGAGTGGAGCCTGCA 364  
 QY 235 SerThrTyrProAspLeuGlyLeuProGluTyrTrpTyrGlyAlaLeuGluTyrValPhe 254  
 Db 365 GTAACCTACAATANTTTGGTTTGGCTCCACATGGTATGGAGCAGTTGAATGATATT 424  
 QY 255 ProGluTyrPalaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274  
 Db 425 CCACATGCGCAAGGCGCATGCGTTGACACTGGTGAACAGTGAACCGTTTGAAGGG 484  
 QY 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThr 294  
 Db 485 GCAATAGCAGTTGCTGATCGGATCTGACAGTTAGCCGGGATCTCATCGGGAATAACA 544  
 QY 295 ThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsn 314  
 Db 545 ACTCTGGAAGGGGATATGGGCTACATGAGCTGTTGAGCAGTAGACAGTCTGTCTTAAT 604  
 QY 315 GlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIlePro 334  
 Db 605 CGAATTACTAATCGAATAGATGTTAATGATTGGAACCCGTCGACAGATGAGCATATTGCT 664  
 QY 335 CysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLys 354  
 Db 665 TCGCATTAATCTCCATCAATGACCTCTCCGAGAGTTCCGAGCAGTCTGATCTGCAAAAG 724  
 QY 355 GluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArg 372  
 Db 725 GAACCTGGGCTTCCCATCCGAACATGATGTCCTCTGATTTGATTTATTGGAAGG 778  
 RESULT 15  
 CD463762  
 LOCUS  
 DEFINITION ETH1\_46\_D07.g1\_A002 Ethylene-treated seedlings Sorghum bicolor cDNA  
 clone ETH1\_46\_D07\_A002 5', mRNA sequence.  
 ACCESSION CD463762  
 VERSION CD463762.1 GI:31385030  
 KEYWORDS EST.  
 SOURCE Sorghum bicolor (sorghum)  
 ORGANISM Sorghum bicolor  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 695)  
 Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S.,  
 Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Salzman, R.,  
 Chua, Tan, N., Gonzalez, M., Lane, S., Miller, V., Nanda, P.,  
 Olaseinde, O., Eastman, A., and Pratt, L.H.  
 An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid  
 (ACC)-treated seedlings  
 Unpublished (2003)  
 Other ESTs: ETH1\_46\_D07.b1\_A002  
 Contact: Cordonnier-Pratt, M.  
 Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 583 0210  
 Email: mmpratt@uga.edu  
 Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in  
 the Human Genome Center, University of Tokyo Institute of Medical  
 Science; plant material and RNA prepared at Texas A & M University;  
 sequencing done in the Laboratory for Genomics and Bioinformatics,  
 University of Georgia. Sequence ends have been trimmed to exclude  
 vector and regions below Phred quality 16. Three-prime sequences  
 are presented as their reverse complement and have been trimmed to  
 exclude polyA.  
 Seq primer: Sugs (CTTCTGCTCTAAAGCTGCG).  
 Location/Qualifiers  
 1..695  
 FEATURES  
 source

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/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="B7x623"
/db_xref="taxon:4558"
/clone="ETH1_46 D07 A002"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Ethylene-treated seedlings"
/note="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA from seedlings grown in hydroponic culture. At 8 days of age, medium was supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic acid (ACC) to induce endogenous ethylene (ETH) production. Roots and shoots were harvested after 27 and 72 hr and material from both time points was combined prior to RNA isolation. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."
ORIGIN
Alignment Scores:
Pred. No.: 2.43e-108 Length: 695
Score: 1036.50 Matches: 195
Percent Similarity: 86.3% Conservative: 6
Best Local Similarity: 83.7% Mismatches: 9
Query Match: 35.8% Indels: 23
DB: 6 Gaps: 3
US-10-628-525A-21 (1-539) x CD463762 (1-695)
Qy 72 GlySerLeuProValAlaLeuAlaAalaArgGlyHisArgValMetValMet----- 89
Db 11 GGAAGCGCGCG-----AGCGGCACCGCCAGCGTGTAGTAGTAGAAGGC 55
Qy 90 -----ProArgTyrLeuAsnGlyThrSerAspLysAsn----- 100
Db 56 ACGGAGCGCGCGCGCGCGCGCGCTCTCTCTTCGCGCCATCCACGCGCACCG 115
Qy 101 -----TyrAlaAsnAlaPheTyrThrGluLysHisIleArgIle 113
Db 116 CGCCCCCTCGTCTCTCCGCAATGCAITTTACAGAAAGACATTCGGATT 175
Qy 114 ProCysPheGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAsp 133
Db 176 CCATGCTTTGGCGGTGAACATGAAGTTACCTTTTCCATGAGTACAGAGATTGAGT 235
Qy 134 TrpValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPhe 153
Db 236 TGGGTGTTTGTGATCATCCCTCATATCACAGACCTGGAAATTTATATGAGATAAGTTT 295
Qy 154 GlyAlaPheGlyAspAanGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAla 173
Db 296 GGTGCTTTTGTGATATCAATCAATTCAGTTCAGATACAGCTCTTCTGCTATGCTGATGAGCT 355
Qy 174 ProLeuLeuLeuGluLeuGlyGlyTyrIleTyrGlyGlnAanCysMetPheValValAsn 193
Db 356 CTTTGTGCTCTGAATTTGGGAGGATATATTATGGACAGAAATTCGATGTTTGTGAAT 415
Qy 194 AspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyVal 213
Db 416 GATTGGATCCAGTCTAGTGCCAGTCTCTTCTGCTGCAAAATATAGACCATATGTT 475
Qy 214 TyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluPro 233
Db 476 TATTAAGACTCCCGCAGCATCTTGTATATACATATTTACACATCAGGGGTAGAGCCT 535
Qy 234 AlaSerThrTyrProAspLeuGlyLeuProProGluTyrTyrGlyAlaLeuGluTrpVal 253
Db 536 GCAAGCACATATCTGACCTTGGTGGTCCACCTGAAATGGTATGGAGCTCTGGAGTGGTA 595
Qy 254 PheProGluTrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAanPheLeuLys 273

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Db 596 TTCCTGTAATGGCAAGGAGGCATCCCTTGACAAAGGCTGAGCGAGTTAATTTTGA 655
Qy 274 GlyAlaValValThrAlaAspArgIleValThrValSer 286
Db 656 GGTGCACTTGTGACAGCAGATCGAATTTGCTACTGCTCAGT 694
RESULT 16
BQ472054 630 bp mRNA linear EST 30-MAY-2002
LOCUS BQ472054 HV Hordeum vulgare subsp. vulgare cDNA clone HV04E12
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BQ472054
VERSION BQ472054.1 GI:21279836
SOURCE EST.
ORGANISM Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 630)
Zhang,H., Potokina,E., Michalek,W., Weschke,W., Stein,N. and
Graner,A.
Barley ESTs from germinating seeds
Unpublished (2002)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 630 Std Error: 0.00
Plate: 4 row: E column: 12
Seq primer: M13rev
Location/Qualifiers
1. 630
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Barke"
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/db_xref="taxon:112509"
/clone="HV04E12"
/tissue_type="germinating seeds"
/dev_stage="germinating seeds (48-96 h)"
/lab_host="Xl10-Gold"
/clone_lib="HV"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); Roots were grown for two days on filter paper at room temperature. Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable. Average insert size is 1 kb"
ORIGIN
Alignment Scores:
Pred. No.: 3.1e-108 Length: 630
Score: 1035.00 Matches: 185
Percent Similarity: 96.5% Conservative: 9
Best Local Similarity: 92.0% Mismatches: 7
Query Match: 35.8% Indels: 0
DB: 5 Gaps: 0
US-10-628-525A-21 (1-539) x BQ472054 (1-630)
Qy 48 ThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeu 67
Db 27 TCACGTAGCATCGTGTGTGACTGTGTGAGCTGCTCTTATGCAAGTCAGGGGCTG 86
Qy 68 GlyAspValCysGlySerLeuProValAlaLeuAlaAalaArgGlyHisArgValMetVal 87

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Db      87  GGAGATGTTTGTGGTTCGTTGCAATGCTCTTGCTCGTGGTCAACGCTGTGATGGTT 146
Qy      88  ValMetProArgTyrLeuAenGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThr 107
Db      147  GTAATCCCGAGATACCTTAATGAGGACCTCTGATAAAACATATGCAAGCATTTATACACC 206
Qy      108  GluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlu 127
Db      207  GGAACACATTAAGATTCATGCTTCGGGGATCACATGAAGTCACCTTTTTCATGAG 266
Qy      128  TyrArgAspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsn 147
Db      267  TATAGAGACAACGTCGATTTGGGTGTTGTTGTATCATCCATCATATCATAGACCAGGAAT 326
Qy      148  LeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCys 167
Db      327  TTGTATGGAGATAAATTTTGGTGCTTTGTGTGATAATCAATTCAGTTACAGATACACTTTC 386
Qy      168  TyrAlaAlaCysGluAlaProLeuLeuLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsn 187
Db      387  TATGCTGCTTGTGAGGCCCACTAATCTTGAATGGGAGATATATTTATGGACAGAT 446
Qy      188  CysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaLys 207
Db      447  TGCATGTTTGTGTGAACGATTTGGCATGCCAGCCTTGTGCCAGTCTTCTTGTGCAAG 506
Qy      208  TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla 227
Db      507  TATAGACCATATGGAGATTTACAGAGATTTCTCCAGCACTCTTGTATATACATAATTTAGCA 566
Qy      228  HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTrpTyr 247
Db      567  CATCAGGTGTGGAGCTGCAAGTACATATCTGATCTGNGATGGCACTGCATATGGTAT 626
Qy      248  Gly 248
Db      627  GGA 629

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RESULT 17
LOCUS   CA818188
DEFINITION CA12E1302IIR_B02 Cabernet Sauvignon Leaf - CA12E1 linear EST 09-DEC-2002
          CDNA clone CA12E1302IIR_B02 3', mRNA sequence.
ACCESSION CA818188
VERSION   CA818188.1 GI:26267125
KEYWORDS EST;
SOURCE   Vitis vinifera
ORGANISM Vitis vinifera
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 877)
AUTHORS   Goes da Silva,F., Lim,H., Iandolo,A., Baek,J., Leslie,A., Xu,J.,
          Jones,K., Walker,M.A. and Cook,D.R.
TITLE     Transcriptional responses of Vitis vinifera to infection by the
          bacterial pathogen Xylella fastidiosa
JOURNAL   Unpublished (2003)
COMMENT   Contact: Doug Cook
          CAES Genome Facility
          UC Davis Department of Plant Pathology
          1 Shields Ave., Davis, CA 95616, USA
          Tel: 530 754 6561
          Fax: 530 754 6617
          Email: drcook@ucdavis.edu
          Seq primer: GCCAACGAATGGTCTAG.
          Location/Qualifiers
            1..877
              /organism="Vitis vinifera"
              /mol_type="mRNA"
              /cultivar="Cabernet Sauvignon"
              /db_xref="taxon:29760"
              /clone="CA12E1302IIR_B02"
FEATURES
source

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/sex="hermaphrodite"
/dev_stage="Mid-season leaf material"
/lab_host="DH5alpha"
/clone_lib="Cabernet Sauvignon Leaf - CA12E1"
/note="Organ: Leaf; Vector: pDNR; Site 1: SfiI; Site 2: SfiI; CA12E1 is a cDNA library of Cabernet Sauvignon leaves. The leaves were collected on July 25, 2001, in Napa Valley, California, and represent leaves in mid-season development. These leaves were verified to be infected with the bacterial pathogen, Xylella fastidiosa, based on a diagnostic assay using PCR and Xylella-specific primer pairs. The plants were asymptomatic at the time of collection, but later developed symptoms. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAACGAGATGGCCATACGCCGGG-3' and
5'-ATTCTAGAGCGGCGGCCACATG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

ORIGIN
Alignment Scores:
Pred. No.:      1.32e-107      Length:      877
Score:          1031.50      Matches:     190
Percent Similarity: 83.2%      Conservative: 38
Best Local Similarity: 69.3%      Mismatches:  45
Query Match:    35.7%      Indels:      1
DB:              6          Gaps:        1

US-10-628-525A-21 (1-539) x CA818188 (1-877)

Qy      264  AspLysGlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAspArgIleVal 283
Db      8   GACACGGGCCAAGCTGTCAATCTCTGAAGGTGCTATTGTGACAGTTGATCGGATACG 67
Qy      284  ThrValSerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGlnGlyLeuAsn 303
Db      68  ACAGTTAGCAAGGGCTATGCTTGGGAGTAAACAACCTCCGAGGTGGATATGCTGTCAT 127
Qy      304  GluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsn 323
Db      128  GAGCTCTCTGACCAATCGAAAGCTGTTATAATGGGATCACAATGGTATTGATGTTTCC 187
Qy      324  AspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSer 343
Db      188  GAATGGGATCCATCTCTCAGATGAGCATATTCCTCTCCATCTACTCTGCTGAAGATCTCT 247
Qy      344  GlyLysAlaLysCysGlyGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363
Db      248  GGGAAAGTTCAATGCAAGATGCTTTGAGAGGAATTAGGCTTCCCATTAGGCCGGAT 307
Qy      364  ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 383
Db      308  TGTCCATTTGATTTGATTCATTGGGAGATTTGGACTACCAAGAAAGGAATCGATGATCGG 367
Qy      384  LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403
Db      368  TTGGCACTCCAGAGCTTATGGAGAGGACGCTCCAAATGGTCTGCTGGGTCTGGGAAC 427
Qy      404  ProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423
Db      428  CCAGAGGACGAAGAGTGGATGAGATGGAATCAACATACACAGGACCAAGTTCGCGGT 487
Qy      424  TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443
Db      488  TGGGTGGATTTAATGTGCCCAATTTTCATAGATAACTGCAAGCTGTGACATCTCTTTG 547
Qy      444  MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463
Db      548  ATGCCATCAGATTCGAACCTTGTGGATTAACCAAGCTCTATGCAATGATATGGGGCT 607
Qy      464  ValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPhe 483

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Db      608 GTACCAGTTGTACATGCGACTGGAGGACTCAGAGATACAGTAGAGAAATTTCAATCCATAT 667
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Db      668 GCTGGAGGAGCGCGGTGAAGGACCGGGTGGACGTTTCTCCCTGTCCAAAAGACAC 727
Qy      503 MetPheValaAspIleAlaAenCysAenIleTyriLeGlnGlyThrGlnValLeuLeuGly 522
Db      728 TATGCTGGCGGCACTGAGAGTTGTCTATCAGGACATACCGGGAACACAAAGCCCTCTCGGA 787
Qy      523 ArgAlaAenGluAlaArgHisValValArgLeuHisValGly 536
Db      788 GAGGTTGATGAGAGAGGAGATGCAAGAAAGATTATACATGGA 829

RESULT 18
LOCUS   CA020001
DEFINITION HV14A20r HV Hordeum vulgare subsp. vulgare cDNA clone HV14A20
5-PRIME, mRNA sequence.
ACCESSION CA020001
VERSION 1
KEYWORDS GI:24297345
SOURCE EST.
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 609)
Zhang,H., Potokina,E., Michalek,W., Weschke,W., Stein,N. and
Graner,A.
Barley ESTs from germinating seeds
Unpublished (2002)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 609 Std Error: 0.00
Plate: 14 row: A column: 20
Seq primer: M13rev.
Location/Qualifiers
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/organism="Hordeum vulgare subsp. vulgare"
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/db_xref="GABI:270043"
/db_xref="taxon:112509"
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/tissue_type="germinating seeds"
/dev_stage="germinating seeds (48-96 h)"
/lab_host="Xl10-Gold"
/clone_lib="HV"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); Roots were grown for
two days on filter paper at room temperature. Due to a
cloning artefact caused by the kit, in most cases the
EcoRI site is NOT present as well as the EcoRI adapter
used for cloning. To excise the insert, restriction sites
upstream EcoRI should be used (e.g. BamHI, SalI, PstI).
NOTE: Also due to the cloning system used Blue/white
selection for recombinants is not 100% reliable.Average
insert size is 1 kb"

ORIGIN
Alignment Scores:
Pred. No.: 1.89e-107 Length: 609
Score: 1028.00 Matches: 189
Percent Similarity: 97.5% Conservative: 5
Best Local Similarity: 95.0% Mismatches: 5
Query Match: 35.5% Indels: 0

RESULT 19
LOCUS   BJ481805
DEFINITION
621 bp mRNA linear EST 23-MAY-2002
K. Sato unpublished cDNA library, strain H602 adult,
heading stage top three leaves Hordeum vulgare subsp. spontaneum
cDNA clone bah61p3 5', mRNA sequence.
ACCESSION BJ481805
VERSION 1
KEYWORDS GI:21160269
SOURCE EST.
ORGANISM Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 621)
Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasi Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..621
/organism="Hordeum vulgare subsp. spontaneum"
/mol_type="mRNA"

FEATURES
source

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Db      161 PheArgTyThrLeuLeuCysTyTrAlaAlaCysGluAlaProLeuIleLeuGluLeuGly 180
Db      12 TTCAAGATACACACTACTTTGCTATGCTGTGTGGAGCCCACTAAATCCTTGAATTGGGA 71
Qy      181 GlyTyriLeTyGlyGlnAenCysMetPheValValAenAaspTtpHisAlaSerLeuVal 200
Db      72 GGATATATTTATGACAGAGTTGCATGTTTGTGTGAACGATTGGCATGCCAGCCTTGTG 131
Qy      201 ProValLeuLeuAlaAlaLysTyArgProTyGlyValTyLysAaspSerArgSerIle 220
Db      132 CCAGTCTCTTCTGCTGCAAAAGTATAGACCATATGGAGTTTACAGAGATTTCTGCAGCACT 191
Qy      221 LeuValIleHisAenLeuAlaHisGlnGlyValGluProAlaSerThrTyProAaspLeu 240
Db      192 CTTGTTATATACATAATTTAGCACATCAGGGGTGGAGCCTGCAAGTACATATCTCTGATCTG 251
Qy      241 GlyLeuProProGluTtpTyGlyAlaLeuGluTtpValPheProGluTtpAlaAaArg 260
Db      252 GGATTGCCACCTGAATGGTATGGAGCTTTAGAAATGGGTATTTCCAGAAATGGCAAGAGG 311
Qy      261 HisAlaLeuAaspLysGlyGluAlaValAenPheLeuLysGlyAlaValValThrAlaAasp 280
Db      312 CATGCCCTTGACAAAGGTGAGGGGTAACTTTTGAAGGTGCAGTTGTGACAGCAGAT 371
Qy      281 ArgIleValThrValSerLysGlyTySerTtpGluValThrThrAlaGluGlyGln 300
Db      372 CGAATTGTGACCGTCAGTCAGGGTTATTTCATGGGGGTGCACACTGCTGAAGGTGGACAG 431
Qy      301 GlyLeuAenGluLeuLeuSerSerArgLysSerValLeuAenGlyLysValAenGlyLys 320
Db      432 GGCTCAATGAGCTCTTAAGCTCCCGAAAAGTGTCTTGAAATGGAATTTGAATGGAAAT 491
Qy      321 AspIleAenAaspTrpAenProAlaThrAaspLysCysIleProCysHisTySerValAasp 340
Db      492 GACATTAATGATTGGAACCCACACCGGACAAAGTGTCTCCCTCATCATTATTCTGTGAC 551
Qy      341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuPro 359
Db      552 GACCTCTCGAAAGGCCAAATGTAAGCTGAATTCAGAGGAGGCTGGGTTTACCT 608

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/strain="H602"
/sub_species="spontaneum"
/db_xref="taxon:77009"
/clone="bah61p3"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"

ORIGIN
Alignment Scores:
Pred. No.: 1.25e-106 Length: 621
Score: 1021.00 Matches: 188
Percent Similarity: 97.0% Conservative: 8
Best Local Similarity: 93.1% Mismatches: 6
Query Match: 35.3% Indels: 0
DB: 3 Gaps: 0

US-10-628-525A-21 (1-539) x BU481805 (1-621)
QY 183 IleTyrGlyGlnAsnCysMetPheValValAsnAspTTPHisAlaSerLeuValProVal 202
Db 14 ATTATGGACAGAGTGCATGTTGTGTGAACGATTGGCATGCCAGCCTTGTGCCAGTC 73
QY 203 LeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuVal 222
Db 74 CTTCTGCTGCAAGATATAGACATATGAGTTTACAGAGATTCGCGACACTCTTGTT 133
QY 223 IleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeu 242
Db 134 ATACATAATTTAGCACATCAGGCTGTGGAGCTGCAGTACATATCTCATCTGGGATTG 193
QY 243 ProProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgHisAla 262
Db 194 CCACCTGAATGTGTAGAGCTTTAGAAATGGGTATTTCCAGATGGGCAGAGGCGATGCC 253
QY 263 LeuAspLysGlyGluAlaValAsnPheLeuLysGlyValAlaValThrAlaAspArgIle 282
Db 254 CTTGACAGGGTGTGGCGGTAACTTTTGAAGGTGCAGTTGTGACAGCAGATCGAAT 313
QY 283 ValThrValSerLysGlyTyrSerTrpGluValThrThrAlaGlnGlyGlyGlnGlyLeu 302
Db 314 GTGACCGTCAGTCAGGGTTATTTCATGGGAGGTCAACAATGCTGTAAGGTGGACAGGCGCTC 373
QY 303 AsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIle 322
Db 374 AATGAGCTCTTAAGCTCCCGAAAGAGTGTCTTGAATGGAATTTGTAATGGAATTCACATT 433
QY 323 AsnAspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspLeu 342
Db 434 AATGATTGGAACCCACACCGGACAGTGTCTCCCTCATCATATTCTGTGACGACCTC 493
QY 343 SerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgPro 362
Db 494 TCTGGAAGGCCCAATTAAGCTGAATTCAGAGGAGCTGGTTTACCTGTAAGGGAG 553
QY 363 AspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIle 382
Db 554 GATGTTCACTGATTTGGCTTTATTGGAAGCTGGATTACCAAGAGGCGATTGATCTCAT 613
QY 383 GlnLeu 384
Db 614 AAAATG 619

RESULT 20
BU027679
LOCUS
DEFINITION
BU027679, yg, ab1 OH EFGHJ sunflower RHA280 Helianthus annuus cDNA
clone OHG7B12, mRNA sequence.
ACCESSION
BU027679
VERSION
BU027679.1 GI:22463199
KEYWORDS
Helianthus annuus (common sunflower)
```

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ORGANISM Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Asteroidae;
Heliantheae; Helianthus.
REFERENCE
1 (bases 1 to 704)
AUTHORS
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Leveille, D., Chevalier, P., Ziegler, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
JOURNAL
Unpublished (2002)
COMMENT
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundo Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
singletons, see http://cgpdb.ucdavis.edu/ for details.
Plate: OHG7 row: B column: 12.
FEATURES
Location/Qualifiers
1..704
source
/organism="Helianthus annuus"
/mol_type="mRNA"
/cultivar="RHA280"
/db_xref="taxon:4232"
/clone="OHG7B12"
/lab_host="E.coli"
/clone_lib="OH EFGHJ sunflower RHA280"
/note="Vector: pBRCDNA5fiab; The library was constructed
from 11 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG TISSUE=shoots environmental stress
TAG LIB=OH EFGHJ sunflower RHA280
TAG_SEQ=TCGCAACGGG"

ORIGIN
Alignment Scores:
Pred. No.: 1.99e-106 Length: 704
Score: 1020.00 Matches: 184
Percent Similarity: 89.3% Conservative: 25
Best Local Similarity: 78.6% Mismatches: 25
Query Match: 35.3% Indels: 0
DB: 5 Gaps: 0

US-10-628-525A-21 (1-539) x BU027679 (1-704)
QY 234 AlaserThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrVal 253
Db 1 GCATCACTTACGGCAATTTTGGATTGCCCCAGAAATGTTACGAGCTTTGGGTGGTA 60
QY 254 PheProGluTyrAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLys 273
Db 61 TTTCTCTACTTGGGCAAGAACACATGCTTTGACACCGCGAGGCTGTTAATGTTCTAAA 120
QY 274 GlyAlaValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluVal 293
Db 121 GGTGCAATTTGTCACCTGCTGACCGGATCTGACAGTTAGCCAGGCTATTCTTGGGAAAT 180
QY 294 ThrThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeu 313
Db 181 ACACACACAGAGGTGGAAATGCTTGTAGACGAGCTTCTTGGTAGTCCGAAGACTGTTTA 240
QY 314 AsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIle 333
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Db 241 AATGGATCACAATGGCATTCATTAATGACTGGAAATCCTCTAGATGCCATATC 300  
 Qy ProCysHisTyrSerValAspLeuSerGlyLysAlaLysCysGlyAlaLeuGln 353  
 Db CCTTCTCATTTACTCTCTTGATGACCTTTTCAGGGAAGATTGAATGCAAGATTGCTCTTCAA 360  
 Qy LysGluLeuGlyLeuProLeuArgProAspValProLeuLeuGlyPheLeuGlyArgLeu 373  
 Db AGGAAATAGGCTCTTCAGTTTCGGCCAGATTGTCTCATTTGATGGGTTTATTGGAGATTG 420  
 Qy AspTyrGlnLysGlyLeuAspLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 393  
 Db GACTACCAAGAGGTATTGACATAATTTCTATCGGAATCTCCAGAAATTTGTCAGAGATGAT 480  
 Qy ValGlnPheValMetLeuGlySerGlyAspProGluLeuGluLeuAspTyrMetArgSerThr 413  
 Db GTTCAGTTTATTAATGCTTGGATCCGAGAAAAAATATATGAAGACTGGATGAGGCCACT 540  
 Qy GluSerLeuPheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHis 433  
 Db GAAGCAACGTTTAAAGATAAATTCCTGGGATGGGTTGGATTCAACGTCCTCATATCTCAC 600  
 Qy ArgIleThrAlaGlyCysAspLeuLeuLeuMetProSerArgPheGluProCysGlyLeu 453  
 Db CGATAACACAGAGATGATATTTACTAATGCCCTCGAGATTCGAGCCATGCGGTTTA 660  
 Qy AsnGluLeuTyrAlaMetGlnTyrGlyThrValProValVal 467  
 Db AATCAGCTGTATGCAATGAGATAGGAACCGTACCAGTGTA 702

## RESULT 21

BM412062 727 bp mRNA linear EST 22-JAN-2002  
 LOCUS EST596389 tomato breaker fruit Lycopersicon esculentum cDNA clone  
 DEFINITION cLEGS8J10 5' end, mRNA sequence.

ACCESSION BM412062

VERSION 1

KEYWORDS 1 (bases 1 to 727)

SOURCE Lycopersicon esculentum (Solanum lycopersicum)

ORGANISM Lycopersicon esculentum

REFERENCE 1 (bases 1 to 727)  
 Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A.,  
 Tsai, J., Bougri, O., Kirkness, E., Uterback, T., Van Aken, S.,  
 Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and  
 Giovannoni, J.

Generation of ESTs from tomato fruit tissue, breaker stage (2002)

Unpublished (2002)

Contact: CUGI

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

This clone is available through the Clemson University Genomics Institute

Seq primer: T3.

Location/Qualifiers

1. 727

/organism="Lycopersicon esculentum"

/mol\_type="mRNA"

/cultivar="TA496"

/db\_xref="taxon:4081"

/clone="cLEGS8J10"

/tissue\_type="Pericarp"

/dev\_stage="Breaker"

/lab\_host="SOLR"

/clone\_lib="tomato breaker fruit"

/notes="Vector: pBluescriptSKmCuadapt; Site 1: EcoRI;

Site 2: XhoI; supplier: Boyce Thompson Institute;

sequencing: The Institute for Genomic Research. Fruit

were harvested at the breaker stage (first sign of

lycopene accumulation on the blossom end of fruit). Fruit  
 were cut in half and the seeds and locules were discarded  
 prior to freezing the pericarp."

## ORIGIN

Alignment Scores: 4.64e-106 Length: 727  
 Pred. No.: 1017.00 Matches: 181  
 Score: 88.4% Conservative: 33  
 Percent Similarity: 74.8% Mismatches: 28  
 Best Local Similarity: 35.2% Indels: 0  
 Query Match: 3 Gaps: 0  
 DB: 3

US-10-628-525A-21 (1-539) x BM412062 (1-727)

Qy 161 PheArgTyrThrLeuLeuCysTyrAlaLaCysGluAlaProLeuLeuLeuGly 180  
 Db 1 TTTGGCTTCACTTGTCTTCTCAGCGCATGTGAGCGCATTTCTTCCACTGGGA 60  
 Qy 181 GlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHisAlaSerLeuVal 200  
 Db 61 GGCTTCACTTATGAGAGAGTCTTGTCTTCGCTAATGATTGGCATGCTTCCCTGGTT 120  
 Qy 201 ProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
 Db 121 CCTTTACTTTTAGCAGCAAGTATCGTCTTATGGTGTTCACAGGATGCTCGTAGTATT 180  
 Qy 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240  
 Db 181 GTCGAATACACAACATTCACATCAGGGAGTGGAGCTGCACCAACCTACAATTTG 240  
 Qy 241 GlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrPalaArgArg 260  
 Db 241 GGATTGCTCTCAATGATGATGAGCATTGATGATATTTCCACATGGGCAAGGGCC 300  
 Qy 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAsp 280  
 Db 301 CATGCGCTTGACACTGGTGAACAGTGAATGTTTGAAGGGGCAATCTCAGTTGCTGAT 360  
 Qy 281 ArgIleValThrValSerLysGlyTyrSerTyrGluValThrAlaGluGlyGln 300  
 Db 361 CGGATATGACAGTATGAGCGGATGATCATGGGAATTAACAATCTCTGAAGGGGATAT 420  
 Qy 301 GlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320  
 Db 421 GGCTACATGAGCTGCTGAGCAGTAGACAGTCACTTCTTAATGGAATTACTAATGNAAT 480  
 Qy 321 AspIleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340  
 Db 481 GATGTTAATGATTGGAACCGTCGACAGATGAGCATATTGCTTCGCATTACTCCATCAAT 540  
 Qy 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGluLysGluLeuGlyLeuProIle 360  
 Db 541 GACCTCTCTGGAAGGCTCAGTGCAAGACTGATCTGCAAAAGAACTGGGCGCTTCAATT 600  
 Qy 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380  
 Db 601 CGACCTGATTGTCGGCTGATTGATTTATTGGAAGGCTGGACTACCAAGAAAGTGTGAC 660  
 Qy 381 LeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
 Db 661 ATAATCTCTGACCAATTCAGAACTTTTTCAGAGAGGATGTCAATTTGTATGCTTGA 720  
 Qy 401 SerGly 402  
 Db 721 TCTGGT 726

## RESULT 22

AY109714

LOCUS

DEFINITION

AY109714

ACCESSION

VERSION

AY109714 2498 bp mRNA linear HTC 25-FEB-2005

Zea mays Cui171\_2 mRNA sequence.

AY109714

AY109714.1 GI:21213541



1710 GGGCGGCGGACCTGGAGGACATGCTGGCGGTTTCGAGTCGGAGCACAGCCACNNNNN 1769  
 QY 422 ArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle 441  
 Db 1770 NNN  
 QY 442 LeuLeuMetProSerArgPheGluProCysGlyLeuAenGlnLeuTyrAlaMetGlnTyr 461  
 Db 1930 CTGCTGATGCGCTCGCGGTTTCGAGCCGTGGCGGCTGAACACAGCTCTACGCCATGGCGTAC 1889  
 QY 462 GlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAenPheAen 481  
 Db 1890 GGGACCGTGGCGGTGGTGGCGCGTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  
 QY 482 ProPheGlyGluAenGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGlu 501  
 Db 1950 CCGTTCACACGACC-----GGGCTCGGTGGGACGTTTCGACCGCGGCGGCGAAC 2000  
 QY 502 AsnMetPheValAspIleAlaAenCys-----AsnIleTyrIleGlnGlyThr 517  
 Db 2001 CGATGATCGACCGGCTCTCGACTGCTCCACGCTCACCGACTACCGGAACTACAGAGAGAGCTGG 2060  
 QY 518 GlnValLeuLeuGlyArgAlaAenGluAlaAenGlyHisValLysArgLeuHisValGlyPro 537  
 Db 2061 CGCGGCTCGAGGCG-----GGCGGCGATGCGCCAGGACCTCGAGCTGGGACCA 2108  
 QY 538 CysArg 539  
 Db 2109 CGCGCG 2114

RESULT 23  
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 LOCUS  
 DEFINITION FGAS060124 Triticum aestivum 808 bp mRNA linear EST 09-NOV-2004  
 aestivum cDNA, mRNA sequence.  
 CV765737  
 EST.  
 CV765737.1 GI:55608403  
 Triticum aestivum (bread wheat)  
 Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.  
 1 (bases 1 to 808)  
 Allard, F., Crosby, W.L., Danyluk, J., Rudes, P., Frick, M., Gaudet, D.,  
 Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Larocque, A.,  
 Links, M.G., McCarthy, E.L., Montoy, A., Muzak, I., Nilson, D.,  
 Penniket, C., Roach, J.L. and Sarhan, P.  
 Functional Genomics of Abiotic Stress In Wheat and Canola Crops  
 Unpublished (2003)  
 Contact: Wm L Crosby  
 Bioinformatics  
 University of Saskatchewan, Department of Computer Science  
 1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
 Saskatchewan, S7N 5A9, Canada  
 Tel: 306 966 1769  
 Fax: 306 966 2033  
 Email: fgas\_est@cs.usask.ca  
 This sequence is the direct result of the Base calling software  
 Phred (default parameters). It is the raw base calls. To aid in the  
 identification of the high quality insert the software Lucy  
 (default parameters) has been run on this sequence. Lucy identified  
 the region [97,720].  
 Plate: WEP044 row: L column: 14.  
 Location/Qualifiers  
 1..808  
 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4565"  
 /clone\_lib="Triticum aestivum FGAS: Library 2 Gate 3"  
 /notes="Organ: Crown and leaf; Vector: pCMV.SPORT6; Aerial  
 parts (crown and leaf) of wheat cultivar Norstar from  
 control and long exposure times to low temperature. 4 mRNA

populations were combined before constructing the library;  
 7 days non-acclimated plants and 1, 23, and 53 days  
 cold-acclimated at 4°C. Non-acclimated and cold-acclimated  
 plants were grown in vermiculite. This is the only library  
 that was done according to the Invitrogen manual, and  
 therefore, a percentage of clones will not have the 3  
 prime end because of NotI digestion within the cDNA."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2,07e-105 Length: 808  
 Score: 1012.00 Matches: 196  
 Percent Similarity: 89.3% Conservative: 13  
 Best Local Similarity: 83.8% Mismatches: 25  
 Query Match: 35.0% Indels: 2  
 DB: 8 Gaps: 0

US-10-628-525A-21 (1-539) x CV765737 (1-808)

QY 304 GluLeuLeuSerSerArgLysSerValLeuAenGlyIleValAenGlyIleAenGlyIleAen 323  
 Db 108 GAGCTCTTAAAGTTCCCGAAAAAGTGTATTGAATGGAATTGTAAATGAATTGATTAAAT 167  
 QY 324 AspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSer 343  
 Db 168 GATTGGAACCCCAACCCACGCAAGTGTCTCCCTCATCATTAATTCTGTGATGACCTCTCT 227  
 QY 344 GlyLysAlaLysCysLysGlyAlaLeuGlnLysGlyLeuGlyLeuProIleArgProAsp 363  
 Db 228 GGAAGGCCAATGTAAGCTGAATTCAGAGAGCTGGGTTTACCTGTAAAGGAGAT 287  
 QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 383  
 Db 288 GTTCTCTGATTGGCTTTATTGGAAGCTGATTTACCAAGAAAGCATTTGACCTCATTTAA 347  
 QY 384 LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403  
 Db 348 ATGGCCATTCAGATCTCATGAGGAGGAGCTGAGTTTGTCTGATCTGGATCTGGGGAT 407  
 QY 404 ProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheAspGly 423  
 Db 408 CCAGTTTTTGAGCGTGGATGAGATCTACGAGTCGAGCTACAGGATAAATTCCTGGTGGT 467  
 QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443  
 Db 468 TGGTTTGGATTAGTGTTCAGTTTCCACAGATAACTGACAGTTTGGGATATATTGTTA 527  
 QY 444 MetProSerArgPheGluProCysGlyLeuAenGlnLeuTyrAlaMetGlnTyrGlyThr 463  
 Db 528 ATGCCATCCAGATTCGAACCTTGGCGTCTTAATCAGCTATATCTATGCAATATGGCACA 587  
 QY 464 ValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAenPheAenProPhe 483  
 Db 588 GTTCTCTGATTTCATGGAACCTGGGGGCTCCCGAGACACAGTCGAGACCTTCAACCCCTTT 647  
 QY 484 GlyGluAenGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAenMet 503  
 Db 648 GGTGCAAAAGGAGAGGAGGTACAGGTTGGCGTCTTCACCGCTAACCGTGGACAGATG 707  
 QY 504 PheValAspIleAlaAenCysAenIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523  
 Db 708 TT-GTGGGATTCGGAACCGGATTCGACATTCAGGAGGACACAGCCGCTCTGGGAGGG 766  
 QY 524 AlaAenGluAlaArgHisValLysArgLeuHisValGlyPro 537  
 Db 767 GCTCATGAAGGAGGAGGATGACAAAAGACA-TAGCTGGGACCA 807

RESULT 24  
 AV111778  
 LOCUS  
 DEFINITION Zea mays Cl171\_1 mRNA sequence.  
 AV111778  
 ACCESSION  
 VERSION AY111778.1 GI:21216368

KEYWORDS	HTC.	Db
SOURCE	Zea mays	1446 GTTGTGGGAGCTTTTACCCAAAGGCTTTAGCGAAGAGGACATCGTGTGTATGTTGTGGTA 1505
ORGANISM	Zea mays	90 ProAargTyrLeuAasnGlyThrSerAspLysAsnTyrAlaAasnAlaPheTyrThrGluLys 109
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	1506 CCAAGGTAT-----GGGACATATGTGGAGCGCTTTGATATATCGGAATC 1547
AUTHORS	1 (bases 1 to 3248) Gardiner, J., Schroeder, S., Polacco, M.L., Sanchez-Villeda, H., Fang, Z., Morgante, M., Landewe, T., Fengler, K., Useche, P., Hanafey, M., Tingey, S., Chou, H., Wing, R., Soderlund, C. and Coe, E.H. Jr.	110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129
TITLE	Anchoring 9,371 maize expressed sequence tagged unigenes to the bacterial artificial chromosome contig map by two-dimensional overgo hybridization	1548 CGGAATACTACAAAGCTCGAGACAGGACCTAGAGTGAAGTAATTTCCATGCAATTTATT 1607
PUBMED	Plant Physiol. 134 (4), 1317-1326 (2004)	130 AspSerValAspTrrpValPheValAspHisProSerTyr---HisArgProGlyAsnLeu 148
REFERENCE	15020742	1608 GATGAGTCGACTTTGTGTTCATTGATGCCCTCTCTTTCCGGCACCGTCAAGATGACATA 1667
AUTHORS	2 (bases 1 to 3248) Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.	149 TyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyr 168
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes	1668 TAT-----NNNNNAAGTAGGACGAAATCATGAAGCGCATGATTTGTTTGAAG 1718
JOURNAL	Unpublished (2002)	169 AlaAlaCysGluAlaProLeuLeuLeuGlyGlyTyrIleTyrGlyGln---Asn 187
REFERENCE	3 (bases 1 to 3248) Coe, E.H.	1719 GTTGTCTGTGAGTTCTTGGCAGCTTCATGCGGTGGTGTGCTACGAGATGGAAT 1778
AUTHORS	Direct Submission	188 CysMetPheValValAsnAspTrrpHisAlaSerLeuValProValLeuLeuAlaLys 207
TITLE	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA	1779 TTGGTGTTCATTGCCCATGATGGCACACTGCATCTCTGCTGTTTATCTGAAGGCATAT 1838
JOURNAL	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.	208 TyrArgProTrrpGlyValTrrpLysAspSerArgSerIleLeuValIleHisAsnLeuAla 227
COMMENT		1839 TACAGAGACCATGGTGTAAATGCAGTACACTCGCTCCGTCCTCATACATAACATCGCC 1898
FEATURES	Location/Qualifiers	228 HisGlnGlyValGluProAlaSerThrTrrpProAspLeuGlyLeuProGluTrrpTyr 247
source	1. .3248 /organism="Zea mays" /mol_type="mRNA" /db_xref="MaizeGDB:630529" /db_xref="taxon:4577" /clone_lib="Maize Mapping Project/DuPont Consensus Library" /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACS in conjunction with the Maize Mapping Project"	1899 CACGAGGCGGTGCTCTGTAGATGAATCCCGTACATGGACTTGCCTGAACACTACTT 1958
ORIGIN		248 GlyAlaLeuGluTrrpValPheProGluTrrpAlaArgHisAlaLeuAspLysGlyGlu 267
Alignment Scores:		1959 CAACATTTTCGAGCTGACGATCCCGTC-----GGTGGCGAG 1994
Pred. No.:	3,16e-104	268 AlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLys 287
Score:	1010.00	1995 CACGCCAACATCTTTGCGCGGGTCTGAAGATGCGACCGGGTGGTACTGTGACGCCG 2054
Percent Similarity:	56.0%	288 GlyTrrpSerTrrpGluValThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSer 307
Best Local Similarity:	42.6%	2055 GGCTACCTGTGGAGCTGAACAGTGAAGCGGCTGGGGCTTCCACGACATCATCCGT 2114
Query Match:	34.9%	308 SerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrrpAsnPro 327
DB:	4	2115 TCTAACGACTGGAAGATCAATGGCATCGTGAACGSCATCGACACCAGGAGTGGAAACCC 2174
US-10-628-525A-21 (1-539) x AY111778 (1-3248)		328 AlaThrAspLysCysIlePro-----CysHisTrrpSerValAspAspLeu--- 342
QY	10 LeuGlyLeuGluProGluGlyIleAlaGluGlySerIleAspAsnThrValValAla 29	2175 AAGGTGGACGTGCACCTTCGGTTCGGACGGCTACACCACTACTCTCTCGAGACATCGAC 2234
Db	1308 GTTGGTGCAATGATGCTGTTCTTTTGAACATTATGGGACAT----- 1352	343 SerGlyLysAlaLysCysGlyValAlaLeuGlnLysGluLeuGlyLeuProIleArgPro 362
QY	30 SerGluGlnAspSerGluIleValValGlyLysGluGlnAlaArgAlaLysValThrGln 49	2235 GCTGGAAGCGCAGTGCAGCGGCTTCGACGGGAGCTGGGCCCTTGGAGTGGCGGCAC 2294
Db	1353 -----GATCTCGGCGCTTTGCGCGGAGAT-----GTTATG 1385	363 AspValProLeuIleGlyPheIleGlyArgLeuAspTrrpGlnLysGlyIleAspLeuIle 382
QY	50 SerIleValPheValThrGlyGluAlaSerProTrrpAlaLysSerGlyGlyLeuGlyAsp 69	2295 GACGTGCCGTGCTCGGCTTCATCGGCGTCTCGATGGACAGAAGGCGGTGGACATCATC 2354
Db	1386 ACGTGATCGTGGTCTGCTGATGTCTTCATGGTGCACAAACAGGTGGTCTTGGAGAT 1445	383 GlnLeuIleIleProAspLeuMetArgLysValGlnPheValMetLeuGlySerGly 402
QY	70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValMet 89	2355 GGGGACCGCATGCGCGTGGATGTCGCGGCGACGACGTGCAGCTGGTGTGATGCTGGCGCCGG 2414



PCR Primers  
 FORWARD: T3 20mer  
 BACKWARD: T7 21mer  
 Plate: 033 row: A column: 05  
 Seq primer: T3 20mer  
 High quality sequence stop: 678.  
 Location/Qualifiers  
 1. .678  
 /organism="Mesembryanthemum crystallinum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3544"  
 /clone="MCT033A05"  
 /tissue\_type="leaf"  
 /dev\_stage="five-week-old"  
 /clone\_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Craesulacean acid metabolism, phase IV (5:30 PM)."  
 /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UnizapXR vector and cDNA synthesis kit."

## FEATURES

source

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,15e-103 Length: 678  
 Score: 991.00 Matches: 176  
 Percent Similarity: 88.9% Conservative: 24  
 Best Local Similarity: 78.2% Mismatches: 25  
 Query Match: 34.3% Indels: 0  
 DB: 6 Gaps: 0

US-10-628-525A-21 (1-539) x CA839938 (1-678)

QY 128 TyrArgAspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsn 147  
 DB 3 TATAGGGATGGTGTTCATTTGGTGTTCATTCCTCTATCAGCGACTGGAAAT 62  
 QY 148 LeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCys 167  
 DB 63 CCTTATGGTGATGATGTTTGGTCTTTGGTGATATACAGTTCGGTTCACCTTGCTTTGC 122  
 QY 168 TyrAlaAlaCysGluAlaProLeuLeuLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsn 187  
 DB 123 CATGCAGCATGTGAAGCTCTCTGTCTCTCCACTTGGAGGTACACTTATGGGGAAG 182  
 QY 188 CysMetPheValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaLys 207  
 DB 183 TGTATGTTCTTGTATGATTTGGATGGCATGCAGGCTTGTGCCAGTACTTTTGGCAGCGAAA 242  
 QY 208 TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla 227  
 DB 243 TACCGTCTTCAGGAGTATATAAGATGCAAGAGCTGTACTGTATACACAACTTTT 302  
 QY 228 HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTrpTyr 247  
 DB 303 CATCAAGTGTGGAGCTGCAGTGACATATGATACTTAGGACTTCCCGGCACTGGTAC 362  
 QY 248 GlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGlyGlu 267  
 DB 363 GGGTCACCTGGAATGGTGTTCGCGAGTGGGCAAGACACATGAACCTTGACAAAGGTGAA 422  
 QY 268 AlaValAsnPheLeuLysGlyAlaValThrAlaAspArgIleValThrValSerLys 287  
 DB 423 GCTGTCAATATTTCTTAAGGAGCCATTTGACCTCGGATAGATACTTACAGTTAGCCAG 482  
 QY 288 GlyTyrSerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSer 307  
 DB 483 GGATATTTCATGGGAATAACAACCTGACAGGTGGATACGGCTTGCACTGAGTTACTAAGC 542  
 QY 308 SerArgLysSerValLeuAsnGlyIleValAsnGlyIleValAsnGlyIleAsnAspTrpAsnPro 327  
 DB 543 AGTCGAAAGTTTCGTACTGAATGGGATTTGAATGGAATTAATPACTTCTCTGAATGCCGCCA 602

QY 328 AlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLys 347  
 DB 603 TCTACTGATGACATATTGCAGCTACTACACTGTTCAGCATCTCTCTGTGAAGGCTCAA 662  
 QY 348 CysLysGlyAlaLeu 352  
 DB 663 TGCAAAGCTGACCTG 677  
 RESULT 27  
 BUSY1816  
 LOCUS  
 DEFINITION BUSY1816 629 bp mRNA linear EST 16-SBP-2002  
 946185B04.y1 946 - tassal primordium prepared by Schmidt lab Zea  
 mays cDNA, mRNA sequence.  
 ACCESSION BUSY1816  
 VERSION BUSY1816.1 GI:22935541  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 629)  
 AUTHORS Walbot,V.  
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford  
 UNIVERSITY  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 946185 row: B column: 04.  
 FEATURES  
 source  
 1. 629  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="OH43"  
 /db\_xref="taxon:4577"  
 /tissue\_type="tassels"  
 /dev\_stage="just after the transition from vegetative to  
 inflorescence development"  
 /lab\_host="XL0LR"  
 /clone\_lib="946 - tassal primordium prepared by Schmidt  
 lab"  
 /note="Organ: tassels; Vector: HybridZAP; Site 1: EcoRI;  
 Site 2: XhoI; George Chuck dissected immature tassels  
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA  
 library in HybridZAP. Sample insert size range was 350 bp  
 to 3 Kb with a 1 Kb average."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 4,02e-102 Length: 629  
 Score: 982.00 Matches: 188  
 Percent Similarity: 99.5% Conservative: 0  
 Best Local Similarity: 99.5% Mismatches: 1  
 Query Match: 33.9% Indels: 1  
 DB: 5 Gaps: 0  
 US-10-628-525A-21 (1-539) x BUSY1816 (1-629)  
 QY 351 AlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIle 370  
 DB 6 GCATTGCAGAGGAGCTGGGTTTACCTATAGGCTGATGTTCTCTGATTCGCTTTATT 65  
 QY 371 GlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeuMet 390  
 DB 66 GGAAGTTGGATTATCAGAAAGGCGCATTCATTCATCACTTATCATCAGATCTCATG 125  
 QY 391 ArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrpMet 410



Db 126 CGGAGAGATGTTCAATTTGTTCATGCTGGATCTGGTGAACCCAGAGCTTGAAGATTGGATG 185

Qy 411 ArgSerThrGluSerIlePheLeuAspLysPheArgGlyTTPValGlyPheSerValPro 430

Db 186 AGATCTACAGAGTGCATCTTCAAGGATAAAATTTCTGGATGGGTTGGATTAGTTGTCCA 245

Qy 431 ValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluPro 450

Db 246 GTTTCCTCCACCAATTAACCTGCGGCTGGCATATATTTGTTAATGCCATCCAGATTCCGAACCT 305

Qy 451 CysGlyLeuAenGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThr 470

Db 306 TGTGCTCTCATACGATATGCTATGCTATGCGATATGCCACAGTTCTGTTGTCCATGCCAACT 365

Qy 471 GlyGlyLeuArgAspThrValGluAenPheAenProPheGlyGluAenGlyGluGlnGly 490

Db 366 GGGGGCCTTAGAGATACCGTGGAGAACTTCAACCTTTCGGTGAAGATGGAGACGGGT 425

Qy 491 ThrGlyTTPAlaPheAlaProLeuThrThrGluAenMetPheValAspIleAlaAenCys 510

Db 426 ACAGGGTGGGCAATTCGCACCCCTTAACACACAGAAACATGTT-GTGGACATTCGGAACCTGC 484

Qy 511 AsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAenGluAlaAenHisVal 530

Db 485 AATATCTACATACAGGAGACACACAGTCTCTCTGGAGAGGCTAATGAGGAGCAATGTC 544

Qy 531 LysArgLeuHisValGlyProCysArg 539

Db 545 AAAAGACTTCACGTGGGACCATGCGC 571

## RESULT 28

## BM412224

## LOCUS

## DEFINITION

EST586551 tomato breaker fruit Lycopersicon esculentum cDNA clone

clEGS9110 5' end, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## Location/Qualifiers

## 1..747

## /organism="Lycopersicon esculentum"

## /mol\_type="mRNA"

## /cultivar="TA496"

## /db\_xref="taxon:4081"

## /clone="clEGS9110"

## /tissue\_type="Pericarp"

## /dev\_stage="breaker"

## /lab\_host="SOLR"

## /notes lib="tomato breaker fruit"

## /clone lib="pBluescriptSKmCuadapt; site 1: EcoRI;

## Site 2: XhoI; supplier: Boyce Thompson Institute;

## sequencing: The Institute for Genomic Research. Fruit

## were harvested at the breaker stage (first sign of

## seq primer: T3.

## Unpublished (2002)

## Contact: CUGI

## Clemson University

## Genomics Institute

## 100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

## This clone is available through the Clemson University Genomics

## Institute

## Seq primer: T3.

## Location/Qualifiers

## 1..747

## /organism="Lycopersicon esculentum"

## /mol\_type="mRNA"

## /cultivar="TA496"

## /db\_xref="taxon:4081"

## /clone="clEGS9110"

## ORIGIN

## Alignment Scores:

## Pred. No.:

## Score:

## Percent Similarity:

## Best Local Similarity:

## Query Match:

## DB:

## US-10-628-525A-21 (1-539) x BM412224 (1-747)

## Qy

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VERSION BQ466504.1 GI:21274286
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 616)
AUTHORS Zhang,H., Potokina,E., Michalek,W., Weschke,W., Stein,N. and
Graner,A.
TITLE Barley ESTs from germinating seeds
JOURNAL Unpublished (2002)
COMMENT Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 616 Std Error: 0.00
Plate: 2 row: 1 column: 15
Seq primer: M3rev.
FEATURES             Location/Qualifiers
     source
       1..616
         /organism="Hordeum vulgare subsp. vulgare"
         /mol_type="mRNA"
         /cultivar="Barte"
         /sub_species="vulgare"
         /db_xref="taxon:112509"
         /clone="HT02L15"
         /tissue_type="endosperm early"
         /dev_stage="0-16 hours after imbibition"
         /lab_host="XL10-Gold"
         /clone_lib="HT"
         /note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of
cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinats is not 100% reliable."

ORIGIN
Alignment Scores:
Pred. No.:      1,238-100      Length:      616
Score:          969.00        Matches:    178
Percent Similarity: 92.6%      Conservative: 9
Best Local Similarity: 88.1%   Mismatches: 15
Query Match:     33.5%        Indels:     0
DB:              5           Gaps:       0

US-10-628-525A-21 (1-539) x BQ466504 (1-616)

QY 300 GlnGlyLeuAsnGluLeuSerArgGlySerValLeuAsnGlyValLeuAsnGly 319
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 6 CGAGGCCCTCAATGAGCTCTTAAGTCCCGAAGAAAGTGTCTGAATGGAATTTGAATGA 65

QY 320 IleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerVal 339
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 66 ATTGACATTAAATGATTGGAACCCACCGACCAAGTGTCTCCCTCATCATTTCTGTGC 125

QY 340 AspAspLeuSerGlyValAlaLysCysValysGlyAlaLeuGlnLysGluLeuGlyLeuPro 359
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 126 GACGACCTCTCTGGAAAGGCCAAATGTAAGCTGAATTCAGAGGAGCTGGGTTTACCT 185

QY 360 IleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIle 379
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 186 GTAAGGGAGGAGTGTTCACATGATTGGCTTTATTGGNAGACTGGATTACCAAGAGGCATT 245

QY 380 AspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeu 399
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 246 GATCTCATTAATAATGCCATTCAGATCTCATGAGGGAAGAGCTACAGTTTGTCTATGCTT 305

```

```

QY 400 GlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAsp 419
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 306 GGATCGGGGATCCCGATTTTTCAGAGCTGGATGAGATCTACCGAGTCGAGCTACAAGGAT 365

QY 420 LysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCys 439
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 366 AATTCCTGGATGGGTTCGATTAGTGTTCAGTTTCCACAGATTAATCGAGGTTC 425

QY 440 AspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMet 459
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 426 GATATATTGTTAATGCCATCCAGATTGAACCTTGGCGTCTTAATCAGCTATATGCTATG 485

QY 460 GlnTyrGlyThrValProValHisAlaThrGlyGlyLeuArgAspThrValGluAsn 479
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 486 CAATATGGTACAGTTCCTGTTTCATGAACTGGGGGCTTCGAGACACGGTGGAGACC 545

QY 480 PheAsnProPheGlyCyluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThr 499
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 546 TTCACCCCTTTGGTGCACAAAGAGAGAGGAGGTACAGGGTGGCGTTCACACCTAAC 605

QY 500 ThrGlu 501
   |||
Db 606 GTGGAA 611

RESULT 30
CK045789
LOCUS
DEFINITION
CK045789
VERSION
CK045789.1 GI:58657109
SOURCE
EST.
ORGANISM
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 593)
AUTHORS Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W.,
Hu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X.,
Zheng,H., Cong,L., Lin,L., Yin,J., Geng,J., Li,G., Shi,J., Liu,J.,
Lv,H., Li,J., Wang,J., Deng,Y., Ran,L., Shi,X., Wang,X., Wu,Q.,
Li,C., Ren,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z.,
Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P.,
Wu,S. and Liu,J.
TITLE The Genomes of Oryza sativa: A History of Duplications
JOURNAL PLoS Biol. 3 (2), e38 (2005)
PUBMED 15685292
COMMENT Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
Fax: 86-571-56805884
Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 593
POLYA=No.
FEATURES             Location/Qualifiers
     source
       1..593
         /organism="Oryza sativa (indica cultivar-group)"
         /mol_type="mRNA"
         /cultivar="PA64s"
         /db_xref="taxon:39946"
         /tissue_type="panicle"
         /cell_type="ferile"
         /dev_stage="heading/flowering"
         /clone_lib="Oryza sativa cv. PA64s panicle ferile cDNA
library"

ORIGIN

```

## Alignment Scores:

Pred. No.:	7.44e-100	Length:	593
Score:	962.00	Matches:	174
Percent Similarity:	94.9%	Conservative:	13
Best Local Similarity:	88.3%	Mismatches:	10
Query Match:	33.3%	Indels:	0
DB:	7	Gaps:	0

US-10-628-525A-21 (1-539) x CK045789 (1-593)

Qy	31	GlulnAspSerGluileValValGlyGluAlaArgAlaLysValThrGlnSer	50
Db	2	GAATTCGGCAGGAGATCATGGTGTGAGGAGCAGCTCAAGCTAAAGTAAACGCGC	61
Qy	51	IleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspVal	70
Db	62	GTTGTCTTTCTTAACCGGTGAAGCTTCTCTTATGCAAGTCAGGTGACCTAGGAGATGTT	121
Qy	71	CysGlySerLeuProValAlaAlaLeuAlaAlaArgGlyHisArgValMetValMetPro	90
Db	122	TGTGGTTTCATGCGCAATTCCTTGTCTTCTGTGTCATCTGTGTGATGGTTGTAATGCCG	181
Qy	91	ArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHis	110
Db	182	AGATACATGACGGGGCTTGAACAAAAATTTTGCACCGCATTTTACACTGAGAGCAC	241
Qy	111	IleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAsp	130
Db	242	ATTAAGATTCCATGCTTTGGCGGAGAACATGAAGTTACTTTTTTCAACGAGTATAGGAT	301
Qy	131	SerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyrGly	150
Db	302	TCGTGTGATTGGGTGTTTGTGTATCATCCCTCATATCATAGACCTGGAAATTTGTATGGA	361
Qy	151	AspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAla	170
Db	362	GATAATTTTGTGCTTTTGGCGATATACATTGATATACACTCCCTGTCTATGCGCGC	421
Qy	171	CysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPhe	190
Db	422	TGTGAAGCCCCATTATTTCTTGAACCTGGGAGGATATATCTATGACAGAAATGCATGTTT	481
Qy	191	ValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaLysTyrArgPro	210
Db	482	GTTGTGAATGATGGCATGCCAGTCTTGTGCCAGTCCCTCTTGTCTGCAAAATATAGACCA	541
Qy	211	TyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla	227
Db	542	TATGTGTGTATACAGGAGATGCCCGAGTGTCTTGTATCATCAATATCTAGCA	592

Search completed: April 1, 2006, 19:23:27

Job time : 8717.03 secs





83	510.5	17.6	1650	3	US-09-252-991A-8097	Sequence 8097, Ap
84	510.5	17.6	2145	3	US-09-252-991A-8205	Sequence 8205, Ap
85	503.5	17.4	2652	3	US-09-115-704-1	Sequence 1, Appli
86	503.5	17.4	2652	3	US-09-780-115-1	Sequence 1, Appli
87	503.5	17.4	3430	3	US-10-163-214-1	Sequence 1, Appli
88	502	17.4	3386	3	US-10-163-214-11	Sequence 11, Appl
89	498	17.2	3453	3	US-10-163-214-5	Sequence 5, Appli
90	456.5	15.8	6027	2	US-08-968-542C-1	Sequence 1, Appli
91	456.5	15.8	6027	3	US-09-554-467A-1	Sequence 1, Appli
92	398.5	13.6	4121	3	US-09-638-524A-1	Sequence 1, Appli
93	394.5	13.6	4122	3	US-10-197-220-84	Sequence 84, Appl
94	332	13.3	1275	3	US-10-163-214-9	Sequence 9, Appli
95	386	13.3	310	3	US-09-118-990A-31	Sequence 31, Appl
96	379.5	13.1	1431	3	US-10-197-220-53	Sequence 53, Appl
97	379.5	13.1	123025	3	US-09-198-452A-1	Sequence 1, Appli
98	379.5	13.1	1230230	3	US-09-438-185A-1	Sequence 1, Appli
99	336.5	11.6	1664976	3	US-08-916-421B-1	Sequence 1, Appli
100	336.5	11.6	1664976	3	US-09-692-570-1	Sequence 1, Appli
101	249.5	8.6	384	3	US-09-118-990A-32	Sequence 32, Appl
102	244.5	8.5	1180	3	US-10-197-220-39	Sequence 39, Appl
103	198	6.8	1664976	3	US-08-916-421B-1	Sequence 1, Appli
104	198	6.8	1664976	3	US-09-692-570-1	Sequence 1, Appli
105	193	6.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
106	193	6.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
107	176.5	6.1	266	3	US-09-313-294A-3737	Sequence 3737, Ap
108	174	6.0	264	3	US-09-107-433-890	Sequence 890, Ap
109	164	5.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
110	164	5.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
111	152.5	5.3	3785	3	US-09-899-718A-1	Sequence 1, Appli
112	151.5	5.2	1293	3	US-09-602-787A-175	Sequence 175, App
113	142.5	4.9	763	3	US-10-197-220-8	Sequence 8, Appli
114	128	4.4	4604	3	US-09-830-807-22	Sequence 22, Appl
115	126	4.4	963	4	US-09-605-703B-2155	Sequence 2155, Ap
116	124.5	4.3	1786	3	US-08-956-171E-618	Sequence 618, App
117	124.5	4.3	1786	3	US-08-781-986A-618	Sequence 618, App
118	121	4.2	1266	3	US-09-602-787A-177	Sequence 177, App
119	119	4.0	540	3	US-09-221-017B-1084	Sequence 1084, Ap
120	114	3.9	1110	3	US-09-543-681A-3342	Sequence 3342, Ap
121	113.5	3.9	2049	3	US-08-481-435-5	Sequence 5, Appli
122	113	3.9	71	2	US-08-572-951-18	Sequence 18, Appl
123	111.5	3.9	1999	3	US-08-961-083-1	Sequence 1, Appli
124	111.5	3.9	1999	3	US-09-536-784-1	Sequence 1, Appli
125	111.5	3.9	1999	3	US-09-765-271-1	Sequence 1, Appli
126	111.5	3.9	1999	3	US-09-765-272A-1	Sequence 1, Appli
127	111.5	3.9	10711	3	US-08-961-527-145	Sequence 145, App
128	110.5	3.8	2260	3	US-09-583-110-1312	Sequence 1312, Ap
129	110.5	3.8	2166	3	US-09-107-433-1102	Sequence 1102, Ap
130	109.5	3.8	30244	3	US-09-949-016-12208	Sequence 12208, A
131	109.5	3.8	30245	3	US-09-949-016-13550	Sequence 13550, A
132	109	3.8	1065	3	US-09-902-540-4644	Sequence 4644, Ap
133	109	3.8	12898	3	US-09-902-540-1000	Sequence 1000, Ap
134	108.5	3.8	1534	2	US-08-588-983-1	Sequence 1, Appli
135	108.5	3.8	1534	2	US-08-588-976-1	Sequence 1, Appli
136	108.5	3.8	2481	2	US-08-290-301-1	Sequence 1, Appli
137	108.5	3.8	2481	3	US-09-013-598-1	Sequence 1, Appli
138	108.5	3.8	2484	2	US-07-841-997A-1	Sequence 1, Appli
139	108	3.7	9992	3	US-09-902-540-952	Sequence 952, App
140	106.5	3.7	2307	3	US-09-949-016-5107	Sequence 5107, Ap
141	106	3.7	1170	3	US-09-902-540-8353	Sequence 8353, Ap
142	106	3.7	6474	3	US-08-961-527-155	Sequence 155, App
143	106	3.7	8056	3	US-09-902-540-874	Sequence 874, App
144	105	3.6	1194	3	US-09-902-540-5572	Sequence 5572, Ap
145	105	3.6	41927	2	US-09-902-540-1268	Sequence 1268, Ap
146	103.5	3.6	2846	2	US-08-365-189-7	Sequence 7, Appli
147	103.5	3.6	2982	2	US-08-365-189-2	Sequence 2, Appli
148	103.5	3.6	2988	2	US-08-365-189-1	Sequence 1, Appli
149	103	3.6	7319	3	US-09-221-017B-510	Sequence 510, App
150	102.5	3.5	660	3	US-09-107-433-1123	Sequence 1123, Ap

ALIGNMENTS

US-08-941-445A-20

; Sequence 20, Application US/08941445A

; Patent No. 6107060

GENERAL INFORMATION:

APPLICANT: Keeling, Peter

APPLICANT: Guan, Hanning

TITLE OF INVENTION: Starch Encapsulation

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSER: Greenlee, Winner and Sullivan, P.C.

STREET: 5370 Manhattan Circle

CITY: Boulder

STATE: CO

COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/941,445A

FILING DATE: 30-SEP-1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/026,855

FILING DATE: 30-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Winner, Ellen P

REGISTRATION NUMBER: 28,547

REFERENCE/DOCKET NUMBER: 89-97

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 499-8080

TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 1620 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: not relevant

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1620

US-08-941-445A-20

Alignment Scores:

Pred. No.: 0 Length: 1620

Score: 2893.00 Matches: 539

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 3 Gaps: 0

US-10-628-525A-21 (1-539) x US-08-941-445A-20 (1-1620)

QY 1 CysValAlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGly 20

DB 1 TSCGTGCGGAGCTGAGCAGGAGGAGCCTCGGCTCTCGAACCTCGAAGGGATTGCTGAAGGT 60

QY 21 SerIleAspAsnThrValValValAlaSerGluGlnAspSerGluIleValValGlyLys 40

DB 61 TCCATCGATACACAGTAGTGTGCAAGTAGCAGAGATTCTGAGATTGTGTTGGAAG 120

QY 41 GluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerPro 60

DB 121 GAGCAAGCTCGAGCTAAAGTACACAAAGCATTGCTTTGTAACCGCGGAGCTTCTCCT 180

QY 61 TyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAla 80

DB 181 TATGCAAAAGTCGGGGGCTTAGGAGATGTTTGTGGTTCATTGCCAGTCTCTTGTCT 240



QY 81 ArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsn 100  
DB 241 CGTGGTCAACCGTGTGATGTTGTAATGCCAGATATTTAAATGGTACCTCCGATAAGAAT 300  
QY 101 TyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHis 120  
DB 301 TATGCAATGCAATTTACACAGAAACACACATTCGGAATCCATGCTTTGGCGGTGAACAT 360  
QY 121 GluValThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisPro 140  
DB 361 GAAGTTACCTCTTCCATAGATAGAGATTCAGTTCAGTGGGTGTTTGTGATCATCCC 420  
QY 141 SerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGln 160  
DB 421 TCATATCACAGACCTGGAAATTTATATGGAGATAAGTTGGTGTCTTTGGGTGAATACAG 480  
QY 161 PheArgTyrThrLeuLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGly 180  
DB 481 TTCAGATACACACTCTTGTGATGCTGCATGTGAGGCTCTTTGATCCTTGAATGGGA 540  
QY 181 GlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrPheIleAlaSerLeuVal 200  
DB 541 GGATATATTTATGACAGAAATTCGATGTTGTTGTCATGATGGCATGCCAGTCTAGTG 600  
QY 201 ProValLeuLeuAlaIleLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
DB 601 CCAGTCTCTTCTGCTGCAAAATATAGACCATATGTTGTTTATAAAGACTCCCGCAGCAT 660  
QY 221 LeuValIleHisLeuLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240  
DB 661 CTGTGATACATAATTTAGCACATCAGGGGTAGAGCTGCAGACATATCTCGACCT 720  
QY 241 GlyLeuProGluTyrPyrGlyAlaLeuGluTyrValPheProGluTyrPalaArgArg 260  
DB 721 GGGTTGCCACTGAATGGTATGGAGCTCGAGTGGGTATTCCTCGAATGGCGAGGAGG 780  
QY 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAsp 280  
DB 781 CATGCCCTTCACAGAGGTGAGCGAGTTAAATTTTGAAGAGTGCAGTTGTGCACAGCAGAT 840  
QY 281 ArgIleValThrValSerLysGlyTyrSerTyrGluValThrThrAlaGluGlyGln 300  
DB 841 CGAATCGTGACTGTCAAGTAGGGTTATCTGTGGAGGTCACACTGCTGAAGGTGGACAG 900  
QY 301 GlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320  
DB 901 GGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACGGAATGTAAATGGAAT 960  
QY 321 AspIleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340  
DB 961 GACATTAATGATGGAAACCTGCCACACAGAAATGTATCCCTGTCAATTTCTGTTGAT 1020  
QY 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIle 360  
DB 1021 GACCTCTCTGGAAGGCCAAATGTAAAGTGCATTCGAGAGGAGCTGGGTTTACCTATA 1080  
QY 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380  
DB 1081 AGGCTGTATGCTCTGATGGCTTTATTTGGAAGGTGGATATTCAGAAAGGCATTTAT 1140  
QY 381 LeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
DB 1141 CTCATTTCACTTATACATACAGATCTCATCGGGAAGATGTTCAATTTGTCTATGCTTGA 1200  
QY 401 SerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLys 420  
DB 1201 TCTGTGACCCAGAGCTTGAAGATTTGGATGAGATCTACAGATCGCATTTCAAGGATAAA 1260  
QY 421 PheArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440  
DB 1261 TTTTCGTGGATGGGTGGATTTAGTTTCCAGTTTCCACCGAATACTGCCGCGCTGGAT 1320  
QY 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460

DB 1321 ATATTGTTAATGTCATCCAGATTCGAACCTTGTGGTCTCAATCAGTATATGCTATGCAG 1380  
QY 461 TyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPhe 480  
DB 1381 TATGGCACAGTTCCTGTGTGTCATGCAACTGGGGGCTTAGAGATACCGTGGAGAACTTC 1440  
QY 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrPalaPheAlaProLeuThrThr 500  
DB 1441 AACCTTTTCGTGAGATGAGAGAGCAGGGTACAGGGTGGGCATTCGCACCCCTAACCCACA 1500  
QY 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520  
DB 1501 GAAACATGTTTGTGGACATTTGGCACTTGCATATATCTACATACAGGGAACAACAAGTCTCTC 1560  
QY 521 LeuGlyArgAlaAlaAsnGluAlaArgHisValLysValArgLeuHisValGlyProCysArg 539  
DB 1561 CTGGGAAGGGCTAATGAAGCAGGCGATGTCAAAAGACTTCACGTGGGACCATGCGCG 1617

## RESULT 2

US-08-941-445A-12  
; Sequence 12, Application US/08941445A  
; Patent No. 6107060  
; GENERAL INFORMATION:  
; APPLICANT: Keeling, Peter  
; APPLICANT: Guan, Hanping  
; TITLE OF INVENTION: Starch Encapsulation  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/941,445A  
; FILING DATE: 30-SEP-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/026,855  
; FILING DATE: 30-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winner, Ellen P  
; REGISTRATION NUMBER: 28,547  
; REFERENCE/DOCKET NUMBER: 89-97  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1752 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1752  
US-08-941-445A-12  
Alignment Scores:  
Pred. No.: 0 Length: 1752  
Score: 2861.00 Matches: 539  
Percent Similarity: 92.5% Conservative: 0



## US-09-345-214-12

## Alignment Scores:

Pred. No.: 0 Length: 2008  
 Score: 2832.00 Matches: 538  
 Percent Similarity: 92.3% Conservative: 0  
 Best Local Similarity: 92.3% Mismatches: 1  
 Query Match: 97.9% Indels: 45  
 DB: 3 Gaps: 1

US-10-628-525A-21 (1-539) x US-09-345-214-12 (1-2008)

QY 1 CysValAlaGluLeuSerArgGlu----- 8  
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 QY 8 ----- 8  
 DB 179 GCGCCCCGCTCGTNGCCCGGCTTCCTCGCGCGCGCGCGCCAGCCACGGGTGAGCCGGCA 238  
 QY 9 -----AspLeuGlyLeuGluProGluGly 16  
 DB 239 TCGACGCGCGCGCGCGCGCGCGCGCGCTCGGTCTCGAACCTGNAAGGG 298  
 QY 17 IleAlaGluGlySerIleAspAsnThrValValAlaIleSerGluGlnAspSerGluIle 36  
 DB 299 ATTGCTGAAGGTTCCATCGATAACACAGTAGTTGTGGCAAGTGGCAAGATTCTGAGATT 358  
 QY 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
 DB 359 GTGGTGGAAAGGAGCAGCTCGAGCTAAGTAACACAAAGCATTGCTTTGTAACCGGC 418  
 QY 57 GluAlaSerProTyrAlaLysSerGlyLeuGlyAspValCysGlySerLeuProVal 76  
 DB 419 GAAGCTTCTCTTATGCANAAGTCTGGGGCTAGAGAGATTGTGGTTCATTGCCAGTT 478  
 QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96  
 DB 479 GCTCTGCTGCTGCTGCTACCGGTGATGGTTGTAATGCCAGATATTTAAATGGTPACC 538  
 QY 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
 DB 539 TCCGATPAAGANTATGCANAATGCATTTTACAGAAANAACACATTCCGATTCATGCTTT 598  
 QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136  
 DB 599 GCGCGTGAAATGAAGTTACTCTTCATGAGTATAGAGATTCAAGTTGAGTGGTGT 658  
 QY 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
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 QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
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 QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196  
 DB 779 CTTGATTTGGGAGGATATATTTATGGACAGAAATTCATGTTTGTGTCAATGATGGCAT 838  
 QY 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
 DB 839 GCCAGTCTAGTGCAGTCCTCTTCTGCTGCAAAATATAGACCATATGCTGTGTTATAAGAC 898  
 QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
 DB 899 TCCGCGAGCATTTCTGTAAATACATAATTTAGCATCAGGGGTAGAGCCTGCAGGACA 958  
 QY 237 TyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256  
 DB 959 TATCTCGACCTGGGTGGCCACCTGAATGATGGAGCTCTGGAGTGGGTATTCCTCTGAA 1018  
 QY 257 TrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276

DB 1019 TGGCGCAGGAGGCATGCCCTTGCAAGGGTGAGGCAGTTTAATTTTGAAGGTGTCAGTT 1078  
 QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
 DB 1079 GTGACAGCAGATCGAATCGTGACTGTCTGTAAGGGTTATTTCGTGGGAGGTACAACTGCT 1138  
 QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316  
 DB 1139 GAAGGTGGACAGGGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTTATTAACCGAATT 1198  
 QY 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
 DB 1199 GTAAATGGAATTGACATTAATGATTGGAACCTCCACACAAATGATATCCCTGTGCTAT 1258  
 QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
 DB 1259 TATCTGTGTGATGACCTCTCTGGAAGGCCAATGTAAAGTGTGATTCAGAGGAGCTG 1318  
 QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
 DB 1319 GGTTTACCTATAAGGCTGATGTTCTCTGATTGGCTTTATTGGNAGTTGGATTATCAG 1378  
 QY 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396  
 DB 1379 AAAGGCATTGATCTCAATCACTTATCATACAGATCTCATGCGGGAAGATGTTCAATTT 1438  
 QY 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416  
 DB 1439 GTCATGCTTGGATCTGCTGACCCAGAGCTTGAAGATTGGAATGATCTCAGAGTGCATC 1498  
 QY 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436  
 DB 1499 TTCAGAGATAAATTTCTGTGATGGTGGATTAGTTTCCAGTTTCCACCCGAATTAAT 1558  
 QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456  
 DB 1559 GCGCGCTGGGATATATGTTAATGCCATCCAGATTCGAACCTTGTGGTCTCAATCAGCTA 1618  
 QY 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuAspThr 476  
 DB 1619 TATGCTATGCAAGTATGGCACAGTTCCTGTGTCCTGCAACTGGGGCCCTTAGAGATACC 1678  
 QY 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrPalaPheAla 496  
 DB 1679 GTGGAGAACTTCAACCTTTCCGTGAGAAATGGAGAGCAGGGTACAGGTGCGCATTCGCA 1738  
 QY 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
 DB 1739 CCCCTAACCCACAGAAACATGTTT-GTGGACATTTGCGAATCTGCAATATCTACATACAGGA 1797  
 QY 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536  
 DB 1798 ACAAGTCTCTCTGGGAAGGGCTAATGAAGCGGCGATGTCAAAAGACTTTCACGTGGGA 1857  
 QY 537 ProCysArg 539  
 DB 1858 CCATGCCG 1866

## RESULT 4

US-09-743-980-12  
 ; Sequence 12, Application US/09743980  
 ; Patent No. 6570008  
 ; GENERAL INFORMATION:  
 ; APPLICANT: E. I. du Pont de Nemours and Company  
 ; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE  
 ; FILE REFERENCE: BB-1147-A  
 ; CURRENT APPLICATION NUMBER: US/09/743,980  
 ; CURRENT FILING DATE: 2001-05-14  
 ; PRIOR APPLICATION NUMBER: 060/094,436  
 ; PRIOR FILING DATE: 1998-07-28  
 ; NUMBER OF SEQ ID NOS: 20

! SOFTWARE: Microsoft Office 97  
! SEQ ID NO 12  
! LENGTH: 2008  
! TYPE: DNA  
! ORGANISM: Zea mays  
! US-09-743-980-12

## Alignment Scores:

Pred. No.: 0 Length: 2008  
Score: 2832.00 Matches: 538  
Percent Similarity: 92.3% Conservative: 0  
Best Local Similarity: 92.3% Mismatches: 1  
Query Match: 97.9% Indels: 45  
DB: 3 Gaps: 1

US-10-628-525A-21 (1-539) x US-09-743-980-12 (1-2008)

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QY 1 CysValAlaGluLeuSerArgGlu----- 8
Db 119 TGGCTCGCGAGCTGAGCAGGAGGGCCGCCGCCGCGCTGCCACCCGCGCTGCTG 178
QY 8 ----- 8
Db 179 GCGCCCCGCTGCTGCCGCTTCTCGCCGCCGCCGCCAGCCCGGTGAGCCGCCA 238
QY 9 -----AspLeuGlyLeuGluProGluGly 16
Db 239 TCGACGCCGCCGCCGCGCCGAGCGCGCTGGGGGACCTCGGTCTCGAACCTGAGGG 298
QY 17 IleAlaGluGlySerIleAspAenThrValValAlaSerGluGlnAspSerGluIle 36
Db 299 ATTGCTGAAGTTCCATCGATAACACAGTAGTTGTGGCAAGTGAGCAAGATTCTGAGATT 358
QY 37 ValValGlyGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56
Db 359 GTGGTTGGAAAGGAGCAAGCTCGAGCTAAAGTAACAACAAAGCATTTGCTTTGTAACCCGC 418
QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76
Db 419 GAAGCTTCTCTATGCAAAAGTCTGGGGGTCTAGGAGATGTTTGTGTTTCATTGCCAGTT 478
QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAenGlyThr 96
Db 479 GCTCTTGCTGCTCGTGGTCACCGTGATGGTTGTAATGCCAGATATTTAAATGTTACC 538
QY 97 SerAspLysAenTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116
Db 539 TCCGATAAGAAATTATGCAAAATGCATTTTACACAGAAAAACACATTGGGATTCATGCTTT 598
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPhe 136
Db 599 GCGGGTGAACATGAAGTTACCTTCTCCATGAGTATAGAGATTCAGTTGACTGGGTGTTT 658
QY 137 ValAspHisProSerTyrHisArgProGlyAenLeuTyrGlyAspLysPheGlyAlaPhe 156
Db 659 GTTGATCATCCCTCATPATCACAGACCTGAAATTTATATGCGATAAAGTTTGGTGCTTTT 718
QY 157 GlyAspAenGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176
Db 719 GGTGATAATCAGTTCAGATACACATCCTTTGCTATGCTGTCATGTGAGGCTCCTTTGATC 778
QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAenCysMetPheValValAenAspTyrHis 196
Db 779 CTTGTAATGGGAGGATATATTTATGACAGAGATTGCATGTTTGTGTCAATGATGGCAT 838
QY 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216
Db 839 GCCAGTCTAGTGCACGCTCTTCTGCTGCAAAATATAGACCATATGTTGTTTATAAAGAC 898
QY 217 SerArgSerIleLeuValIleHisAenLeuAlaHisGlnGlyValGluProAlaSerThr 236
Db 899 TCCCGCAGCATTTCTGTGTAATACATAATTTAGCACATCAGGGGTGAGAGCTCGAAGCACA 958
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Db 959 TATCTCTGACCTTGGGTGGCCACTGAATGTTATGGAGCTCTGGAGTGGGTATTCCTTGAA 1018
QY 257 TyrAlaArgArgHisAlaLeuAspLysGlyGluAlaValAasnPheLeuLysGlyAlaVal 276
Db 1019 TGGCGCAGGAGCATGCCCTTGACAAGGGTGAGGCAGTTAAATTTTTTGAAGGTGCAGTT 1078
QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrGluValThrAla 296
Db 1079 GTGACAGCAGATCGAATCGTGACTGTCAATAAGGGTTATTCGTGGAGGTCACACTGCT 1138
QY 297 GluGlyGlyGlnGlyLeuAenGluLeuSerSerArgLysSerValLeuAenGlyIle 316
Db 1139 GAAGGTGGACAGGGCTCAATGAGCTTTAAGCTCCAGAAAGAGTGTATTAAACGGAATT 1198
QY 317 ValAenGlyIleAspIleAenAspTyrAenProAlaThrAspLysCysIleProCysHis 336
Db 1199 GTAAATGGAATTCACATTAATGATTGGAACCTGCGCACAGACAAATGTATCCCTGTCAT 1258
QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356
Db 1259 TATTCGTGTGATGACTCTCTGGAAGGCCAAATGTAAAGGTGCATTGCAGAAAGGAGCTG 1318
QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
Db 1319 GGTTCACCTATTAAGGCTGATGTTCTCTGATTTGCTTTATTGGAAGGTGGATATATCAG 1378
QY 377 LysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPhe 396
Db 1379 AAAGGCATTGATCTCATTCACCTTATCATCCAGATCTCATCGGGAAGATGTTCAATTT 1438
QY 397 ValMetLeuGlySerCysAspProGluLeuGluAspTyrMetArgSerThrGluSerIle 416
Db 1439 GTCATGCTTGGATCTGGTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATC 1498
QY 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436
Db 1499 TTCAGAGTAATATTTCTGGATGGGTGGATTTAGTTTCCAGTTTCCACCGAATAACT 1558
QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAenGlnLeu 456
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QY 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476
Db 1619 TATGCTATGAGTATGGCACAGTCTCTGTGTCCATGCAACTGGGGGCTTTAGAGATACC 1678
QY 477 ValGluAenPheAsnProPheGlyGluAenGlyGluGlnGlyThrGlyTyrAlaPheAla 496
Db 1679 GTGGAGAACTTCAACCTTTCCGTGGAATGGAGAGCAGGTACAGGGTGGGCATTCGCA 1738
QY 497 ProLeuThrThrGluAenMetPheValAspIleAlaAenCysAenIleTyrIleGlnGly 516
Db 1739 CCCCTAAACACAGAAAAACATGTT- GTGGACATTTGGCACTGCAATATCTACATACAGGA 1797
QY 517 ThrGlnValLeuLeuGlyValArgAlaAenGluAlaArgHisValLysArgLeuHisValGly 536
Db 1798 ACACAGTCTCTCTGGGAAGGGCTAATGAAGCAGGCATGTCAAAGACATTCACGTGGGA 1857
QY 537 ProCysArg 539
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## RESULT 5

US-09-345-214-5  
; Sequence 5, Application US/09345214  
; Patent No. 6392120  
; GENERAL INFORMATION:  
; APPLICANT: Lightner, Jonathan E.  
; APPLICANT: Broglie, Karen E.  
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE  
; TITLE OF INVENTION: EXPRESSION TO PRODUCE STARCHES IN GRAIN CROPS









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QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysGlyAlaLeuGlnLysGluLeu 356
Db 1286 TATTCCTGTTGATGACCTCTCTGGAAGGCCAAATGTAAGGTGCATTCAGAGGAGCTG 1345
QY 357 GlyLeuProileArgProAspValProLeuileGlyPheileGlyArgLeuAspTyrGln 376
Db 1346 GGTTCACCTATAAGGCGCTGATGTTCTCTGATTTGGCTTTATTGGAAGATTGGATTATCAG 1405
QY 377 LysGlyLeuAspLeuileGlnLeuileProAspLeuMetArgGluAspValGlnPhe 396
Db 1406 AAAGGCATTGATCTCAATCAACTATATCAACAGATCTCATCGGGAAGATGTTCAATTT 1465
QY 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerile 416
Db 1466 GTCATGCTTGGATCTGGTACCCAGAGCTTGAGATTGGATGAGATCTACAGATCGATC 1525
QY 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgileThr 436
Db 1526 TTCAAGGATAAATTCGTGATGGGTTCGATTAGTGTTCAGTTTCCACCGAATAACT 1585
QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456
Db 1586 GCGGCTGCGATATATGTTAATGTCATCCAGATTCGAACCTTGTGTTCTCAATCAGCTA 1645
QY 457 TyrAlaMetGlnTyrGlyThrValProValHisAlaThrGlyGlyLeuArgAspThr 476
Db 1646 TATGCTATCGATATGCGACAGTCTCTGTGTCATGCAACTGGGGCCCTTAGAGTACC 1705
QY 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAla 496
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QY 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrileGlnGly 516
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QY 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536
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QY 537 ProCysArg 539
Db 1885 CCATGCCGC 1893

RESULT 8
US-09-931-297-1
; Sequence 1, Application US/09931297
; Patent No. 6635804
; GENERAL INFORMATION:
; APPLICANT: Jens Koesmann
; TITLE OF INVENTION: Nucleic acid molecules encoding soluble
; starch synthases from maize
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/931,297
; FILING DATE: 16-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/192,909
; FILING DATE: <Unknown>
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; APPLICATION NUMBER: DE 196 19 918.2
; FILING DATE: 17-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley, Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: GFB-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-96-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2383 base pairs
; TYPE: nucleotide
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; TISSUE TYPE: endosperm
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..1950
; OTHER INFORMATION: /function= "starch synthesis"
; /product= "soluble starch synthase"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-931-297-1

Alignment Scores:
Pred. No.: 0 Length: 2383
Score: 2818.00 Matches: 534
Percent Similarity: 92.1% Conservative: 3
Best Local Similarity: 91.6% Mismatches: 2
Query Match: 97.4% Indels: 45
DB: 3 Gaps: 1

US-10-628-525A-21 (1-539) x US-09-931-297-1 (1-2383)
QY 1 CysValAlaGluLeuSerArgGluAsp----- 9
Db 146 TCGGTTCGGAGCTGAGCAGGAGGCGCCCGCGCGCGATGCCACCCGCGCTGCTG 205
QY 9 ----- 9
Db 206 GCGCCCCGCTCGTGCCTCGGCTTCCTCTCGCGCGCGCGCGCGAGCCGCGGTCGAGCGCGCA 265
QY 10 -----LeuGlyLeuGluProGluGly 16
Db 266 TTGACGCCCGCGCGCTGCTGCCGACGCCGCGCTGGGGGTCTCTCGGTCTCGAACCTGAAGG 325
QY 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36
Db 326 ATTGCTGAAGGTTCATCGATACACAGTAGTGTGTGGCAAGTGAGCAAGATTCTGAGATT 385
QY 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56
Db 386 GTGGTTGGAAGAGCAGCTCAGCTAAGTAAGTAACAAACATTTGTTTGTAACTGGC 445
QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76
Db 446 GAAGCTCTCTTATGCAAAAGTCTGGGGTCTAGGAGATGTTTGTGTTTCATTGCCAGTT 505
QY 77 AlaLeuAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96
Db 506 GCTCTTGCTGCTCGTGGTCCACCGTGTGATGTTGTAATGCCAGATATTTAAATGGTACC 565
QY 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116
Db 566 TCCGATAGAAATTATGCAATGCAATTTTACACAGAAACACATTCGGATTTCATGCTTT 625
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136
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Db 686 GTTGATCATCCTCATATACAGACCTGGAAATTTATATGAGATAGATTGGTGGCTTTT 745  
Qy 157 GlyAspGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuLeu 176  
Db 746 GGTGATTAATCAGTTTCAGATACACACTCCTTTGGCTATGCTGATGAGGCTCCTTTGGTC 805  
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis 196  
Db 806 CTTGAATGGGAGGATATATTATGGACAGATTTGCATTTTGTGTCAATGATGGCAT 865  
Qy 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 866 GCCAGTCTAGTGGCAGTCTCTTGTCTGCAAAATATAGACCATATGCTGTGTTATAAAGAC 925  
Qy 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
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Qy 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
Db 1046 TGGCGAGGAGGAGCATGCCCTTGACAGGGTGAGCAGTAAATTTTTTGAAGGTGAGTT 1105  
Qy 277 ValThrAlaAspArgIleValThrValSerIleGlyTyrSerTyrGluValThrAla 296  
Db 1106 GTGACAGCAGATCGAATCGTGACTGTCTAGTAAGGGTTATTTCATGGGAGGTACAACTGCT 1165  
Qy 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle 316  
Db 1166 GAGGTGGACAGGGCCTCATAGCTCTTAAAGTCCAGAAAGAGTGTATTAAAGGGAAAT 1225  
Qy 317 ValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHis 336  
Db 1226 GTAAATGGAATTGACATTAATGATTGGAACCTGCCACAGCAAAATGTATCCCTGTGCAT 1285  
Qy 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
Db 1286 TATTCCTGTGATCCTCTCTGGAAAGGCCAAATGTAAAGTGCATTCGAGAAAGGAGCTG 1345  
Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
Db 1346 GGTTCATCTAATAGGCTGATGTTCTCTGATTTGGCTTTATGGAAGATTGGATTATCAG 1405  
Qy 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396  
Db 1406 AAAGGCATTCATCTCATTCATCATACAGATCTCATGCGGGAAGATGTTCAATTT 1465  
Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIle 416  
Db 1466 GTCATGCTTGGATCTGGTACCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATC 1525  
Qy 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436  
Db 1526 TTCAGAGATAAATTTGCTGAGUGGTGGATTGATTTAGTGTTCAGATTTCCCAACCGAATACT 1585  
Qy 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456  
Db 1586 GCGGCTGCGATATATGTTAATGCCATCCAGATTCGAACTTGTGGTCTCATACAGCTA 1645  
Qy 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
Db 1646 TATGCTATGCAATGATGCAAGTCTCTGTGTCATGCAACTGGGGGCTCTAGAGATACC 1705  
Qy 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAla 496  
Db 1706 GTGGAGAACTTCAACCTTTTCGGTGAGAAATGGAGACAGGGTACAGGGTGGGCATTCGCA 1765

Qy 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
Db 1766 CCCTTAACCAACAGAAACATGTT-GTGGACATTCGGAACCTGCAATATCTCATACAGGA 1824  
Qy 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536  
Db 1825 ACAACAGTCTCTCTGGGAAGGCTTAATGAAGCGAGGCTATGTCAAAAGACTTCACGTGGA 1884  
Qy 537 ProCysArg 539  
Db 1885 CCATGCCGC 1893  
RESULT 9  
US-08-572-951-1  
; Sequence 1, Application US/08572951  
; Patent No. 5824790  
; GENERAL INFORMATION:  
; APPLICANT: KEBLING, PETER L.  
; APPLICANT: KNIGHT, MARY E.  
; APPLICANT: GUAN, HANPING  
; TITLE OF INVENTION: MODIFICATION OF STARCH  
; TITLE OF INVENTION: SYNTHESIS IN PLANTS  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: Pillsbury Madison & Sutro LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/572,951  
; FILING DATE: 15-DEC-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/346,602  
; FILING DATE: 29-NOV-1994  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/263,921  
; FILING DATE: 21-JUN-1994  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul N. Kokulis  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 222957/1.02.15C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2990 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-572-951-1  
Alignment Scores:  
Pred. No.: 8,45e-316 Length: 2990  
Score: 2757.00 Matches: 523  
Percent Similarity: 90.9% Conservatives: 8  
Best Local Similarity: 89.6% Mismatches: 8  
Query Match: 95.3% Indels: 45  
DB: 2 Gaps: 1

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QY	8 -----	8
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QY	9 -----AspLeuGlyLeuGluProGluGly 16	
Db	838 TCGACGCGCGCCCGCTGCGCGCGCGCGCTGGGGGACCTCGGTCTCGAACCCTGAGGG	897
QY	17 lIeAlaGluGlySerIleAspAenThrValValAlaSerGluGlnAspSerGluIle 36	
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QY	37 ValValGlyGlyGluGlnAlaArgAlaIysValThrGlnSerIleValPheValThrGly 56	
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Db	1078 TGCCTCTGCTGCTGGGGTCACCGTGTGATGGTTGTAATGCCACAGACATTTAAATGGTAC	1137
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QY	136 eValAspHisProSerTyrHiAArgProGlyAenLeuTyrGlyAspIysPheGlyAlaPh 156	
Db	1258 TGTGTATCATCCCTCATATACAGACCTCGAAATTTATATGGAGATAAGTTTGGTCTTT	1317
QY	156 eGlyAspAenGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuI 176	
Db	1318 TGGTGATAATCAGTTCAGATACACATCTCTTGTATGCTGCGATGAGGCTCTTTGTG	1377
QY	176 eLeuGluLeuGlyGlyTyrIleTyrGlyGlnAenCysMetPheValValAsnAspTyrHi 196	
Db	1378 CCTTGAATTGGGAGGATATATTATGGACAGAAATTCATGTTGTTGTCATGATTGGCA	1437
QY	196 sAlaSerLeuValProValLeuLeuAlaIalysTyrArgProTyrGlyValTyrIlysAs 216	
Db	1438 TGCAGCTTAGAGCCAGTCTCTTCTGCTGCAAAATATAGACCATATGTTGTTTATAAGA	1497
QY	216 pSerArgSerIleLeuValIleHisAenLeuAlaHisGlnGlyValGluProAlaSerTh 236	
Db	1498 CTCGCCGACAGTCTTGTATACATAAATTAGACATCAGGGGTGAGAGCCCTGCAAGCAC	1557
QY	236 rTyrProAspLeuGlyLeuProProGluTyrTyrGlyAlaLeuLeuGluTyrValPheProG 256	
Db	1558 ATATCTTGACCTTGGGTGGCCACTGAATGATGAGAGCTCTGGAGTGGGTATTCCTGA	1617
QY	256 uTrpAlaArgArgHisAlaLeuAspIysGlyGluAlaValAenPheLeuIysGlyAlaVa 276	
Db	1618 ATGGGCGAGGAGCATGCCCTTGACAAAGGCTGAGGCAAGTTAAATTTTGAAGGTGCACT	1677
QY	276 lValThrAlaAspArgIleValThrValSerIysGlyTyrSerTyrGluValThrThrAl 296	
Db	1678 TGTGACAGCAGATCGAATCGTACTGCTAGTAGGGTTATTATGAGGAGGTACAACTGC	1737
QY	296 aGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgIysSerValLeuAsnGlyI 316	
Db	1738 TGAAGGTGGACAGGGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACCGGAAT	1797
QY	316 eValAenGlyIleAAspIleAAsnAspTyrAsnProAlaThrAspIysCysIleProCysHi 336	
Db	1798 TGTAAATGGAATTGCAATTAATGATGGAAACCTGTCACAGACAAATGATATCCCTGTCA	1857
QY	336 sTyrSerValAspAspLeuSerGlyIysAlaIysCysIysGlyAlaLeuGlnIysGluLe 356	
Db	1858 TTATTCTGTGTAGTACCTCTCTTGAAGGCTAAATGTAAGGTGCAATTCGAAGAGAGCT	1917
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QY	376 nIysGlyIleAspLeuIleGlnIleIleProAspLeuMetArgGluAspValGlnPh 396	
Db	1978 GAAAGCATTTGATCTCAATTCATATACAGATCTCATCGGAAGAATTTGCAATT	2037
QY	396 eValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIl 416	
Db	2038 TGTCTATGCTTGGATCTGGTGACCCAGAGCTTGAAGATTGAGATCTACAGAGTCGAT	2097
QY	416 ePheIysAspIysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleTh 436	
Db	2098 CTTCAAGGATAAATTTCTGTGGATGGTTGATTTAGTGTTCAGTTTCCACCGAATAAC	2157
QY	436 rAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAenGlnLe 456	
Db	2158 TCGCGGTGGCATATATTTGTTAATGCCATCCAGATTCGAACCTTGTGGTCTCAATCAGCT	2217
QY	456 uTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspTh 476	
Db	2218 ATATGCTATGCAAGTATGGCAGATTCCTCTTGTCCATGCACTGGGGGCTTAGAGATAC	2277
QY	476 rValGluAenPheAsnProPheGlyGluAenGlyGluGlnGlyThrGlyTyrPalaPheAl 496	
Db	2278 CGTGGAGAACTTCAACCTTTCCGTGAGAAATGGAGAGCAGGGTACAGGGTGGGCATTCCG	2337
QY	496 aProLeuThrThrGluAenMetPheValAspIleAlaAenCysAenIleTyrIleGlnGl 516	
Db	2338 ACCCTTAACACAGAAACATGTTTGTGGACATTCGCAACTGCAATATCTACATACAGGG	2397
QY	516 YThrGlnValLeuLeuGlyArgAlaAenGluAlaArgHisValIysArgLeuHisValGl 536	
Db	2398 AACACAGTAAATATGGGAAGGCTAATGAGCCAGGCAATGTCNAAGAGTTCACTGGG	2457
QY	536 YProCysArg 539	
Db	2458 ACCATGCCGC 2467	
RESULT 10		
US-09-345-214-6/c		
; Sequence 6, Application US/09345214		
; Patent No. 6392120		
; GENERAL INFORMATION:		
; APPLICANT: Lightner, Jonathan E.		
; APPLICANT: Broglie, Karen E.		
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE		
; FILE REFERENCE: BB-1147		
; CURRENT APPLICATION NUMBER: US/09/345,214		
; CURRENT FILING DATE: 1999-06-30		
; EARLIER APPLICATION NUMBER: 060/094,436		
; EARLIER FILING DATE: 1998-07-28		
; NUMBER OF SEQ ID NOS: 20		
; SOFTWARE: Microsoft Office 97		
; SEQ ID NO 6		
; LENGTH: 1528		
; TYPE: DNA		
; ORGANISM: Zea mays		
US-09-345-214-6		
Alignment Scores:		

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Pred. No.: 3,44e-304 Length: 1528
Score: 2655.00 Matches: 495
Percent Similarity: 99.8% Conservative: 0
Best Local Similarity: 99.8% Mismatches: 1
Query Match: 91.8% Indels: 1
DB: 3 Gaps: 0

US-10-628-525A-21 (1-539) x US-09-345-214-6 (1-1528)

QY 44 ArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAlaLys 63
DB 1527 CGAGCTAAAGTAACACAAAGCATTTGCTTTGTAAACCGCGGAAGCTTCTCTTATGCAAG 1468
QY 64 SerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHis 83
DB 1467 TCTGGGGGCTCAGGAGATGTTTGTGGTTCATTGCCAGATTGCTCTGTGCTGCTGCTCAC 1408
QY 84 ArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsn 103
DB 1407 CGTGTGATGTTGTAATGCCAGATATTTAAATGGTACCTCCGATGAAGAAATTAATGCAAT 1348
QY 104 AlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThr 123
DB 1347 GCATTTTACACAAAAACATTCGGATTCATGCTTTGGCGGTGNAACATGAAGTTACC 1288
QY 124 PhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSerTyrHis 143
DB 1287 TTCTTCCATGAGPATAGAGATTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1228
QY 144 ArgProGlyAsnLeuTyrGlyAspLysPheGlyValPheGlyAspAsnGlnPheArgTyr 163
DB 1227 AGACCTGGAAATTTATGAGATAAGTTTGGTGTCTTTTGGTGTGATTAATCAGTTTCAGATAC 1168
QY 164 ThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyTyrIle 183
DB 1167 ACACTCCTTTGCTATGCTGATGTGAGGCTCCTTTGATCTTTGAATGGGAGGATATAT 1108
QY 184 TyrGlyGlnAsnCysMetPheValValAsnAspTyrHisAlaSerLeuValProValLeu 203
DB 1107 TATGGACAGAAATGCAATGTTTGTGTCAATGATGGCATGCCAGTCTAGTGCAGTCTCT 1048
QY 204 LeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIle 223
DB 1047 CTGTGCAAAATATAGACATATGTTGTTTATAAGACTCCCGCAGCATTTCTTGAATA 988
QY 224 HisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuPro 243
DB 987 CATAATTTAGCACATCAGGCTGTAGAGCTTGCAGGCACATATCCTGACCTTGGTGGCCA 928
QY 244 ProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeu 263
DB 927 CCTGAATGCTATGAGCTCTGGAGTGGGTATTCCTGTAATGGCGAGGAGGATGCCCTT 868
QY 264 AspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleVal 283
DB 867 GACAAGGGTGGAGCAGTTAAATTTTTGAAGGTGCAGTTGTGACACGACATCGAATCGTG 808
QY 284 ThrValSerLysGlyTyrSerTyrGluValThrAlaGluGlyGlyGlnGlyLeuAsn 303
DB 807 ACTGTCAAGTAAGGTTATTCGTGGAGGTCAACATGCTGTAAGGTGGACAGGCGCTCAAT 748
QY 304 GluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsn 323
DB 747 GAGCTCTTAAGCTCCAGAAAGAGTGATTAACCGGAATTTGTAATGGAATTCACATTAA 688
QY 324 AspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspLeuSer 343
DB 687 GATTGGAACCTTGGCCACAGCAAAATGATCCCTCTGTCATTATTCGTGATGACCTCTCT 628
QY 344 GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363
DB 627 GGAAGGCCCAATGTAAAGTGCATTTGCAGAGGAGCTGGGTTTACCTATTAAGGCTGAT 568
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QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 383
DB 567 GTTCTCTCATTTGGCTTTATTTGAAGGTTGGATTATCAGAAAGCATTTGATCTCATTTCAA 508
QY 384 LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403
DB 507 CTTATCATACCAGATCTCATGCGGGAAGATGTTCAATTTGTCTGCTGGATCTGGTGAC 448
QY 404 ProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423
DB 447 CCAGACCTTGAAGATTGGATGAGATCTACAGAGTCGATCTTCAAGGATAAATTTCTGGA 388
QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443
DB 387 TGGGTTGGATTTAGTCTTCAGTTTCCACCGAATAACTGCCGCTGCGATATATTGTTA 328
QY 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463
DB 327 ATGCCATCCAGATTTCAACCTTTGTGTCTCAATCAGCTATATGCTATGCAATATGGCACA 268
QY 464 ValProValValHisAlaThrGlyLeuArgAspThrValGluAsnPheAsnProPhe 483
DB 267 GTTCTGTTGTCCATGCAACTGGGGCCCTAGAGATCCGTTGAGAACTTCAACCTTTTC 208
QY 484 GlyLeuAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMet 503
DB 207 CGTGAGATGGAGAGCAGGTTACAGGTTGGCATTCGCACCCCTAACACAGAAACATG 148
QY 504 PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523
DB 147 TT-GTGGACATTTGCCGAATCTCAATATCTACATACAGGGAACACAACTCTCTCTGGAAGG 89
QY 524 AlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
DB 88 GCTAATGAAGCGAGCATGTCAAAAGACTTCACGTGGGACCATGCCGC 41
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## RESULT 11

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US-09-743-980-6/c
; Sequence 6, Application US/09743980
; Patent No. 6570008
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE
; FILE REFERENCE: BB-1147-A
; CURRENT APPLICATION NUMBER: US/09/743,980
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 060/094,436
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 1528
; TYPE: DNA
; ORGANISM: Zea mays
US-09-743-980-6
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```
Alignment Scores:
Pred. No.: 3,44e-304 Length: 1528
Score: 2655.00 Matches: 495
Percent Similarity: 99.8% Conservative: 0
Best Local Similarity: 99.8% Mismatches: 1
Query Match: 91.8% Indels: 1
DB: 3 Gaps: 0
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US-10-628-525A-21 (1-539) x US-09-743-980-6 (1-1528)

```
QY 44 ArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAlaLys 63
DB 1527 CGAGCTAAAGTAACACAAAGCATTTGCTTTGTAAACCGCGGAGCTTCTCTTATGCAAG 1468
QY 64 SerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHis 83
```

1467 TCTGGGGCTAGGAGATGTTTGTGGTTTCATTGGCCAGTTGCTCTTGTCTGCTGCTGCTCAC 1408  
QY 84 ArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsn 103  
Db 1407 CGTGTGATGGTTGTAAATGCCCGAGATATTTAAATAGGTACCTCCGATGAAGAAATATGCAAT 1348  
QY 104 AlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyClyHisGluValThr 123  
Db 1347 GCATTTTACACAGAAACACATTCGGATTCGATTCGATCTTTGGCGGTGAACATGAAGTTACC 1288  
QY 124 PhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSerTyrHis 143  
Db 1287 TTCTTCCATAGATAGAGATTGAGTTGATGGTGTGTTGATCATCCCTCATATCAC 1228  
QY 144 ArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyr 163  
Db 1227 AGACCTGGAAATTTATATGAGATAAGTTTGGTGCTTTTGGTGATAATCAGTTTCAGATAC 1168  
QY 164 ThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIle 183  
Db 1167 ACATCTCTTGTATGCTGCATGTGAGGCTCTTTGATCTTGAATTGGAGGATATATT 1108  
QY 184 TyrGlyGlnAsnCysMetPheValValAsnAspTyrPheHisAlaSerLeuValProValLeu 203  
Db 1107 TATGGACAGAAATGCATGTTGTGTGTCATGATTGGCATGCCAGTCTAGTCCAGTCTCTT 1048  
QY 204 LeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIle 223  
Db 1047 CTTGCTGCAAAATATAGACCATATGTTGTATATAAGACTCCCGCAGCATTTCTTGTATA 988  
QY 224 HisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuPro 243  
Db 987 CATATTTAGCACATCAGGGGTAGAGCTGCAGCACATATCCTGACCTTGGGTGCCA 928  
QY 244 ProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeu 263  
Db 927 CCGAATGTTATGGAGCTCTGGAGTGGGTATTTCCCTGAATGGCGAGGAGCATGCCCTT 868  
QY 264 AspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleVal 283  
Db 867 GACAGGGGTGAGCGAGTTAAATTTTGAAGGTGCAGTTGTGCACGACATCGAATCGTG 808  
QY 284 ThrValSerLysGlyTyrSerTyrGluValThrThrAlaGluGlyGlyGlnGlyLeuAsn 303  
Db 807 ACTGTCAGTAAGGTTATTCGTGGAGGTCACACTGCTGAAGGTGGACAGGCGCTCAAT 748  
QY 304 GluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsn 323  
Db 747 GAGCTCTTAAGCTCCAGAAAGAGTGTATTAACCGGAATTTGTAATGGAATTCACATTAAT 688  
QY 324 AspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSer 343  
Db 687 GATTGGAACCCCTGCCACAGCAAAATGTATCCCTCTGTCAATTTCTGTGATGACCTCTCT 628  
QY 344 GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363  
Db 627 GGAAGGCCAATGTAAAGTGCATTCGAGAGAGCTGGGTTTACCTATAGGCGCTGAT 568  
QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 383  
Db 567 GTTCTCTGATTTGCTTTATGGAAGTTGGATTATCAGAAAGGCATTGATCTCATTCAA 508  
QY 384 LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403  
Db 507 CTTATCATACCAAGTCTCATGCGGAAGATGTTCAAATTTGTCTGCTTGGATCTGGTGAC 448  
QY 404 ProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423  
Db 447 CCAGAGCTTGAAGATTGGATGAGATCTACAGAGTGCATCTTCAGGATTAATTTCTGGA 388  
QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443  
Db 387 TGGGTTGGATTTAGTGTTCAGTTTCCCACCGAATAAATCTGCCGGCTGCCATATATTGTTA 328

QY 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463  
Db 327 ATGCCATCCAGATTCGAACCTTTGTGTCTCAATCAGCTATATGCTATGCAGTATGCGACA 268  
QY 464 ValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPhe 483  
Db 267 GTTCTGTTGTCCATGCAACTGGGGCCCTTAGAGATACCGTGGAGAACTTCAACCCCTTTC 208  
QY 484 GlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMet 503  
Db 207 GGTGAGATGGAGAGCAGGGTACAGGGTGGGCATTCGCACCCCTTAACACACAGAAACATG 148  
QY 504 PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523  
Db 147 TT-GTGGACATTCGCAACTGCAATATCTACATACAGGGGAACACAAAGTCTCTCTGGGAAG 89  
QY 524 AlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
Db 88 GCTAATGAAGCGAGGCATGTCAAAAGACTTCACGTGGGACCATGCCGC 41

## RESULT 12

US-09-508-377-11  
; Sequence 11, Application US/09508377  
; Patent No. 6916976  
; GENERAL INFORMATION:  
; APPLICANT: KALEEN, ZHONGYILI  
; APPLICANT: MORELL, MATTHEW  
; APPLICANT: RAHMAN, SADEQU  
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION IN PLANTS  
; FILE REFERENCE: 054270/0126  
; CURRENT APPLICATION NUMBER: US/09/508,377  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: AU PP 2509  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: PCT/AU98/00743  
; PRIOR FILING DATE: 1998-09-11  
; PRIOR APPLICATION NUMBER: AU PP 9108  
; PRIOR FILING DATE: 1997-09-12  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 2662  
; TYPE: DNA  
; ORGANISM: Triticum tauschii  
US-09-508-377-11

## Alignment Scores:

Pred. No.:	1,448-281	Length:	2662
Score:	2467.50	Matches:	464
Percent Similarity:	51.8%	Conservative:	30
Best Local Similarity:	86.2%	Mismatches:	41
Query Match:	85.3%	Indels:	4
DB:	3	Gaps:	2

US-10-628-525A-21 (1-539) x US-09-508-377-11 (1-2662)

QY 2 ValAlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGlySer 21  
Db 539 GTGGGGGAACTCGCG---CCGACCTCTGCTC-----GAAGGGATTGCTGAGGATTC 589  
QY 22 IleAspAsnThrValValValAlaSerGluGlnAspSerGluIleValValGlyLysGlu 41  
Db 590 ATCGACACATTAATGTTGGCTGCGAGTGCAGGAGATCTGAGATCATGATCGGAATGAG 649  
QY 42 GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61  
Db 650 CAACCTCAAGCTAAAGTTACAGTAGCATCGTGTGTGTGTGACCTGGTGAAGCTCTCTTAT 709  
QY 62 AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaArg 81  
Db 710 GCAAAGTCAGGGGGCTGGGAGATGTTTGTGTTGTTTACCAATTCCTTCTGCTGCTGCT 769



QY 82 GlyHisArgValMetValMetProArgTyrIleuAsnGlyThrSerAspLysAsnTyr 101  
Db 770 GGTCAACGCTGGTGGTGTGAATCCCAAGATACCTTGAATGGGCTCTCTGATAAAACTAT 829  
QY 102 AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu 121  
Db 830 GCAAAAGGCATATACACTGGGAGCACATTAAGATTCAATGCTTTGGGGGATCACATGAA 889  
QY 122 ValThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSer 141  
Db 890 GTGACCTTTTTCATGAGTATAGACACACGTCGATTGGGTGTGTGTCGATCATCCGTCA 949  
QY 142 TyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161  
Db 950 TATCATAGACAGAGAGTATATATGGAGATAATTTTGGTGTCTTTTGTGTGATAATACAGTTC 1009  
QY 162 ArgTyrThrLeuLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluGlyGly 181  
Db 1010 AGATACACACTCTCTTGTCTATGCTGCATGCGAGGCCCACTAATCTTGAATTGGGAGGA 1069  
QY 182 TyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValPro 201  
Db 1070 TATATTTATGACAGAAATTCGATGTTGTGTGAACGATTGGCATGCCAGCCTTGTGCCA 1129  
QY 202 ValLeuLeuAlaIalysTyrArgProTyrGlyValTyrIysAspSerArgSerIleLeu 221  
Db 1130 GTCTCTTCTGCTGCAAAATATAGACCATACGGTGTGTACAGAGATTCCCGCAGCACCCCTT 1189  
QY 222 ValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGly 241  
Db 1190 GTTATACATATTTAGACATCAGGCTCTCGAGCTCGCATATCTCTGATCTGGGA 1249  
QY 242 LeuProProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHis 261  
Db 1250 TTGCCACCTGAATGGTATGAGCTTTAGAATGGGTATTTCCAGAAAGGAGCAGCTCGTGCAGCAGATCGA 1309  
QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArg 281  
Db 1310 GCCCTTGACAAAGGTGAGGAGTTAACTTTTGAAGAGGAGCAGCTCGTGCAGCAGATCGA 1369  
QY 282 IleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGly 301  
Db 1370 ATTGTGACCTGCTCAGGCTTATTCATGGAGGTCAACTGCTGAAGGTGACAGGCG 1429  
QY 302 LeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp 321  
Db 1430 CTCAATGAGCTCTTAAGCTCCGAAAGAGTATTTGAATGGAATTTGAATGGAATGAC 1489  
QY 322 IleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp 341  
Db 1490 ATTAATGATTTGGAAAGCCCAACACAGCAAGTGTCTCCCTCATCATTAATCTGTGATGAC 1549  
QY 342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg 361  
Db 1550 CTCTCTGAAAGGCCAAATGAAGCTGAATTCAGAGAGAGCTGGTTTACTCTGTAAGG 1609  
QY 362 ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381  
Db 1610 GAGGATGTTCTCTGATTTGCTTTATTTGGAAGACTGGATTACCAAGAAAGGCATTGATCTC 1669  
QY 382 IleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer 401  
Db 1670 ATTAATAAGGCCATTCACAGCTCATGAGGAGGAGCTGCAGTTTGTCTGCTTGGATCT 1729  
QY 402 GlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPhe 421  
Db 1730 GGGATCCCAATTTTGAAGCTCGATGAGATCTACCGAGTCGAGTTACAGGATAAATTC 1789  
QY 422 ArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle 441  
Db 1790 CGTGGATGGTGGATTAGTGTTCAGATTTCACACAGATACTACGAGTTCGGATATA 1849  
QY 442 LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461

Db 1850 TTGTTAATGTCATCCAGCTTGAACCTTGTGGTCTTAATCAGCTATATGCTATGCAATAT 1909  
QY 462 GlyThrValProValValHisAlaThrGlyGlyLeuArgPheThrValGluAsnPheAsn 481  
Db 1910 GGTACAGTCTCTGTAGTTCATGGAACCTGGGGGGCTCCGAGACACAGTCCGAGACCTTCAAC 1969  
QY 482 ProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGlu 501  
Db 1970 CCTTTTGGTCAAAAGAGAGAGGAGGTACAGGTGGGGCTTCTCACCGCTAACCGTGGAC 2029  
QY 502 AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu 521  
Db 2030 ARGATGTT-GTGGGCATTTGCCAACCGCGATGTGCACATTCAGGGAGCACAGCGCTCTG 2088  
QY 522 GlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
Db 2089 GGAGGGCTCATGAGCGAGGCATGACGAAGACCATACGTGGGACCATGCCGC 2142

RESULT 13  
US-09-196-390-1  
; Sequence 1, Application US/09196390  
; Patent No. 6307125  
; GENERAL INFORMATION:  
; APPLICANT: Block, Martina  
; APPLICANT: Loz, Horst  
; APPLICANT: Lutticke, Stephanie  
; APPLICANT: Walter, Lennart  
; APPLICANT: Froberg, Claus  
; APPLICANT: Kosmann, Jens  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES  
; TITLE OF INVENTION: FROM WHEAT WHICH ARE INVOLVED IN STARCH  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/196,390  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 196 21 588.9  
; FILING DATE: 29-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 196 36 917.7  
; FILING DATE: 11-SEP-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP97/02793  
; FILING DATE: 28-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley, Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: AGREVO-9  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2239 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA



NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/952,677  
FILING DATE: 14-Sep-2001  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/196,390  
FILING DATE: 19-No. 6734339-1998  
APPLICATION NUMBER: DE 196 21 588.9  
FILING DATE: 29-MAY-1996  
APPLICATION NUMBER: DE 196 36 917.7  
FILING DATE: 11-SEP-1996  
APPLICATION NUMBER: PCT/EP97/02793  
FILING DATE: 28-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: AGREVO-9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Triticum aestivum L.  
STRAIN: cv. Florida  
HAPLOTYPE: ca. 21 d Caryopses  
IMMEDIATE SOURCE:  
LIBRARY: cDNA library in pBluescript sk (-)  
CLONE: TaSSS  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3..2017  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-952-677-1

Alignment Scores:  
Pred. No.: 1,42e-281 Length: 2239  
Score: 2466.50 Matches: 464  
Percent Similarity: 91.8% Conservative: 29  
Best Local Similarity: 86.4% Mismatches: 41  
Query Match: 85.3% Indels: 4  
DB: 3 Gaps: 2

US-10-628-525A-21 (1-539) x US-09-952-677-1 (1-2239)

QY 2 ValAlaGluLeuSerArgGluAspLeuGluProGluGlyLeuAlaGluGlySer 21  
Db 30 GTGGGGAACTCGCG---CCCGACCTCTCGTC-----GAAGGGATTGCTGAGGATTCC 80  
QY 22 IleAspAsnThrValValValAlaSerGluGlnAspSerGluIleValGlyLysGlu 41  
Db 81 ATCGACAGCATAATTGGCTGCTCAAGTGACGAGGATTCTGAGATCATGATGCGAATGAG 140  
QY 42 GlnAlaGAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61

Db 141 CAACCTCAAGCTAAAGTTACACGTAGCATCGTGTGTGTGAGCTGCTCCTTAT 200  
QY 62 AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAalaArg 81  
Db 201 GCAAGTCAAGGGGGTGGGAGATGTTTGGTTCGTTACCAATTCCTTCCTGCTCGT 260  
QY 82 GlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr 101  
Db 261 GGTCAACCGAGTGATGGTTGTAATGCCAAGTACTTAAATGGGTCTCTGATAAAACCTAT 320  
QY 102 AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu 121  
Db 321 GCAAAGGCATTATACACTCGCAAGCACATTAAAGATTCCATGCTTTGGGGATCATCATGAA 380  
QY 122 ValThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSer 141  
Db 381 GTGACCTTTTTCATGAGTATAGACACAGCTCGATGGGTGTTTGTGATCATTCCTGCA 440  
QY 142 TyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161  
Db 441 TATCAGACACCAAGGTTTATATGAGATAAATTTTGGTCTTTTGGTGATATCATGTTTC 500  
QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluGlyGly 181  
Db 501 AGATACACACTCCTTTGCTATGCTGATGCGAGGCCCACTAATCTTGAATTGGGAGGA 560  
QY 182 TyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHisAlaSerLeuValPro 201  
Db 561 TATATTTATGGACAGAAATTCATGTTTGTGTGACGATGGCATGCGACCTTTGTGCCA 620  
QY 202 ValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeu 221  
Db 621 GTCTTTCTTGTGCAAAATATAGACCATACGGGTGTTTACAGAGATTTCCCGCAGCACCTT 680  
QY 222 ValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGly 241  
Db 681 GTTATACATAAATTTAGCACATCAGGGGTGGAGCCTGCAAGTACATATCTGATCTGGGA 740  
QY 242 LeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaAspArgHis 261  
Db 741 TTGCTCTCTGAAATGATGAGCTTTAGATGGGTATTTCCAGATGGGCGACAGGAGCAT 800  
QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArg 281  
Db 801 GCCCTTGACAAGGGTGGAGCAGTTAACTTTTGAAGGAGCAGCTGTGACAGCAGATCG 860  
QY 282 IleValThrValSerLysGlyTyrSerTyrGluValThrAlaGluGlyGlnGly 301  
Db 861 ATTTGACCGTCAGTCAGGGTTATTTCATGGGAGGTCAACTGCTGAAGGTGACAGGCG 920  
QY 302 LeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp 321  
Db 921 CTCATGAGCTCTTAAGCTCCCGAAAGATGATTGAATGGATTTGAATGAATGAATGAC 980  
QY 322 IleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp 341  
Db 981 ATTAATGATTGGAACCCACACAGCAAGTGTCTCCCTCATCATTTATTTCTGTCGATGAC 1040  
QY 342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg 361  
Db 1041 CTCCTCTGGAAGGCCCAATGTAAGCTGAATGTCAGAGAGAGTTGGGTTCCTCTGAAGG 1100  
QY 362 ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381  
Db 1101 GAGGATGTTCTCTGATTGGCTTTATTGGAAGACTGATTACCCAGAAAGGCAATTGATCTC 1160  
QY 382 IleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer 401  
Db 1161 ATTAATAATGGCCATTCACAGAGCTCATGAGGGAGGAGTGCAATTTGTCATGCTTGATCT 1220  
QY 402 GlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPhe 421

Db 1221 GGGGATCCAAATTTTGAAGCGCTGGATGAGATCTACCGAGTCGAGTTTACAAGGATAAAATTC 1280  
QY 422 ArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle 441  
Db 1281 CGTGGATGGTGGATTTAGTGTTCAGTTCCTCCACAGAATAACTGACGGTTGCGATATA 1340  
QY 442 LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461  
Db 1341 TTGTAAATGCCATCCGAGATTGAACCTTCGGGTCTTAATCAGCTATATCTATGCAATAT 1400  
QY 462 GlyThrValProValValHisAlaThrGlyLeuArgAspThrValGluAsnPheAsn 481  
Db 1401 GGTACAGTTCCTGTAGTTTCATGAACTGGGGGCTCCCGAGACACATCGAGACCTTCAAC 1460  
QY 482 ProPheGlyLeuAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGlu 501  
Db 1461 CTTTTTGGTGCAAAGGAGGAGGGGTACAGGGTGGCGCTTCTACCGCTAACCGTGGAC 1520  
QY 502 AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu 521  
Db 1521 AAGATGTT-GTGGGCATTCGGAACCGCGATGTCGACATTCAGGAGCACAAAGCCGTCCTG 1579  
QY 522 GlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCys 538  
Db 1580 GGAGGGGCTCATGAAGCGAGGCATGACGAAGACCATACGTGGGACCATGC 1630

## RESULT 15

US-09-674-824-1  
; Sequence 1, Application US/09674824  
; Patent No. 6890732  
; GENERAL INFORMATION:  
; APPLICANT: Lorz, et al  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES DERIVED FROM WHEAT  
; FILE OF INVENTION: WHICH ARE INVOLVED IN THE SYNTHESIS OF STARCH  
; FILE REFERENCE: AGR 1998/M 205/ FLH514413-3848  
; CURRENT APPLICATION NUMBER: US/09/674,824  
; CURRENT FILING DATE: 2000-02-16  
; PRIOR APPLICATION NUMBER: PCT/EP99/03156  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: DE 198 20607.0  
; PRIOR FILING DATE: 1998-05-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 2771  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (280)..(2547)  
US-09-674-824-1

Alignment Scores:  
Pred. No.: 2,028-281 Length: 2771  
Score: 2466.50 Matches: 464  
Percent Similarity: 91.8% Conservative: 29  
Best Local Similarity: 86.4% Mismatches: 41  
Query Match: 85.3% Indels: 4  
DB: 3 Gaps: 2

US-10-628-525A-21 (1-539) x US-09-674-824-1 (1-2771)

QY 2 ValAlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGlySer 21  
Db 562 GTGGGGAACTCGCG---CCCGACTCTCGTCTC-----GAAGGGATTGCTGAGGATTC 612  
QY 22 IleAspAsnThrValValAlaSerGluGlnAspSerGluIleValValGlyLysGlu 41  
Db 613 ATCGACAGCATAAATTGTGCTGCTCAAGTGCAGGAGGATTCAGATCATGAGTCGAATGAG 672  
QY 42 GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61  
Db 673 CAACCTCAAGCTAAAGTTACACGTAGCATCGTGTGTTGTGACCTGGTGAAGCTGCTCCTTAT 732

QY 62 AlaLysSerGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAarg 81  
Db 733 GCAAAGTCAGGGGGTGGAGATGTTGTGGTCTGTACCAATGCTCTTGTCTCGT 792  
QY 82 GlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr 101  
Db 793 GGTCAACCGAGTGATGGTTGTAATGCAAGATACTTAAATGGTCTCTCTGATAAAACTAT 852  
QY 102 AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGlu 121  
Db 853 GCAAAAGGCAATTATACACTCCGAAGCACATTAAGATTCCATGCTTTGGGGGATCACATGAA 912  
QY 122 ValThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSer 141  
Db 913 GTGACCTTTTTCATGAGTATAGACAAACGTCGATGGGTGTTGTGCATCATCCGTC 972  
QY 142 TyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161  
Db 973 TATCACAGACCAAGAAATTTATATGAGATAATTTTGGTGTCTTTGGTGTATAATCAGTTC 1032  
QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluGlyGly 181  
Db 1033 AGATACACACTCTTGTCTATGCTGCATCCGAGGCCCACTAATCTTGAATTGGGAGA 1092  
QY 182 TyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrPheAlaSerLeuValPro 201  
Db 1093 TATATTTATGGACAGAAATTCATGTTGTGTGAACGATGGCANTGCCAGCTTGTGCCA 1152  
QY 202 ValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeu 221  
Db 1153 GTCCCTTCTTGTGCAAAATATAGACCATACGCGTGTTCACAGAGATTCCCGCAGCACCTT 1212  
QY 222 VallIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGly 241  
Db 1213 GTTATACATAAATTTAGCACATCAGCGGTGGAGCCCTGCAAGTACATATCTGATCTGGGA 1272  
QY 242 LeuProGluTyrTyrGlyValAlaLeuGluTyrValPheProGluTyrAlaArgArgHis 261  
Db 1273 TTGCTCTCTGAATGTATGGAGCTTTAGATGGGTATTTCCAGAAATGGGCAAGGAGCAT 1332  
QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArg 281  
Db 1333 GCCCTTGACAGGGGTGAGCGAGTTAACTTTTGAAGGAGCAGTGTGTGACACAGATCGG 1392  
QY 282 IleValThrValSerLysGlyTyrSerTyrGluValThrThrAlaGluGlyGlnGly 301  
Db 1393 ATTGTGACCGCTCAGTCAGGGTTATTCATGGGAGGTCAACAACCTGCTGAAGGTGACAGGC 1452  
QY 302 LeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp 321  
Db 1453 CTCATGAGCTCTTAAGCTCCGAAATAAGTGTATTTGAATGGAAATTTGAATGGAAATGAC 1512  
QY 322 IleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp 341  
Db 1513 ATTAATGATGGAAACCCCAACACACAGCAAGTGTCTCCCTCATCATTAATTTCTGTCGATGAC 1572  
QY 342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleAarg 361  
Db 1573 CTCTCTGAAAAGGCCAAATGTAAAGCTGAATGGCAAGGAGGTGGGTGTACTGTGAAGG 1632  
QY 362 ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381  
Db 1633 GAGGATGTTCTCTGATTTGGCTTTATTTGAAGACTGGATTTACCAAGAGGCATTTGATCTC 1692  
QY 382 IleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer 401  
Db 1693 ATTAATAATGGCCATTTCCAGAGCTCATGAGGAGGAGCGTCAATTTGTCTGATCTGATCT 1752  
QY 402 GlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPhe 421  
Db 1753 GGGGATCCAAATTTTGAAGGGCTGGATGAGATCTACCGAGTCGAGTTTACAAGGATAAAATTC 1812

QY 422 ArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle 441  
Db 1813 CGTGGATGGGTGGATTTAGTTTCCAGTTTCCACAGAAATAAATCGCAGGTGGCATATA 1872  
QY 442 LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461  
Db 1873 TTGTTAATGCATCGAGATTGAACCTTGGCTTTAATCAGCTATATGCTATGCAATAT 1932  
QY 462 GlyThrValProValValHisAlaThrGlyCysLeuArgAspThrValGluAsnPheAsn 481  
Db 1933 GGTACAGTTCTGTAGTTTCATGGAACCTGGGGCCCTCCGAGACACAGTCGAGACCTTCAAC 1992  
QY 482 ProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGlu 501  
Db 1993 CCTTTTGGTCAAAAGAGAGAGGGGTACAGGGGTGGCGCTTCTCACCGCTAAACCGTGGAC 2052  
QY 502 AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu 521  
Db 2053 AAGATGTT-GTGGGCAITTCGACCGGATGTCGACATTGAGGGAGCACAAGCGGTCTG 2111  
QY 522 GlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCys 538  
Db 2112 GGAGGGGCTCATGAAGCGAGGCATGACGAAGACCATACGTGGGACCATGC 2162

## RESULT 16

US-09-345-214-11  
; Sequence 11, Application US/09345214  
; Patent No. 6392120  
; GENERAL INFORMATION:  
; APPLICANT: Lightner, Jonathan B.  
; APPLICANT: Broglie, Karen B.  
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE  
; FILE OF INVENTION: EXPRESSION TO PRODUCE STARCHES IN GRAIN CROPS  
; FILE REFERENCE: BB-1147  
; CURRENT APPLICATION NUMBER: US/09/345,214  
; CURRENT FILING DATE: 1999-06-30  
; EARLIER APPLICATION NUMBER: 060/094,436  
; EARLIER FILING DATE: 1998-07-28  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 11  
; LENGTH: 1415  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-345-214-11

## Alignment Scores:

Pred. No.: 1 05e-231 Length: 1415  
Score: 2043.00 Matches: 388  
Percent Similarity: 89.8% Conservative: 0  
Best Local Similarity: 89.8% Mismatches: 0  
Query Match: 70.6% Indels: 44  
DB: 3 Gaps: 1

US-10-628-525A-21 (1-539) x US-09-345-214-11 (1-1415)

QY 1 CysValAlaGluLeuSerArgGlu----- 8  
Db 119 TGCGTCGCGAGCTGAGCAGGAGGGCGCGCGCGCGCGCTGCCACCGCGCTGCTG 178  
QY 8 ----- 8  
Db 179 GCGCCCGCGCTGTCGCGCGCTTCTCGCGCGCGCGCGCGCGCGCGCTGAGCGCGCA 238  
QY 9 -----AspLeuGlyLeuGluProGluGly 16  
Db 239 TCGACGCGCGCGCGCTGCGCGCGCGCGCGCTGCGGTCTCGAACCTGAAGGG 298  
QY 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36  
Db 299 ATTGCTGAAGTTCCATCGATACACAGTAGTTGTGGCAAGTCGAGCAAGATTCTGAGATT 358  
QY 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56

RESULT 17

US-09-743-980-11

Db 359 GTGGTTGGAAAGGAGCAAGCTCGAGCTAAAGTAACAACAAGCATTTGCTTTGTAACCGC 418  
QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
Db 419 GAAGCTTCTCTTATGCAAAAGTCTGGGGGTCTAGGAGATGTTTGTGTGTTTCAATGCCAGTT 478  
QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96  
Db 479 GCTCTTGTCTCTGTGTCTACCGTGTGATGTTGTAATGCCAGATATTTAAATGGTACC 538  
QY 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
Db 539 TCCGATAAAGAAATATGCAATGCAATTTTACACAAAAACACATTCGGAATTCATGCTTT 598  
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPhe 136  
Db 599 GGGGTGACACAGTAGTACCTTCTTCCATGAGTATAGAGATTCAGTTGATGGGTGTTT 658  
QY 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
Db 659 GTTGATCATCTCTCATATCACAGACCTGGAAATTTATATCGAGATAAGTTTGGTCTTTT 718  
QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
Db 719 GGTGATAATCAGTTCAGATACACATCTCTTGTCTATGCTGCATGTGAGGCTCTCTTGCATC 778  
QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis 196  
Db 779 CTTGAATTTGGAGGATATTTATGACAGANTTCATGTTTGTGTGTTGTTCAATGATGGCAT 838  
QY 197 AlaSerLeuValProValLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 839 GCCAGTCTAGTGCAGTCTCTTCTGTCGCAAAATATAGACCATATGCTGTTTATAAAGAC 898  
QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
Db 899 TCCGCGAGCATTTCTTGTATAACATAATTTAGCACATCAGGGTGTAGAGCCTGCAAGACA 958  
QY 237 TyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256  
Db 959 TATCTCGACTTGGGTGGCACCCTGAATGATGGAGCTCTGGAGTGGGTATTTCCCTGAA 1018  
QY 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
Db 1019 TGCGCGAGGAGCATGCTCCCTTGACAGGGTGGAGCATTAATTTTGAAGGTGCAGTT 1078  
QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrGluValThrAla 296  
Db 1079 GTGACAGCAGATCGAATCGTACTGTCTAGTAAGGGTTATTCGTGGGAGGTCACAACTGCT 1138  
QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle 316  
Db 1139 GAAGGTGGACAGGGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACCGGAAT 1198  
QY 317 ValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHis 336  
Db 1199 GTAAATGGAATTGACATTAATGATTGGAACCTCGCCACAGACAAATGATCCCTGTGCAT 1258  
QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysGlyGlyAlaLeuGlnLysGluLeu 356  
Db 1259 TATTCCTGTTGATGACCTCTCTGAAAGGCCAAATGTAAAGGTGCATTCGACAGAGGAGCTG 1318  
QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
Db 1319 GGTTCACCTATTAAGGCTGATGTTCTCTGATTTGGCTTTTATTGGAAGGTTGGATTATCAG 1378  
QY 377 LysGlyIleAspLeuIleGlnLeuIleIleProAsp 388  
Db 1379 AAAGCATTTGATCTCATTCACTTATCATACCAGAT 1414





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; APPLICATION NUMBER: PCT/EP95/04415
; FILING DATE: 09-NOV-1995
; PRIORITY INFORMATION:
; APPLICATION NUMBER: DE P 44 41 408.0
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James P.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agrevo-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2360 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Solanum tuberosum
; STRAIN: cv. Desire
; TISSUE TYPE: leaf tissue
; IMMEDIATE SOURCE:
; LIBRARY: cDNA-library in Lambda ZAPII
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 68..1990
; US-08-836-567-9

Alignment Scores:
Pred. No.: 1,42e-215 Length: 2360
Score: 1910.00 Matches: 360
Percent Similarity: 78.9% Conservative: 74
Best Local Similarity: 65.5% Mismatches: 93
Query Match: 66.0% Indels: 24
DB: 3 Gaps: 6

US-10-628-525A-21 (1-539) x US-08-836-567-9 (1-2360)

QY 10 LeuGlyLeuGluProGluGlyIleAlaGluGlySerIle-----ValAlaSerGluGln 32
DB 290 TTGGGTGCTGAGAGAGATGGT-----TCGGCTCTGTGTGGTTCATTTGATTCCTCA 343
QY 23 -----AspAenThrValVal-----ValAlaSerGluGln 32
DB 344 CATTCCTGTGAGAGAGATGCAACAAATGGTAGAATCTCATGATATTTGTAGCCAAATGATAGA 403
QY 33 Asp-----SerGluIleValValGlyLysGluGlnAlaAlaArgAlaLysValThrGlnSer 50
DB 404 GATGACTTGAGTGAGGATACCTGAGGAGATGGAGGAAACCCCAATCAAAATTAACCTTTCAAT 463
QY 51 IleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspVal 70
DB 464 ATCATTTTGTACTGCTGAGCAGCTCCCATATTTCTAAGACTGCTGGATGAGGATGAGT 523
QY 71 CysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValValMetPro 90
DB 524 TGTGGTCTTTGCAATGCGCATAGCTGCTCGGGGTCAATCGTGTATGCTGCTTCACT 583
QY 91 ArgTyrLeuAen---GlyThrSerAspLysAenTyrAlaAenAlaPheTyrThrGluLys 109
DB 584 AGGTATTTGAATGGAGTCTCCTCAGATGAAAGTAGCCCAATGCTGTGACCTTTGATGTG 643
QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129
DB 644 CGGGCCACTGTCTCATTTGTTGGTGTGTCACAGAAAGTAGCCCTTCTACCATGAATACAGG 703
QY 130 AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAenLeuTyr 149
DB 704 GCAGGTGTTGATGGGTATTTGGGACCCTCTCTTACTGACAGACTGGAAGCCCATAT 763
QY 150 GlyAspLysPheGlyAlaPheGlyAspAenGlnPheArgTyrThrLeuLeuCysTyrAla 169
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DB 764 GGTGATATTTATGGTGCATTTGGTGATAATCAGTTTGGTTCATCTTGTCTTCACGCCA 823
QY 170 AlaCysGluAlaProLeuIleLeuGluLeuGlyTyrIleTyrGlyGlnAenCysMet 189
DB 824 GCATGTGAGGCCCATTTGGTCTTCTCACTGGAGGGTTCTACTATGAGAGAGTGTGTT 883
QY 190 PheValValaAenAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyrArg 209
DB 884 TTCTCGCTAAATGATTTGGCATGCTGCCCTGGTTCTTTACTTTTAGCGGCAAGATATCGT 943
QY 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAenLeuAlaHisGln 229
DB 944 CCTATATGGTGTTTACAGGATGCTCGTAGTATTTGTCATACACACATTTGCACATCAG 1003
QY 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyVala 249
DB 1004 GGATGTGAGCTGCAGTACCTACATAATTTGGGTTTGGCTCCACATGATATGGAGCA 1063
QY 250 LeuGluTrpValPheProGluTrpAlaArgHisAlaLeuAspLysGlyGluAlaVal 269
DB 1064 GTTGAATGATATTTCCCATGCGGCAAGCGCATGCGCTTGACACTGCTGGAACAGTG 1123
QY 270 AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr 289
DB 1124 AACGTTTTGAAAGGGCAATAGCAGTTGCTGATCGGATACTGACACTTAGCCAGGATAC 1183
QY 290 SerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAenGluLeuLeuSerArg 309
DB 1184 TCATGGGAATTAACAACCTCTGGAAGGGGATATGGGCTACATGAGCTGTGAGCAGTAGA 1243
QY 310 LysSerValLeuAenGlyIleValAenGlyIleAspIleAenAspTrpAenProAlaThr 329
DB 1244 CAGTCTGTTCTTAATGGAATTAATAATGGAATAGATGTTAATGATGGAACCCGTCGACA 1303
QY 330 AspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLys 349
DB 1304 GATGACATATTTGCTTCGCATTAATCCATCAATGACCTCTCCGGAAGGTTTCAAGTCAAG 1363
QY 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe 369
DB 1364 ACTGATCTGCAAAAGGAACTGGGCTTCATATTCGACCTGATGTTGCTCTGATGATTT 1423
QY 370 IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeu 389
DB 1424 ATTGGAAGCTGACTTACCAGAAAGGTGTGACATAATCTCTGTCACCAATTTCCAGAACTT 1483
QY 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrp 409
DB 1484 ATGCAGAAATGATGTCCAAGTTGTAATGCTTGGATCTGTTGAGAAACAATATGAAGACTGG 1543
QY 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerVal 429
DB 1544 ATGAGACATACAGAAATCTTTTAAAGACAATTTCTGGTCTTGGGTTGATTAATGTT 1603
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DB 1604 CCAGTTTCTCATAGGATACACAGGATGCGACATACATATTTGATGCTCCCTCAAGATTCGAA 1663
QY 450 ProCysGlyLeuAenGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469
DB 1664 CGGTGTGGCTTAACCAATTTGATGCAATGAGATATGGCACCACATCTATTTGTTTCATAGC 1723
QY 470 ThrGlyGlyLeuArgAspThrValGluAenPheAenProPheGlyGluAenGly---Glu 488
DB 1724 ACGGGGGGCTTAAGAGACACAGTGAAGGATTTTAATCCATATGCTCAAGAGGAATAGGT 1783
QY 489 GlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAenMetPheValAspIleAla 508
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QY 509 AsnCysAenIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAlaArg 528
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QY 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyr 409
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QY 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerVal 429
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QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449
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QY 450 ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469
Db 1664 CCGTGTGGCTTAAACCAATTTGATGCAATGAGATATGGACCATACCTATTGTTCTAGC 1723
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RESULT 20
US-08-836-567-3
; Sequence 3, Application US/08836567
; Patent No. 6130367
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; APPLICANT: Springer, Franziska
; APPLICANT: Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,567
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04415
; FILING DATE: 09-NOV-1995
; PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: DE P 44 41 408.0
/ FILING DATE: 10-NOV-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Haley Jr., James F.
/ REGISTRATION NUMBER: 27,794
/ REFERENCE/DOCKET NUMBER: Agrevo-4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-596-9000
/ TELEFAX: 212-596-9090
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1758 base pairs
/ TYPE: nucleotide
/ STRANDEDNESS: unknown
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ HYPOTHEetical: NO
/ ANTI-SENSE: NO
/ ORGANISM: Solanum tuberosum
/ STRAIN: cv. Berolina
/ TISSUE TYPE: tuber tissue
/ IMMEDIATE SOURCE:
/ LIBRARY: cDNA-library in pBluescriptSKII+
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..1377
/ OTHER INFORMATION: /function= "Polymerization of
/ OTHER INFORMATION: starch"
/ OTHER INFORMATION: /product= "Starch synthase"
US-08-836-567-3
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Alignment Scores:
Pred. No.: 1,96e-184 Length: 1758
Score: 1645.50 Matches: 304
Percent Similarity: 81.7% Conservative: 63
Best Local Similarity: 67.7% Mismatches: 70
Query Match: 56.9% Indels: 13
DB: 3 Gaps: 5
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US-10-628-525A-21 (1-539) x US-08-836-567-3 (1-1758)

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QY 115 CysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyr 134
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QY 275 AlaValThrAlaAspArgHisValThrValSerLysGlyTyrSerTrpGluValThr 294
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QY 295 ThrAlaGluGlyGlnGlyLeuAAsnGluLeuLeuSerSerArgLysSerValLeuAAsn 314
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Db 646 GGAATTAATTAATGGAATAGATGTTAATGATGGAACCCGTGCACATGAGCATATCGCT 705
QY 335 CysHisTyrSerValAspAspLeuSer-----GlyLeuAlaLysCysLysGlyAlaLeu 352
Db 706 TCGCATTAATCCATCAATGACCTCTCCCTCCCTGGAAAGTTTCAGTGCAGACTGATCTG 765
QY 353 GlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArg 372
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QY 413 ThrGluSerIlePheLysAspLysPheArgGlyTrrpValGlyPheSerValProValSer 432
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QY 433 HisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGly 452
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QY 453 LeuAAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGly 472
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RESULT 21
US-09-606-304-3
; Sequence 3, Application US/09606304
; Patent No. 6483010
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; Abel, Gernot
; Springer, Franziska
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
```

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;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/606,304
; FILING DATE: 28-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,567
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE P 44 41 408.0
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agrevo-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1758 base pairs
; TYPE: nucleotide
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Solanum tuberosum
; STRAIN: cv. Berolina
; TISSUE TYPE: tuber tissue
; IMMEDIATE SOURCE:
; LIBRARY: cDNA-library in pBluescriptSKII+
; OTHER INFORMATION: CDS
; FEATURE:
; LOCATION: 1..1377
; OTHER INFORMATION: /function= "Polymerization of
; starch"
; /product= "Starch synthase"
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
;
; US-09-606-304-3
;
; Alignment Scores:
; Pred. No.: 1,966-184 Length: 1758
; Score: 1645.50 Matches: 304
; Percent Similarity: 81.7% Conservative: 63
; Best Local Similarity: 67.7% Mismatches: 70
; Query Match: 56.9% Indels: 13
; DB: 3 Gaps: 5
;
; US-10-628-525A-21 (1-539) x US-09-606-304-3 (1-1758)
;
; QY 95 GlyThrSerAspLysAsnTyrAlaAAsnAlaPheTyrThrGluLysHisIleArgIlePro 114
; Db 1 GGCACGAGC-----AATGCTGTTGACCTGTGATGCGGGGCCACTGTGCCAT 45
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US-08-941-445A-10  
; Sequence 10, Application US/08941445A  
; Patent No. 6107060  
; GENERAL INFORMATION:  
; APPLICANT: Keeling, Peter  
; APPLICANT: Guan, Hanning  
; TITLE OF INVENTION: Starch Encapsulation  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/941,445A  
; FILING DATE: 30-SEP-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/026,855  
; FILING DATE: 30-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winner, Ellen P  
; REGISTRATION NUMBER: 28,547  
; REFERENCE/DOCKET NUMBER: 89-97  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2097 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..2097  
US-08-941-445A-10  
Alignment Scores:  
Pred. No.: 2,88e-123 Length: 2097  
Score: 1130.50 Matches: 254  
Percent Similarity: 57.2% Conservative: 64  
Best Local Similarity: 45.7% Mismatches: 159  
Query Match: 39.1% Indels: 80  
DB: 3 Gaps: 11  
US-10-628-525A-21 (1-539) x US-08-941-445A-10 (1-2097)  
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STATE: New York  
 COUNTRY: USA  
 ZIP: 10020

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/606,304  
 APPLICATION NUMBER: 08/836,567  
 FILING DATE: 10-NOV-1994  
 FILING DATE: 28-Jun-2000  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/836,567  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: DE P 44 41 408.0  
 FILING DATE: 10-NOV-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Haley Jr., James F.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: Agrevo-4

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-596-9000  
 TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2793 base pairs  
 TYPE: nucleotide  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 ORIGINAL SOURCE:  
 ORGANISM: Solanum tuberosum  
 STRAIN: cv D, sir, e  
 TISSUE TYPE: leaf tissue  
 IMMEDIATE SOURCE:  
 LIBRARY: cDNA-library in Lambda ZAPII  
 OTHER INFORMATION: CDS

FEATURE:  
 LOCATION: 242..2542  
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
 US-09-606-304-7

Alignment Scores:  
 Pred. No.: 1,43e-120 Length: 2793  
 Score: 1109.50 Matches: 240  
 Percent Similarity: 61.2% Conservative: 65  
 Best Local Similarity: 48.2% Mismatches: 162  
 Query Match: 38.4% Indels: 32  
 DB: 3 Gaps: 9

US-10-628-525A-21 (1-539) x US-09-606-304-7 (1-2793)

Qy 50 SerileValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAsp 69  
 Db 1070 AACATTATTTTGGTGGCTTCAGAAATCGCGTCCATGCTCTAAAACAGGTGGGCTTGGAGAT 1129

Qy 70 ValCysGlySerLeuProValAlaLeuAlaArgGlyHisArgValMetValMet 89  
 Db 1130 GTTGTGGAGCATTACCCAAAGCTTTGGCTCGACGTGGCCACAGAGTTATGGTTGGCA 1189

Qy 90 ProArgTyrLeuAsn-----GlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThr 107  
 Db 1190 CTCTGTATGACACTATCTGACCTCAAGATCTGGTGAAGAAAATTTATAAAGTT 1249

Qy 108 GluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlu 127  
 Db 1250 GAT-----GGTCAGGATGTGGAAGTGACTTACTTCCAAAGCT 1285

Qy 128 TyrArgAspSerValAspTrpValPheValAsp---HisProSerTyrHisArgProGly 146  
 Db 1286 TTATTATGATGGTGGATTTTGTTCATTGTGACAGTCATATGTTTAGACACATGGGAAC 1345

Qy 147 AsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeu 166  
 Db 1346 AACATTTACGGA-----GGGAACCGTGGGATATTTTAAAACGCATGGTTTATTT 1396

Qy 167 CysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGln 186  
 Db 1397 TCAAAAGCAGCGATTGAGGTTCTTGGCATGTTCCTCATGTGGTGGGTCTGCTATGGAGAT 1456

Qy 187 ---AsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAla 205  
 Db 1457 GGAATTTTATGCTTCAATGATGGCATCTGCTTTATTCGCAATATATCGATAA 1516

Qy 206 AlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsn 225  
 Db 1517 GCTTATTATCGTGACAATGGAATTAAGACTATACAAGATCTGCTCTGGTGAATTCATAAC 1576

Qy 226 LeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGlu 245  
 Db 1577 ATCGCTCATCAGGTCGTGTCCTTTGGAGGATTTTTCATATGTAGATCTTCCACCACAC 1636

Qy 246 TrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgHisAlaLeuAspLys 265  
 Db 1637 TATATGGACCTTTCAAGTTGTATGACCAGTA-----GGA 1672

Qy 266 GlyGluAlaValAsnPheLeuLysGlyAlaValAlaValThrAlaAspArgIleValThrVal 285  
 Db 1673 GGTGAGCATTTCAAATTTTCCGGCTGGTCTAAAGACACGACAGATCGTGTAGTTACAGTT 1732

Qy 286 SerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeu 305  
 Db 1733 AGTCATGGATATTTCATGGNACTTAAAGACTTCCCAAGGTGGTGGGAGTTGCATCAGATA 1792

Qy 306 LeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrp 325  
 Db 1793 ATTAATGAGAACGATTGGAATTTACAGGATTTGTGAATGGGATGATGATACAAAAGAGTGG 1852

Qy 326 AsnProAlaThrAspLysCysIlePro-----CysHisTyrSerValAspAsp 341  
 Db 1853 AACCTGTAGTTGGAGCTTCACTTACAGTCAGATGGTGTACATGACTTCTCTTGGACAGC 1912

Qy 342 Leu---SerglyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIle 360  
 Db 1913 CTACAGACTGGCAAGCCTCAATGTAAAGCTGATTCAGAGGAACTTGGTTTACCAAGTT 1972

Qy 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380  
 Db 1973 CGTGTATGATGTCCCACTGATCGGTTTCAATTGGAGGCTTGACCCACAAAGGGTGTGAT 2032

Qy 381 LeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
 Db 2033 CTGATTGTGAGGCCAGTCGTTGGATGATGGGTGAGGATGTACAACTGCTCATGTTGGGG 2092

Qy 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys 420  
 Db 2093 ACGGGGAGCGGTGACCTTGAACAGATGCTAAGGCAATTTGAGTGTCAACACCAATGATAAA 2152

Qy 421 PheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440  
 Db 2153 ATTAGAGGATGGTGGTGGTTCCTCTGTGAAGACTTCTCATCGTATACTGCTGGTGCAGAC 2212

Qy 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460  
 Db 2213 ATTCTGCTCATGCTTCTAGATTGAGCCTTGGGACTGGAACAGCTTTATGCAATGAAA 2272

Qy 461 TyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPhe 480  
 Db 2273 TATGGGACTATTCTCTGTGTTTTCATGAGTAGGAGGACTCAGAGATACTGTGAGCCCTTT 2332

Qy 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThr 500  
 Db 2333 GATCCTTTTAAATGATCA-----GGACTGGGGGTGACCTTCAGTAGGCGCTGAGCT 2383

Qy 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520

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Db 2384 AGCCAGCTGATCCACGCAATTAGGAATGCTTACTGAC-TTATCGTGAATACAAAAAGAG 2442
Qy 521 LeuGlyArgAlaAsnGluAlaArgHisVallysArgLeuHisValGlyProCys 538
Db 2443 TTGGAGGGGATTACAGACCGCTTGTATGACACAGACTTAAGTTGGGATAATGC 2496

RESULT 26
US-09-388-743-25
; Sequence 25, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Lan
; TITLE OF INVENTION: No. 6423886el Starch Synchase Polynucleotides and Their
; FILE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 2418
; TYPE: DNA
; ORGANISM: Typha latifolia
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)... (2418)
US-09-388-743-25

Alignment Scores:
Pred. No.: 6.63e-120 Length: 2418
Score: 1103.00 Matches: 243
Percent Similarity: 59.7% Conservative: 78
Best Local Similarity: 45.2% Mismatches: 176
Query Match: 38.1% Indels: 42
DB: 3 Gaps: 12

US-10-628-525A-21 (1-539) x US-09-388-743-25 (1-2418)
Qy 15 GluGlyIleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSer 34
Db 574 GAAGACTTGTAGAGCAAAATGGATAGTGTACATGTC-----AAAGAT 618
Qy 35 GluIleValValGlyIysGluGln-----AlaArgAlaIysValThr 48
Db 619 GATTTGAATCTCTGGGAAGAAATAGGTTCTCTTCTTCTTGGCTGGGCAATGTC--- 675
Qy 49 GlnSerIleValPheValThrGlyGluAlaSerProTyrAlaIysSerGlyIleGly 68
Db 676 ATGAACATCATCATAGTAGTGTCTGCAGAAATGTGCTCTTGGTCCAAAACAGCGTGGCTTGA 735
Qy 69 AspValCysGlySerLeuProValAlaLeuAlaArgGlyHisArgValMetValVal 88
Db 736 GATGTTGCAGAGCATTGCCAAGGCTTTGCCAGAGAGGACATAGGGTCATGGTTGTG 795
Qy 89 MetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGlu 108
Db 796 GCACCAAGGTATGCAAACTATGCTGAACCCCAAGATATAGGAGTCCGCAAAATACTACAAG 855
Qy 109 LysHisIleArgIleProCysPheGlyGluHisGluValThrPhePheHisGluTyr 128
Db 856 GTTCAT-----GGCGAGGATATGGAAGTAACCTATTATTCATGCTTAT 897
Qy 129 ArgAspSerValAspTrpValPheValAspHisProSerTyr---HisArgProGlyAsn 147
Db 898 ATCGAGGTGTGATTTGTTTATGGATAGTCAGACTTCGCTCACCAGGGGGAATCGT 957
Qy 148 LeuTyr---GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeu 166
Db 958 ATTTATGAGGGAACCGAGTG-----GATATCTTAAACGATGATGTTTGTTC 1005
Qy 167 CysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyTyrIleTyrGlyGln 186

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Db 1006 TGCAAGGCAGCTGTAGAGGTTCTTGGCATGTTCCATGTGGTCTCTGTATGAGAT 1065
Qy 187 ---AsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAla 205
Db 1066 GGTAAATTTGGCTTTTCATCAGCAATGATTGGCATACTGCTCTCTTGGCTGTTTATCTGAAG 1125
Qy 206 AlalysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsn 225
Db 1126 GCATATTATCGTCAATGCTTGATGATGATGCTCGTCTGTTCTGTTGGTAAATACAAAC 1185
Qy 226 LeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProProGlu 245
Db 1186 ATAGCCACCAGCGTCTGCTGCTGTAGATGACTTCAAAATTTGGGGCTTGGCCGATCAC 1245
Qy 246 TrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLys 265
Db 1246 TACTGGACCTTTTCAGATTGTATGACCCCGTC-----GGA 1281
Qy 266 GlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAspArgIleValThrVal 285
Db 1282 GGTGAACACCTCAATATTTTGTGCTGGCTGAGACTGCTGACCGAGTGGTTACTGTT 1341
Qy 286 SerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeu 305
Db 1342 AGCCATGTTTATGCTGAGGAGCTGAAAAACATCAGAAGTGGTTGGGGCTTACATGAAT 1401
Qy 306 LeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrp 325
Db 1402 ATAAATGAAGTAGTAAGTTTCAAGTATTGTAATGGCATTGATGCAAGAGGAGTGG 1461
Qy 326 AsnProAlaThrAspLysCysIlePro-----CysHisTyrSerValAspAsp 341
Db 1462 AGCCCGAATTTGATGTGCACCTTAATCCGATGGATACACAATATTCTCTAGTACT 1521
Qy 342 LeuSer---GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIle 360
Db 1522 TTAGAGATGGTAAAGCCAGTATGTAAGGCTGCTTTCAGCGAGAGTGGCTGCTGCTGTT 1581
Qy 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380
Db 1582 CGTGATATGTATCCCATTCATTGCAATTCATTGGAAGGTTAGACCACCAAGAGCGCTGAT 1641
Qy 381 LeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400
Db 1642 CTCAATTCGCGAGGCCATGCTTGGATGTGATGCTCATGATGTTCAAGTAGTCAATGTTAGGC 1701
Qy 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys 420
Db 1702 ACGGGAGGCAAGACCTTGAGAATTTTACTGAGGAACCTTTGAGGGTCAACACAGGGACAA 1761
Qy 421 PheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440
Db 1762 GTTAGAGATGGGTGTCATTTTCAGTAAAGATGGCGCATAGAAATTACAGCAGGTGCGCAC 1821
Qy 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460
Db 1822 ATCCTCATGATGCTTCGAGGTTTGAGCCATGCGGATTCGACCCAGCTTTACGCATGATG 1881
Qy 461 TyrGlyThrValProValValHisAlaThrGlyIleLeuArgAspThrValGluAsnPhe 480
Db 1882 TATGGAACCATCTCCAGTGGTGCATGCTGTGGGGGCTTTAGAGATACAGTCAATTT 1941
Qy 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThr 500
Db 1942 GATCTCTTCAACAGAGTCT-----GGTCTGGTTGGACCTTCACAGGGCAGAGGCA 1992
Qy 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520
Db 1993 GGAAGACTCATCGTCATTGTAATACTGCTT-GAATACATACTGGAATACAGGACAG 2051
Qy 521 LeuGlyArgAlaAsnGluAlaArgHisVallysArgLeuHisValGlyProCys 538

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Db 2052 TTGGAAGGCTCTTCAACACAGAGGATGATCAAGATCTTTAGCTGGGATAATGC 2105

RESULT 27

US-10-044-543-25

; Sequence 25, Application US/10044543

; Patent No. 6734341

; GENERAL INFORMATION:

; APPLICANT: Singletary, George

; APPLICANT: Zhou, Lan

; TITLE OF INVENTION: No. 6734341el Starch Synthase Polynucleotides

; TITLE OF INVENTION: and Their Use in the Production of New Starches

; FILE REFERENCE: 1144D

; CURRENT APPLICATION NUMBER: US/10/044,543

; CURRENT FILING DATE: 2002-01-11

; PRIOR APPLICATION NUMBER: 09/388,743

; PRIOR FILING DATE: 1999-09-02

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 25

; LENGTH: 2418

; TYPE: DNA

; ORGANISM: Typha latifolia

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(2418)

US-10-044-543-25

Alignment Scores:

Pred. No.:	6.63e-120	Length:	2418
Score:	1103.00	Matches:	243
Percent Similarity:	59.7%	Conservative:	78
Best Local Similarity:	45.2%	Mismatches:	176
Query Match:	38.1%	Indels:	42
DB:	3	Gaps:	12

US-10-628-525A-21 (1-539) x US-10-044-543-25 (1-2418)

Qy	15	GluclylealaGluGlySerIleAspAenThrValValValAalaSerGluGlnAspSer	34
Db	574	GAAGATCTTGTAAGCAACAAATTGGATAGTGATCATGTC-----AAAGAT	618
Qy	35	GlutleValValGlyLysGluGln-----AlaArgAlaLysValThr	48
Db	619	GATTTGAATCTGGGGAAGAAATAGAGGTCTCTCTCTTTGGCTGGGCAATGTC---	675
Qy	49	GlnSerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGly	68
Db	676	ATGAACATCATAGTAGTTGCTGCAGAAATGTGCTCTTGGTCCAAACACAGGTGGGCTTGA	735
Qy	69	AspValCysGlySerLeuProValAlaLeuAlaArgGlyHisArgValMetValVal	88
Db	736	GATGTTCCAGGAGCATTTGCCAAGGCTTTGGCCAGAAGAGACATAGGGGTGCTGGTGTG	795
Qy	89	MetProArgTyrLeuAenGlyThrSerAspLysAenTyrAlaAenAlaPheTyrThrGlu	108
Db	796	GCACCAAGGTATGGAACATATGCTGAACCCACAGATATAGAGTCCGCAANTACTACAAG	855
Qy	109	LysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlyTyr	128
Db	856	GTTCAT-----GGCAGGATATGGAAGTAACTTATTTCATGCTTAT	897
Qy	129	ArgAspSerValAspTrpValPheValAspHisProSerTyr---HisArgProGlyAsn	147
Db	898	ATGCACGGTGTGAATTTTGTATGATAGTCCAGACTTCGCTACCGGGGAATTCGT	957
Qy	148	LeuTyr---GlyAspLysPheGlyAlaPheGlyAspAenGlnPheArgTyrThrLeuLeu	166
Db	958	ATTATGAGGGAACCCAGTG-----GATATCTTAAACGATGATTTTGTTC	1005
Qy	167	CysTyrAlaAlaCysGluAlaProLeuLeuLeuGlyGlyTyrIleTyrGlyGln	186
Db	1006	TGAAGCAGCTGTAGAGGTTCTTTGGCATGTTCCATGTGGTGGCTCTCTGTATGAGAT	1065

RESULT 28



US-09-345-214-16/c  
 ; Sequence 16, Application US/09345214  
 ; Patent No. 6392120  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lightner, Jonathan E.  
 ; APPLICANT: Broglie, Karen E.  
 ; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE  
 ; TITLE OF INVENTION: EXPRESSION TO PRODUCE STARCHES IN GRAIN CROPS  
 ; FILE REFERENCE: BB-1147  
 ; CURRENT APPLICATION NUMBER: US/09/345.214  
 ; CURRENT FILING DATE: 1999-06-30  
 ; EARLIER APPLICATION NUMBER: 060/094,436  
 ; EARLIER FILING DATE: 1998-07-28  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 16  
 ; LENGTH: 1798  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; US-09-345-214-16

Alignment Scores:  
 Pred. No.: 6.24e-119 Length: 1798  
 Score: 1093.00 Matches: 244  
 Percent Similarity: 58.2% Conservative: 73  
 Best Local Similarity: 44.8% Mismatches: 167  
 Query Match: 37.8% Indels: 62  
 DB: 3 Gaps: 12

US-10-628-525A-21 (1-539) x US-09-345-214-16 (1-1798)

Qy	10	LeuGlyLeuGluProGluGlyLeuAlaGlySerLeuAspLeuValValAla 29
Db	1601	GTGGTGCAGATGATGCTGGTCTCTTTTGAACATATATGGGACAAAT-----1557
Qy	30	SerGluGlnAspSerGluLeuValValGlyLeuGlnAlaArgAlaLysValThrGln 49
Db	1556	-----GATYCTGGGCTTTGGCCGGGAGAAAT-----GTTATG 1524
Qy	50	SerLeuValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAsp 69
Db	1523	AACGTGATCGTGGTGGCTGCTGAATGTTCTCCATGGTGGTGAACAGGTGCTTGGAGAT 1464
Qy	70	ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValMet 89
Db	1463	GTGTGGGAGCTTTTACCAAGGCTTTAGCGGAGAGAGACATCGTGTATGTTGTGTA 1404
Qy	90	ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109
Db	1403	CCAAGGTAT-----GGGACTATGTGGAAAGCCTTTGATATGGGAATC 1362
Qy	110	HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129
Db	1361	CGGAAATACTACAAAGCTGCAGCAGCAGGACCTAGAGTGAATATTTCCATGATTTAT 1302
Qy	130	AspSerValAspTrpValPheValAspHisProSerTyr---HisArgProGlyAsnLeu 148
Db	1301	GATGGAGTCGACTTTGTGTTTCAATGATGCTCTTTTCGGCAGCAGCTCAAGATGACATA 1242
Qy	149	TyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyr 168
Db	1241	TATGGG-----GGAGTAGCGAGGAAATCATGAAGCGCAGATTTTGTGTTGCAAG 1191
Qy	169	AlaAlaCysGluAlaProLeuIleLeuGluLeuGlyTyrIleTyrGlyGln---Asn 187
Db	1190	GTGTGTTGAGGTCTCTTGGCAGCTTCCATGCGGTGGTGTGTGCTACGGAGATGGAAT 1131
Qy	188	CysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaLys 207
Db	1130	TTGGTGTTCATTCGCAATGATTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1071
Qy	208	TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla 227

RESULT 29

US-09-743-980-16/c

; Sequence 16, Application US/09743980

Db	1070	TACAGAGACCATGGGTTAATGCAGTACACTCGCTCCGTCTCTCATACATACATACGCGC 1011
Qy	228	HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyr 247
Db	1010	CACCGGGCGGTGCTCTGTAGATGAATTCCTGATGACTTGCCTTGAACACTACTCTT 951
Qy	248	GlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGlyGlu 267
Db	950	CAACATTTTCGAGCTGTACGATCCGTC-----GGTGGCGAG 915
Qy	268	AlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLys 287
Db	914	CAGCCCAACATCTTTGCCGCGGTCTGAAGATCGCAGACCGGGTGGTGTGACTGTGAGCGC 855
Qy	288	GlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuSer 307
Db	854	GGCTACTGTGGAGCTGAAGACAGTGGAGGGCGGTGGGGCTTCCACGACATCTCCGT 795
Qy	308	SerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnPro 327
Db	794	TCTAACGACTGGAAGATCAATGCGATCGTGAACCGCATCGACACACAGGAGTGAACCCC 735
Qy	328	AlaThrAspLysCysIlePro-----CysHisTyrSerValAspAspLeu--- 342
Db	734	AAGGTGACCTGTCACCTCGCGTCCGACCGCTACACCAACTACTCTCTCGAGACACTCGAC 675
Qy	343	SerGlyLysAlaLysCysValGlyAlaLeuGlnLysGlyLeuGlyLeuProIleAspPro 362
Db	674	GCTGGAAAGCGGAGTGCAGAGCGGCTGCGACGGGAGCTGGGCTTGGAGTGGCGAC 615
Qy	363	AspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIle 382
Db	614	GAGTGGCTGCTCGCTCTCATCGCGCTCTGATGGACAGAGGCGCGTGGACATCATC 555
Qy	383	GlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGly 402
Db	554	GGGGACCGCTGCGTGGATCGCGGGGACAGCTGCGTGTGATGTCTGGGACACCGG 495
Qy	403	AspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArg 422
Db	494	CGCGCGACCTTGAACGAATGCTGACGACTTGGAGCGGGAGCATCCCAACAGGTGCGC 435
Qy	423	GlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeu 442
Db	434	GGGTGGTGGTCTCTCGTGGCTATGCGGCATCGCATCAGCGCGCGCGCGACGTGCTG 375
Qy	443	LeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGly 462
Db	374	GTGATGCCCTCCGCTTCCAGCCCTCGCGGCTGAAACGAGCTCTACGCGATGGCATACGC 315
Qy	463	ThrValProValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnPro 482
Db	314	ACGTGCTCTGTGTGACCGCGTGGCGGGCTCAGGGACACCGTGGCGCGCTTGCACCGC 255
Qy	483	PheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsn 502
Db	254	TTT-----AGCGACCGCGCTCGGTGGACTTT-----225
Qy	503	MetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu----- 520
Db	224	-----GACCGCGCGAGGCCAACAGCTGATCGA--GGCGCTCAGGACACTCGCTCGA 175
Qy	521	-----LeuGlyArgAlaAsnGluAlaArgHisValLysArg 532
Db	174	CAGTACCGGAACACTACGAGGAGCTGGAGAGTCTCCAGGCGCGCGCATGTCCGAGGA 115
Qy	533	LeuHisValGlyPro 537
Db	114	CCTCAGCTGGGACCA 100

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; Patent No. 6570008
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE
; FILE OF INVENTION: EXPRESSION TO PRODUCE STARCHES IN GRAIN CROPS
; FILE REFERENCE: BB-1147-A
; CURRENT APPLICATION NUMBER: US/09/743,980
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 060/094,436
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Zea mays
; US-09-743-980-16

Alignment Scores:
Pred. No.: 6,24e-119 Length: 1798
Score: 1093.00 Matches: 244
Percent Similarity: 58.2% Conservative: 73
Best Local Similarity: 44.8% Mismatches: 167
Query Match: 37.8% Indels: 62
DB: 3 Gaps: 12

US-10-628-525A-21 (1-539) x US-09-743-980-16 (1-1798)

QY 10 LeuGlyLeuGluProGluGlyLeuAlaGluGlySerIleAspAsnThrValValValAla 29
   :::::
DB 1601 GTTGTGCAGATGATCGTCTTTTGAACATATATGGGACAAT----- 1557

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DB 1556 -----GATTCTGGGCTTTGGCCGGGGAAT-----GTTATG 1524

QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69
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QY 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValValMet 89
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QY 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109
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QY 149 TyrGlyAspPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyr 168
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QY 208 TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla 227
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QY 288 GlyTyrSerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSer 307
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; Sequence 15, Application US/09345214
; Patent No. 6392120
; GENERAL INFORMATION:
; APPLICANT: Lightner, Jonathan E.

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; APPLICANT: Broglie, Karen E.
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE
; FILE REFERENCE: BB-1147
; CURRENT APPLICATION NUMBER: US/09/345,214
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 060/094,436
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Zea mays
US-09-345-214-15

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Best Local Similarity: 44.8% Mismatches: 167
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US-10-628-525A-21 (1-539) x US-09-345-214-15 (1-2019)

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Qy 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAlaAlaPheTyrThrGluLys 109
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Qy 110 HisileArgileProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129
Db 444 CGGNAATACTACAAGCTGAGGACAGGACCTAGAGTGAACATTTTCCATGCAATTATT 503
Qy 130 AspSerValAspTrpValPheValAspHisProSerTyr---HisArgProGlyAsnLeu 148
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Qy 149 TyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyr 168
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Db 615 GTTGTCTGTTGAGTTCTTGGCAGCTTCATGCGGTGGTGTGTGCTACGGAGATGGAAAT 674
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 2, 2006, 00:58:46 ; Search time 2546.51 Seconds  
(without alignments)  
1750.313 Million cell updates/sec

Title: US-10-628-525A-21

Perfect score: 2893

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Database : Published Applications NA Main:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	2818	97.4	2383	3	US-09-931-297-1
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QY 301 GlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320
Db 901 GGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACGGAATTTGTAATGGAAT 960
QY 321 AspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340
Db 961 GACATTAATGATTGGAAACCTGCCAGACAAATGATATCCCTGTCAATATCTGTGTAT 1020
QY 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIle 360
Db 1021 GACCTCTCTGGAAGGCCAAATGTAAAGGTGCATTCAGAGAGGAGCTGGGTACCTATA 1080
QY 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380
Db 1081 AGGCCTGATGTTCTCTGATGGCTTTATTTGAAGGTGGATATTCAGAAAGGCATTTGAT 1140
QY 381 LeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400
Db 1141 CTCAATCAACTTATATACAGATCTCATCGGGAAGATGTTCAATTTGTTCATGCTTGA 1200
QY 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys 420
Db 1201 TCTGGTGACCCAGAGCTTGAGATTGGATGAGATCTACAGAGTCGATCTTCAAGGATAAA 1260
```

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QY 421 PheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440
Db 1261 TTTTCGTGGATGGGTGGATTAGTTTCCAGTTTCCACCGAATAACTGCCGGCTGGAT 1320
QY 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460
Db 1321 ATATTGTTAATGTCATCCAGATTCCGAACCTTGTGGTCTCAATCAGCTATATGCTATGCAG 1380
QY 461 TyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPhe 480
Db 1381 TATGSCACAGTTCTGTTGTCATGCACCTGGGGGCTTAGAGATACCGTGGAGAACTTC 1440
QY 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThr 500
Db 1441 AACCTTTTCGTCGAGATGAGAGCAGGGTACAGGGTGGCAATTCGACCCCTAACCCACA 1500
QY 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520
Db 1501 GAAACATGTTTGTGACATTCGAACTGCAATATCTACATACAGGGAACACAAGTCCCTC 1560
QY 521 LeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
Db 1561 CTGGGAAGGCTAATGAGCGGCGCATGTCAAAAGACTTCACCTGGGACCATGCGCG 1617

RESULT 2
US-10-336-753-52
; Sequence 52, Application US/10336753
; Publication No. US20030226176A1
; GENERAL INFORMATION:
; APPLICANT: Guan, Hanning
; APPLICANT: Keeling, Peter L.
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; TITLE OF INVENTION: HOSTS
; FILE REFERENCES: 2461-52
; CURRENT APPLICATION NUMBER: US/10/336, 753
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US/09/402, 254
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/06660
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/042, 939
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 1749
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)..(1749)
US-10-336-753-52

Alignment Scores:
Pred. No.: 0 Length: 1749
Score: 2861.00 Matches: 539
Percent Similarity: 92.5% Conservative: 0
Best Local Similarity: 92.5% Mismatches: 0
Query Match: 98.9% Indels: 44
DB: 6 Gaps: 1

US-10-628-525A-21 (1-539) x US-10-336-753-52 (1-1749)
QY 1 CysValAlaGluLeuSerArgGlu----- 8
Db 1 TCGTCCGAGCTGAGCAGAGGGGGCCGCGCGCGCTGCCACCCGCGTGTGCTG 60
QY 8 ----- 8
Db 61 GCGCCCCGCTCGTGTGCGCGGCTTCCTTCGCGCGCGCGCGCGCCACGGGTGAGCCGGCA 120
QY 9 -----AspLeuGlyLeuGluProGluGly 16
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Db 121 TCAGCCCGCCGCCCTGCGCCGACGCGCGCTCGGTCTCGAACCTGAAGGG 180  
Qy 17 IleAlaGluGlySerIleAspThrValValValAlaSerGluGlnAspSerGluIle 36  
Db 181 ATTGCTGAAGGTTCCATTCGATTAACACAGTAGTGTGGCAAGTACAGAAATTCGAGATT 240  
Qy 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
Db 241 GTGGTTTGGAAAGGAGCAGCTCGAGCTAAGTAACACAAAGCATTGCTTTGTAAACGGC 300  
Qy 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
Db 301 GAAGCTTCTCCTTATGCAAAAGTCTGGGGGTCTAGGAGATGTTTGTGGTTCATTGCCAGTT 360  
Qy 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96  
Db 361 GCTCTTGTCTGCTGGTCCGCGTACCGTGTGGTGTGTAATCCCAAGATATTAAATGGTACC 420  
Qy 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
Db 421 TCCGATAAGATTATGCAATGCAATTTACACAGAAACACATTCGGATTCCATGCTTT 480  
Qy 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPhe 136  
Db 481 GCGGGTGAACATGAAGTTACCTTCTTCCATGAGTATAGAGATTCACTTCACTGGGTGTTT 540  
Qy 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
Db 541 GTTGATCATCCCTCATATCACAGACTCGGAATTTATATGGAGATAAGTTTGGTGTCTTT 600  
Qy 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
Db 601 GGTGATAAATCAGTTACAGATACACACTCTTTCGTATGCTGCATGTGAGGCTCTTTGATC 660  
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis 196  
Db 661 CTTGAATGGGAGGATATATTTATGACAGAAATTCATGTTGTTGTCATGATTGGCAT 720  
Qy 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 721 GCAGTCTAGTGCCAGTCTCTTCTGTCGCAAAATATAGACCATATGTTGTTTATATAAGAC 780  
Qy 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
Db 781 TCCCGCAGCATCTTCTGTAATACATATTTAGCACATCAGGGTGAGAGCTCGACACACA 840  
Qy 237 TyrProAspLeuGlyLeuProGluTyrPyrGlyAlaLeuGluTyrPyrValPheProGlu 256  
Db 841 TATCCTGACCTTGGGTGGCCACCTGAATGGTATGGAGCTCTGGAGTGGGTATTTCCCTGAA 900  
Qy 257 TrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
Db 901 TGGCGGAGGAGGATGCCCTTGACAGGGGTGAGGCAGTTAAATTTTGAAGGTCGAGTT 960  
Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrGluValThrThrAla 296  
Db 961 GTGACAGCAGATCGAATCTGACTGTCTAGTAGGGTTATTCGTGGAGGTCACTGCT 1020  
Qy 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle 316  
Db 1021 GAAGGTGACAGGGCCCTCAATGAGTCTTAAAGTCCAGAAAGAGTGTATTAACCGAATT 1080  
Qy 317 ValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHis 336  
Db 1081 GTAATGGAAATTTGACATTAATGATTGGAACCTCGCCACACAGAAATGTATCCCTGTGAT 1140  
Qy 337 TyrSerValAspAspLeuSerGlyTysAlaLysCysLysGlyValAlaLeuGlnLysGluLeu 356  
Db 1141 TATTCTGTTGATGACCTCTCTGGAAGGCCAAATGTAAAGTGCAATTCAGAAAGGAGCTG 1200  
Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
Db 1201 GGTTTTACCTATAAGGCCCTGATGTTCTCTGATGGCTTTTATTGGAAGGTTGGAATTATCAG 1260

Qy 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396  
Db 1261 AAAGGCATTGATCTCATTTCAACTTATACACAGATCTCATCGGGAAGATGTTCAATTT 1320  
Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIle 416  
Db 1321 GTCATGCTTGGATCTGGTCACCCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATC 1380  
Qy 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436  
Db 1381 TTCAAGGATAAAATTTCTGGTGGTGGATTAGTGTTCAGTTCACCGAATAAAT 1440  
Qy 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456  
Db 1441 GCGGGCTGGATATATTGTTAATGCCATCCAGATTCGAACCTTGTGGTCTCAATCAGCTA 1500  
Qy 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
Db 1501 TATGCTATGCAGTATGGCACAGTTCCTGTGTCCATGCAACTGGGGGCTTAGAGATACC 1560  
Qy 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAla 496  
Db 1561 GTGGAGAACTTCAACCTTTTCGTGAGAAATGGAGATGGAGACAGGTACAGGGTGGCATTCGCA 1620  
Qy 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
Db 1621 CCCCTAACACAGAAACATGTTTGTGGACATTCGCAATTCGCAATTCACATACAGGA 1680  
Qy 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536  
Db 1681 ACACAAGTCTCTCTGGGAAGGCTAATGAAGCGAGGCATGTCAAAAGACTTCACGTGGGA 1740  
Qy 537 ProCysArg 539  
Db 1741 CCATGCCGC 1749

RESULT 3  
US-10-628-525-12  
; Sequence 12, Application US/10628525  
; Publication No. US20040185114A1  
; GENERAL INFORMATION:  
; APPLICANT: Keeling, Peter  
; Guan, Hanning  
; TITLE OF INVENTION: Starch Encapsulation  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/628,525  
; FILING DATE: 28-Jul-2003  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/941,445  
; FILING DATE: 30-SEP-1997  
; APPLICATION NUMBER: US 60/026,855  
; FILING DATE: 30-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winner, Ellen P  
; REGISTRATION NUMBER: 28,547  
; REFERENCE/DOCKET NUMBER: 89-97  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080



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RESULT 4
US-10-109-048-1142
; Sequence 1142, Application US/10109048
; Publication No. US20040107461A1
; GENERAL INFORMATION:
; APPLICANT: COMMURI, PADMA
; APPLICANT: KEELING, PETER L.
; APPLICANT: RAMIREZ, NONA
; APPLICANT: MCKEAN, ANGELA
; APPLICANT: GAO, ZHONG
; APPLICANT: GUAN, HANPING
; TITLE OF INVENTION: GLUCAN CHAIN LENGTH DOMAINS
; FILE REFERENCE: 2461-76
; CURRENT APPLICATION NUMBER: US/10/109,048
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/279,720
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 1154
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1142
; LENGTH: 2991
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2709)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-109-048-1142

Alignment Scores:
Pred. No.: 0 Length: 2991
Score: 2861.00 Matches: 539
Percent Similarity: 92.5% Conservative: 0
Best Local Similarity: 92.5% Mismatches: 0
Query Match: 98.9% Indels: 44
DB: 7 Gaps: 1

US-10-628-525A-21 (1-539) x US-10-109-048-1142 (1-2991)
QY 1 CysValAlaGluLeuSerArgGlu----- 8
Db 719 TGCCTCGCGAGCTGACGACGAGGAGGGCCGCGCCGCGCTGCCGCCCGCGCTGCTG 778
QY 8 ----- 8
Db 779 GCGCCCCCGCTCGTGCCCGGCTTCCTCGCGCCGCGCGCCGCGCCGCGCGCA 838
QY 9 ----- AspLeuGlyLeuGluProGluGly 16
Db 839 TCGACGCCGCCCGCTGCTGCCACGCCGCGCTGGGGGACCTGGTCTCGAACCTGNAGGG 898
QY 17 IleAlaGluGlySerIleAspAenThrValValAlaSerGluGlnAspSerGluIle 36
Db 899 ATTGCTGAAGGTTCCATCATCAACAGTAGTGTGGCAAGTGAGCAAGATTCTGAGATT 958
QY 37 ValValGlyGlyGluGlnAlaArgAlaIysValThrGlnSerIleValPheValThrGly 56
Db 959 GTGGTGGAAAGAGCAGCTCGAGCTAAAGTAACACAAAGCATTGTCTTTGTAACCCGC 1018
QY 57 GluAlaSerProTyrAlaIysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76
Db 1019 GAAGCTTCTCTTATGCAAGTCTGGGGGTCTAGGAGATGTTGTGGTTCATTGCCAGTT 1078
QY 77 AlaLeuAlaAArgGlyHisArgValMetValMetProArgTyrLeuAenGlyThr 96
Db 1079 GCTCTGTCTGCTCGTGGTCAACGCTGATGGTGTAAATGCCAGATATTAAATGGTACC 1138
QY 97 SerAspLysAsnTyrAlaAenAlaPheTyrThrGluIysGlyHisIleArgIleProCysPhe 116
Db 1139 TCCGATAAGAAATTATGCAATGCATTTTACACAGAAAAACACATTCGGGATTCATGCTTT 1198
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136
1199 GCGCGTGAACATGAAGTTACCTTCTCCATGATATAGAGATTCACTTACCTGGGTGTTT 1258
137 ValAspHisProSerTyrHisArgProGlyAenLeuTyrGlyAspLysPheGlyAlaPhe 156
1259 GTTGATCATCCCTCATATCACAGACCTGGAATTTATATGGAGATAAGTTTGGTGTCTTT 1318
157 GlyAspAenGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaPheLeuIle 176
1319 GGTGATAATCAGTTTCAGATACACACTCCCTTCTCTATGCTGCATGTAGAGGCTCTCTTTGATC 1378
177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAenCysMetPheValValAenAspTrpHis 196
1379 CTTGAATTGGGAGGATATATTATGCAGAGAATTGCATGTTGTGTCAATGATTCGCAT 1438
197 AlaSerLeuValProValLeuLeuAlaIalysTyrArgProTyrGlyValTyrLysAsp 216
1439 GCCAGTCTAGTCCAGTCTCTCTGCTGCANAAATATAGACCATATGCTGTATATAAGAC 1498
217 SerArgSerIleLeuValIleHisAenLeuAlaHisGlnGlyValGluProAlaSerThr 236
1499 TCCCGCAGCAATTCCTTGTAAATACATATTTAGCACATCAGGGGTAGAGCCTGCAAGACA 1558
237 TyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256
1559 TATCTGACCTTGGGTGCCACCTGATGGTATGAGGCTCTGGAGTGGGTATTCCTCGAA 1618
257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAenPheLeuLysGlyAlaVal 276
1619 TGGGCGAGGAGCATGCCCTTGCAAGGGTGAGGCAGTTAAATTTTGAAGGTGCAGTT 1678
277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296
1679 GTGACAGCAGATCGAATCGTACTGTCTAGTAAGGGTTATTCGTGGAGGTCACACTGCT 1738
297 GluGlyGlyGlnGlyLeuAenGluLeuSerSerArgLysSerValLeuAenGlyIle 316
1739 GAAGGTGGACAGGGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGATTAACCGGAAT 1798
317 ValAenGlyIleAspIleAenAspTrpAenProAlaThrAspLysCysIleProCysHis 336
1799 GTAAATGGAATTTGACATTAATGATGGAACCTGCCACAGACAAATGTATCCCTGTCTAT 1858
337 TyrSerValAspAspLeuSerGlyValAlaIysCysValysGlyValLeuGlnLysGluLeu 356
1859 TATTCGTGTGATGACCTCTCTGAAAGGCCAAATGTAAAGGTGCATTCGAGAGGAGCTG 1918
357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
1919 GGTTTACCTATAAGGCTGATGTTCTCTGATTTGGCTTTATTTGGAAGGTTGGATTATCAG 1978
377 LysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPhe 396
1979 AAAGGCATTGATCTCAATTCATATACAGATCTCATCGCGGAAGATGTTCATATTT 2038
397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416
2039 GTCATGCTTGGATCTGGTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGATGCATC 2098
417 PheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr 436
2099 TTCAAGGATAAATTTTCGTGGATGGGTGGATTTAGTGTTCAGTTTCCACCGAATAACT 2158
437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAenGlnLeu 456
2159 GCCGGCTGCGATATATTTGTTAATGCCATCCAGATTCGAACTTGTGGTCTCAATCAGTA 2218
457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476
2219 TATGCTATGCAATGGCACAGTTCTCTGTTTCCATGCAACTCTGGGGCCCTTAGAGATACC 2278
477 ValGluAenPheAsnProPheGlyGluAenGlyGluGlnGlyThrGlyTrpAlaPheAla 496
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Db 2279 GTGAGAACTTCAACCCCTTCGTGAGAAATGAGAGCGGGTACAGGGTGGGCATTTCGCA 2338  
Qy 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAniIleTyrIleGlnGly 516  
Db 2339 CCCCTAACCAAGAAACATGTTTGTGACATTGCGAACTGCAATATCTACATACAGGGA 2398  
Qy 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValIleValIleValGly 536  
Db 2399 ACACAGTCTCTCTGGGAAGGCTTAATGAAGCGAGGATGTCTCAAAAGACTTTCAGTGGGA 2458  
Qy 537 ProCysArg 539  
Db 2459 CCATGCCGC 2467

RESULT 5  
US-10-425-115-54073/c  
; Sequence 54073, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 54073  
; LENGTH: 3123  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)-(3123)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_149315C.1  
US-10-425-115-54073

Alignment Scores:  
Pred. No.: 0 Length: 3123  
Score: 2861.00 Matches: 539  
Percent Similarity: 92.5% Conservative: 0  
Best Local Similarity: 92.5% Mismatches: 0  
Query Match: 98.9% Indels: 44  
DB: 8 Gaps: 1

US-10-628-525A-21 (1-539) x US-10-425-115-54073 (1-3123)  
Qy 1 CysValAlaGluLeuSerArgGlu-----8  
Db 2273 TGGTTCGGAGCTGAGCAGGAGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCTG 2214  
Qy 8 -----8  
Db 2213 GCGCCCGCGCTCGTGGCGCGCTTCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 2154  
Qy 9 -----AspLeuGlyLeuGluProGluGly 16  
Db 2153 TCAGCGCGCGCGCGCTGCGCGAGCGCGCGCTGGGGGACCTCGGTCTCGAACCTGAAGGG 2094  
Qy 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36  
Db 2093 ATTGCTGAAGTTCATCGATACACAGTATGTGGCAAGTGGCAAGATTCAGATT 2034  
Qy 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
Db 2033 GTGGTTGGAAGGAGCAAGCTCGAGCTAAAGTAACAAAGCAATGTCTTTTGTAAACCGGC 1974  
Qy 57 GluAlaSerProTyrAlaLysSerGlyLeuGlyAspValCysGlySerLeuProVal 76

Db 1973 GAAGCTTCTCCTTATGCAAAAGTCTGGGGGTCTAGGAGATGTTGTGTGTTCAATGCCAGTT 1914  
Qy 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96  
Db 1913 GCTCTTGTCTGCTGTGTGTCACTGGTGTGTGTGTGTATGATGCCAGATATTTAAATGGTACC 1854  
Qy 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
Db 1853 TCCGATAAAGAAATATGCAAAATGCATTTTACACAGAAAAACACATTCCGATTCCATGCTTT 1794  
Qy 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136  
Db 1793 GCGGGTGAACATGAAGTTACCTTCTTCATGAGTATAGAGATTCAAGTTCAGTGGGTGTT 1734  
Qy 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
Db 1733 GTTGATCATCCCTCATATCACAGCCTGGAAATTTATATGGAGATAAGTTTGGTGTCTTT 1674  
Qy 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
Db 1673 GGTGATAATCAGTTTCAGATACACACTCTTGTCTGTATGCTGATGCTGAGGCTCTCTTCATC 1614  
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196  
Db 1613 CTGGAATTGGAGAGATATATTTATGACAGAAATGCAATGTCATGTTGTGTCATGATTGGCAT 1554  
Qy 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 1553 GCCAGTCTAGTGCAGTCTCTTGTGTCGAAATATATAGACCATATGTTGTTTATAAGAC 1494  
Qy 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
Db 1493 TCCCGCAGCATCTCTGTAATACATAATTTAGCACATCAGGGTGTAGAGCTCTGCAAGCACA 1434  
Qy 237 TyrProAspLeuGlyLeuProGluTyrProGluTyrGlyAlaLeuGluTyrValPheProGlu 256  
Db 1433 TATCTGACCTTGGGTGGCCCTGAAATGGTATGGAGCTCTGGAGTGGGTATTCCCTGAA 1374  
Qy 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyValAlaVal 276  
Db 1373 TGGCGCAGGAGCATGCCCCCTTGACAGGGGTGAGCGAGTAAATTTTGAAGGTGCGAGTT 1314  
Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
Db 1313 GTGACAGCAGATCGAATCGTGAATCGTGAAGGGTATTTCGTGGAGGTCACAACTGCT 1254  
Qy 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316  
Db 1253 GAAGGTGGACAGGGCTCAATGAGCTCTTAAAGCTCCAGAAAGAGTGTATTAAACGGGAAT 1194  
Qy 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
Db 1193 GTAAATGGAAATGACATTAATGATTGGAACTCTGCCACAGCAAAATGATCCCTGTGAT 1134  
Qy 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysGlyGlyAlaLeuGlnLysGluLeu 356  
Db 1133 TATTCCTGTGATGACCTCTCTGAAAGGCCAAATGTAAGGTGCAITTCGAGAGGAGCTG 1074  
Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
Db 1073 GGTTCATCTATAGGGCTCATGTTCTCTGATTTGGCTTTTATTGGAAGTTGGATTATCAG 1014  
Qy 377 LysGlyIleAspLeuIleGlnLeuIleLeuProAspLeuMetArgGluAspValGlnPhe 396  
Db 1013 AAAGCATTTGATCTCATCTCACTTATCATACAGATCTCATGCGGAGAGATGTTCAATTT 954  
Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416  
Db 953 GTCATCTTGGTCTCTGTCACCCAGCTTGAAGATTGGATGAGATCTACAGAGTCGATC 894  
Qy 417 PheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr 436  
Db 893 TTCAGAGTAAATTTTCGTGGATGGGTGGATTAGTGTTCAGTTTCCAGTTTCCCAACCAACT 834

437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAanGlnLeu 456  
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457 TyrAlaMetGlnTyrGlyThrValProValHisAlaThrGlyGlyLeuArgAspThr 476  
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497 ValGluAanPheAsnProPheGlyGluAanGlyGluGlnGlyThrGlyTrpAlaPheAla 496  
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517 ProLeuThrThrGluAanMetPheValAspIleAlaAanCysAsnIleTyrIleGlnGly 516  
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537 ThrGlnValLeuLeuGlyArgAlaAanGluAlaArgHisValLysArgLeuHisValGly 536  
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ORGANISM: Zea mays  
TISSUE TYPE: endosperm  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2..1950  
OTHER INFORMATION: /function= "starch synthesis"  
/product= "soluble starch synthase"  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-931-297-1  
Alignment Scores:  
Pred. No.: 0 Length: 2383  
Score: 2818.00 Matches: 534  
Percent Similarity: 92.1% Conservative: 3  
Best Local Similarity: 91.6% Mismatches: 2  
Query Match: 97.4% Indels: 45  
DB: 3 Gaps: 1  
US-10-628-525A-21 (1-539) x US-09-931-297-1 (1-2383)  
QY 1 CysValAlaGluLeuSerArgGluAsp----- 9  
Db 146 TCGGTGCGGAGCTGAGCAGGAGGCGCCCGCGCCGCGATGCCACCCCGCTGCTG 205  
QY 9 ----- 9  
Db 206 GCGCCCCCGCTCGTCCCGCGCTTCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCA 265  
QY 10 -----LeuGlyLeuGluProGluGly 16  
Db 266 TTGACGCCCGCGCGCTGCCGCGCGCGCTGGGGGTCTCGGTGTCGAACCTGAAGG 325  
QY 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36  
Db 326 ATTGCTGAAGTTCCATCGATAACACAGTAGTTGTGGCAAGTGGAGCAAGATTCTGAGATT 385  
QY 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
Db 386 GTGGTTGGNAAGGAGCAGCTGAGCTAAAGTAAACACAAACATTGCTTTGTAATGGC 445  
QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
Db 446 GAAGCTTCTCTTATGCAAAAGTCTGGGGTCTAGGAGATGTTTGTGGTTCATTGCCAGTT 505  
QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrIleuAsnGlyThr 96  
Db 506 GCTCTGTGCTGCTGGTGCACCGTGTGATGTTGTAATGCCAGATATTAATGTTATCC 565  
QY 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
Db 566 TCCGATAGAAATTATGCAATGCAATTTACACAGAAAACACATTCGGATTCCATGCTTT 625  
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136  
Db 626 GCGCGTGAACATGAAGTTACCTTCTCCATGATAGTAGAGATTTCAGTTCAGTGGGTGTT 685  
QY 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
Db 686 GTTGATCATCCCTCATATACAGACCTGGAATTTATATGGAGATAAGTTTGGTGTCTTT 745  
QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
Db 746 GGTGATATCAGTTCCAGATACACATCTCTTCTGCTATGCTGATGAGAGCTCTCTTGGTC 805  
QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196  
Db 806 CTTGAATTGGGAGGATATATTTATGGACAGAATTGCAATGCTGTTGTTGTTGTTGTTGTTG 865  
QY 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 866 GCCAGTCTAGTGCCAGTCTCTTCTGCTGCAAAATATAGACCATATGCTGTTTATTAAGAC 925  
QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236



Db 926 TCCGCGAGCATCTTGTAAATACATAAATTGACATCAGGGTGTAGAGCCCTGCAAGCAC 985  
Qy 237 TyrProaspLeuGlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGlu 256  
Db 986 TATCTGACCTTGGTGGCCACCTGAATGGTATGAGCTCTGGAGTGGTATTCCTCTGAA 1045  
Qy 257 TrpAlaArgArgHisAlaLeuAspGlyGlyAlaValIleAsnPheLeuLysGlyAlaVal 276  
Db 1046 TGGCGAGGAGGCGATGCCCTTGACAGGGTGAGCAGTATATTTTGAAGGTGCGAGTT 1105  
Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
Db 1106 GTGACACAGATCGAATCGTGACTGTCTAGTAAGGGTTATTCATGGGAGGTACAACTGCT 1165  
Qy 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle 316  
Db 1166 GAAGGTGACAGGCGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAAGCGAAT 1225  
Qy 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
Db 1226 GTAAATCGAATTGACATTAATGATTGGAACCTGCCACAGACAAATGTATCCCTGTGAT 1285  
Qy 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
Db 1286 TATTCTGTTGATGACCTCTCTGGAAGGCCAAATGTAAAGTGCATTCGGAAGAGGCTG 1345  
Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
Db 1346 GGTATTACCTATAAGCCCTGATGTTCTCTGATTGCTTTATTGAAGATGGATTATCAG 1405  
Qy 377 LysGlyIleAspLeuIleGlnLeuIleIleProaspLeuMetArgGluAspValGlnPhe 396  
Db 1406 AAAGGCAATGATCTCAATCACTTATCATCCAGATCTCATGCGGAAGATGTTCAATTT 1465  
Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416  
Db 1466 GTATGCTTGATCTGTTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATC 1525  
Qy 417 PheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr 436  
Db 1526 TTCAAGGATAAATTTCTGTGATGGTGGATTGATGTTCCAGTTTCCACCCGCAATAACT 1585  
Qy 437 AlaGlyCysAspIleLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456  
Db 1586 GCCGGCTCGCATATATTGTTAATGCCATCCAGATTCCGAACCTTGTGTCTCAATCAGCTA 1645  
Qy 457 TyrAlaMetGlnTyrGlyThrValProValIleAlaThrGlyGlyLeuArgAspThr 476  
Db 1646 TATGCTATGAGTATGGCAGATTCCTGTTGTCATGCAACTGGGGGCCCTTAGAGATACC 1705  
Qy 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAla 496  
Db 1706 GTGGAGAACTTCAACCTTTCGGTGAGATGGAGACGGGTACAGGGTGGGCAATTCGCA 1765  
Qy 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
Db 1766 CCCCTAACCCACAGAAAACATGTTTGTGCAATTCGCAACTGCAATATCTACATACAGGGA 1824  
Qy 517 ThrGluValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536  
Db 1825 ACACAAGTCTCTCTGGGAGGGCTAATGAAGCGAGGCGATGTCAAAAGACTTTCACGTGGGA 1884  
Qy 537 ProCysArg 539  
Db 1885 CCATGCGC 1893

## RESULT 7

US-10-767-701-13043  
; Sequence 13043, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 13043  
; LENGTH: 2670  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS52\_1  
US-10-767-701-13043

Alignment Scores:  
Pred. No.: 0 Length: 2670  
Score: 2753.00 Matches: 522  
Percent Similarity: 90.3% Conservative: 6  
Best Local Similarity: 89.2% Mismatches: 11  
Query Match: 95.2% Indels: 47  
DB: 7 Gaps: 1

US-10-628-525A-21 (1-539) x US-10-767-701-13043 (1-2670)

Qy 1 CysValAlaGluLeuSerArgGlu-----8  
Db 270 TGGTTCGGGAGTGTAGCAGGAGGGTCCCGCGCCGACGCGCGCGCGCTGCCACCCGCG 329  
Qy 8 -----8  
Db 330 CTGCTGGCGCGCCCGCTCGTGGCCGCTTCTCTCGCGCGCGCTCCGAGCCGAGGGTGAG 389  
Qy 9 -----AspLeuGlyLeuGluPro 14  
Db 390 CCGCGCTGCACACCGCGCGCCCTGCGCGAGCGCGGTCTCGCGACCTCGGTCTCCAACT 449  
Qy 15 GluGlyIleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSer 34  
Db 450 GAAGGATTCGTGAGGGTTCATCGATGACACAGTAGTGTGGCAAGTAGCAGATTCT 509  
Qy 35 GluIleValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheVal 54  
Db 510 GAGATCGTGGTGGAAAGGAGCAAGCTCGAGCTAAAGTAACACAAAGCATTGTCTTGTA 569  
Qy 55 ThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeu 74  
Db 570 ACTGGCGAAGCTTCTCTTATGCANAAGTCTGGGGGCTTAGGAGATGTTGTGTTCATTG 629  
Qy 75 ProValAlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsn 94  
Db 630 CCAGTTGCTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 689  
Qy 95 GlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIlePro 114  
Db 690 GGTACCTCTGATAAGAAATTCGCAATGCAATTTTACACAGAAAGCACATTTCGGATTCCA 749  
Qy 115 CysPheGlyGlyGluHisGluValThrPhePheHisGluTyrThrArgAspSerValAspTrp 134  
Db 750 TGTCTTGGCGGGTGAACATGAAGTTACCTTTTTCATGATGATGATGATGATGATGATGAT 809  
Qy 135 ValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGly 154  
Db 810 GTGTTTGTGATCATCCCTCATATACAGACCTGGAAATTTATATGGAGATAAGATTGGT 869  
Qy 155 AlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaPro 174  
Db 870 GCTTTTGGTGAATAATCAGTTCAGATACACGCTCTTGTCTATGCTGCTGCTGCTGCTGCT 929  
Qy 175 LeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAsp 194  
Db 930 TTGGTCTTGAATTTGGGAGGATATATTTATGGACAGAAATTCGATGTTGTGTGTAATGAT 989

QY 195 TrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyr 214  
Db 990 TGCATGCCAGTCTAGTGCAGTCCTTCTGTCAAATAATATAGACCATATGCTGTTTAT 1049  
QY 215 LysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAla 234  
Db 1050 AAAGACTCCGCGAGCATCTTGTAATACATATTTAGACATCAGGGTGTAGAGCCTGCA 1109  
QY 235 SerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPhe 254  
Db 1110 AGCACATATCCTGACCTGGGTGGCCACCTGAATGTTATGGAGCTCTGGAGTGGTATTC 1169  
QY 255 ProGluTyrAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheIleLysGly 274  
Db 1170 CTTGAATGGCAAGGAGGATGCCCTTGACAGGGTGAGCGAGTTAAATTTTGAAGGT 1229  
QY 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrGluValThr 294  
Db 1230 GCAGTTGTGCACAGCAGATCGAATTTGTGACTGTCTAGTAAGGTTATTCATGGGAGGTACA 1289  
QY 295 ThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsn 314  
Db 1290 ACTGCTGAAGGTGGACAGGGTCTCAATGAGCTCTTAAGCTCCCGAAAGAGTGTATTAAC 1349  
QY 315 GlyIleValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCysIlePro 334  
Db 1350 GGAATTTGTAATGGAATTCACATTAATGATGGAACCTCGCAGCGACAAATGTATCCCT 1409  
QY 335 CysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLys 354  
Db 1410 TGTCAATTATCTGTTGATGACCTCTCTGGAAAGCCAAATGTAAAGTGCATTCAGAG 1469  
QY 355 GluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAsp 374  
Db 1470 GAGCTGGGTTTACCTATAAGGCTGAAGTTCCTCTGATGGTTTTATTGGAAGATTGGAT 1529  
QY 375 TyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspVal 394  
Db 1530 TATCAGAAAGGCAATGATCTCATTCAACTTATCATACCAATCTCATGCGGAGCAGCGTT 1589  
QY 395 GlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGlu 414  
Db 1590 CAATTGTCTATGCTTGGATCTGGTGACCCAGAGCTCGAAGACTGGATGAGATCTACAGAG 1649  
QY 415 SerIlePheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArg 434  
Db 1650 TCGGACTTCAAGGATAAAATTCGTGGATGGGTGGATTTAGTGTTCAGTTTCCACCACCA 1709  
QY 435 IleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsn 454  
Db 1710 ATAACCTGCCGGCTGCCATATATTTGTAATGCCATCCAGATTCGAACCTTGTGGTCTCAAT 1769  
QY 455 GlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArg 474  
Db 1770 CAGCTATATGCTATGCAGTATGGCAGATTCCTGTGTCCATGCAACTGGGGCCCTTAGA 1829  
QY 475 AspThrValGluAsnPheAsnProPheGlyGluAsnGlyGlnGlyThrGlyTyrAla 494  
Db 1830 GATACTGTGGAGAACTTCAACCTTTTCGGTGGAATGGAGAAACAGGGGTACAGGGTGGCA 1889  
QY 495 PheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIle 514  
Db 1890 TTCGACCCCTAACCCAGGAAACATGTT- GTGGACATTCGCAACTGCAATTTCCACATA 1948  
QY 515 GlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHis 534  
Db 1949 CAAGGAGCACAAATCTTCCTGGGAGGGCTCATGAGAGGGGCATGTCAAAGACTTTCAC 2008  
QY 535 ValGlyProCysArg 539  
Db 2009 GTGGGACCATGCCGC 2023

RESULT 8

US-10-425-115-184334  
; Sequence 184334, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 184334  
; LENGTH: 1988  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MPT4577\_996C.1  
US-10-425-115-184334

Alignment Scores:  
Pred. No.: 7,01e-314 Length: 1988  
Score: 2681.00 Matches: 499  
Percent Similarity: 99.8% Conservatives: 3  
Best Local Similarity: 99.2% Mismatches: 1  
Query Match: 92.7% Indels: 1  
DB: 8 Gaps: 0

US-10-628-525A-21 (1-539) x US-10-425-115-184334 (1-1988)

QY 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
Db 2 ATGGTTGGAAGAGGAGCAGCTCGAGTAAAGTAAACACAAACATTCCTCTTTGTAACGTGC 61  
QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
Db 62 GAAGCTTCTCCTTATGCAAAAGTCTGGGGGTCTAGGAGATGTTTGTGGTTCATTGCCAGTT 121  
QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96  
Db 122 GCTCTTGTCTCTGTTGGTCAACGTCGTGATGGTTGTAATGCCAGATATTTAAATGGTACC 181  
QY 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
Db 182 TCCGATAAGAAATATGCAAAATGCAATTTTACACAGAAAAACACATTCGGATTCATGCTTT 241  
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPhe 136  
Db 242 GCGGTGAACATGAAGTGTACCTTCTTCATGATATAGAGATTCAGTTGACTGGGTGTTT 301  
QY 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
Db 302 GTTGATCATCCCTCATATCACAGACCTCGAAATTTATATGGAGATAAGTTTGGTCTTTT 361  
QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
Db 362 GGTGATAATCAGTTTCAGATACACATCTCTTTGCTATGCTGTCATGTGAGGCTCTCTTTGGTC 421  
QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis 196  
Db 422 CTGTAATTTGGGAGGATATATTTATGACAGAAATTCATGCTGTTGTGTCATGATGGCAT 481  
QY 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 482 GCCAGTCTAGTCCAGTCTCTTCTGTCGCAAAATATAGACCATATGCTGTTTATAAGAC 541  
QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
Db 542 TCCCGCAGCATTTGTAATACATAATTTAGCACATCAGGGGTAGAGCCTGCAGACACA 601

QY 237 TyrProAspLeuGlyLeuProProGluTrpTyrGlyAlaLeuGluTrpValPheProGlu 256  
 Db 602 TATCTGACCTTGGTTGCCACCTGGAATGGTATGGAGCTCTGGAGTGGTATCCCTGAA 661  
 QY 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAenPheLeuLysGlyAlaVal 276  
 Db 662 TGGCGAGGAGCATGCCCTGACAGGGTGAGCAGTTAATTTTTTGAAGGTGCGATT 721  
 QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
 Db 722 GTGACAGCAGATCGAATCGTGACTGTAGTAAGGGTTATTCATGGAGGTCCACAACTGCT 781  
 QY 297 GluGlyGlyGlnGlyLeuAenGluLeuSerSerArgLysSerValLeuAenGlyLe 316  
 Db 782 GAAGGTGGACAGGCGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACCGAAT 841  
 QY 317 ValAenGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
 Db 842 GTAAATGGAATTGACATTAATGATGGAACTGCGCCACAGACAAATGATCCCTGTGAT 901  
 QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
 Db 902 TATCTCTGATGACCTCTCTGGAAGGCCAAATGTAAAGTGCATTCAGAGGAGCTG 961  
 QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
 Db 962 GGTATTACCTAAGGCTGATGTTCTCTGATGGCTTTATTTGGAAGATTGGATTATCAG 1021  
 QY 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396  
 Db 1022 AAGGCATTCATCTCACTTATCATACAGATCTCATGGGAGAGATTCAATTT 1081  
 QY 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416  
 Db 1082 GTCATGCTTGGATCTGGTACCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATC 1141  
 QY 417 PheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr 436  
 Db 1142 TTCAGAGATAAATTTCTGGTGGTGGTGGATTTAGTGTTCCAGTTTCCACCGAATAACT 1201  
 QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAenGlnLeu 456  
 Db 1202 GCCGGCTGCAATATTTTAAAGCCATCCAGATTGCAACTTTGTGTCTCAATCAGTA 1261  
 QY 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
 Db 1262 TATGCTATGCAGTATGACAGTCTCTGTGTCATGCCAATCTGGGGCTTAGAGATACC 1321  
 QY 477 ValGluAenPheAsnProPheGlyGluAenGlyGluGlnGlyThrGlyTrpAlaPheAla 496  
 Db 1322 GTGGAGAACTTCAACCTTTCCGTGGAATGGAGAGCAGGTACAGGGTGGGCATTCGCA 1381  
 QY 497 ProLeuThrThrGluAenMetPheValAspIleAlaAenCysAenIleTyrIleGlnGly 516  
 Db 1382 CCCTTAACACAGAAACATGTT- GTGGACNTTGGCACTGCAATATCTACATACAGGGA 1440  
 QY 517 ThrGlnValLeuLeuGlyArgAlaAenGluAlaArgHisValLysArgLeuHisValGly 536  
 Db 1441 ACACAAGTCTCTCTGGAGGGCTAATGAAGCGAGGCAATGTCAAAGACTTCAAGTGGGA 1500  
 QY 537 ProCysArg 539  
 Db 1501 CCATGCCG 1509

## RESULT 9

US-10-425-114-19497

; Sequence 19497, Application US/10425114

; Publication No. US2004003488A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E.

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Uses Thereof for Plant Improvement

; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; NUMBER FILING DATE: 2003-04-28

; SEQ ID NO 19497

; LENGTH: 1855

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3150-035-F10\_FLI

US-10-425-114-19497

## Alignment Scores:

Pred. No.: 1,41e-296 Length: 1855  
 Score: 2538.00 Matches: 471  
 Percent Similarity: 99.8% Conservative: 0  
 Best Local Similarity: 99.8% Mismatches: 1  
 Query Match: 87.7% Indels: 1  
 DB: 7 Gaps: 0

US-10-628-525A-21 (1-539) x US-10-425-114-19497 (1-1855)

QY 68 GlyAspValCysGlySerLeuProValAlaLeuAlaAaArgGlyHisArgValMetVal 87  
 Db 1 GGAGATGTTTGGTTCATTCGCGAGTTCCTCTGCTGCTCGTGTACCGTGTGATGGTT 60  
 QY 88 ValMetProArgTyrLeuAenGlyThrSerAspLysAsnTyrAlaAenAlaPheTyrThr 107  
 Db 61 GTAATGCCAGATATTAAATGGTACTCCGATAAGAAATATGCAATGCAATTTACACA 120  
 QY 108 GluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlu 127  
 Db 121 GAAAAACACATTCGGATTCATGCTTTGGCGGTGAACATGAAATGACCTTTCTTCATGAG 180  
 QY 128 TyrArgAspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsn 147  
 Db 181 TATAGAGATTCAGTTCAGTGGGTGTTGTGTATCATCCCTCATATCAGACCTGGAAAT 240  
 QY 148 LeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCys 167  
 Db 241 TTATATGGAGATAAGTTTGTGCTTTTGTGTAATAATCAGTTTCAGATACACACTCTTTC 300  
 QY 168 TyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsn 187  
 Db 301 TATGCTGCATGTGAGGCTCTTTTGAATTCGAGGATATATTTATGGACAGAAAT 360  
 QY 188 CysMetPheValValAenAspTrpHisAlaSerLeuValProValLeuAlaAlaLys 207  
 Db 361 TGCATGTTTGTGTCATGATGATGGCATGCCAGTCTAGTCCAGTCTCTTCTGTGCANAA 420  
 QY 208 TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAenLeuAla 227  
 Db 421 TATAGACCATATGCTGTTTATAAAGACTCCCGCAGCATTCCTGTAATACATAATTTAGCA 480  
 QY 228 HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTrpTyr 247  
 Db 481 CATCAGGGTGTAGAGCTCTCAAGCACATATCTGACCTTTGGGTGGCCACCTGATGTAT 540  
 QY 248 GlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGlyGlu 267  
 Db 541 GGAGCTCTGGAGTGGGTATTCCTGTAATGGCGAGGAGGATGCCCTTGAAGAAGGTGAG 600  
 QY 268 AlaValAenPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLys 287  
 Db 601 GCAGTTAAATTTTGAAGGTGCAGTTGTGACAGCAGATCGAATCGTGTGCTGCTAGTAAG 660  
 QY 288 GlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAenGluLeuLeuSer 307  
 Db 661 GGTATTCTGGAGGTCAAACTGCTGAAGGTGGACAGGGCCTCAATGAGCTCTTAAGC 720

QY 308 SerArgLysSerValLeuAenGlyIleValAenGlyIleAspIleAenAspTrpAenPro 327  
 Db 721 TCCAGAAAGAGTGATTAACCGAATTGAATGGAATTGACATTAATGATTGGAACCCCT 780  
 QY 328 AlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyIlyAlaLys 347  
 Db 781 GCCACAGACAAATGTATCCCTGTCTATTATCTGTGATGACCTCTCTGGAAGGCCAA 840  
 QY 348 CysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIle 367  
 Db 841 TGTAAAGGTGCATTGACAGAGGAGCTGGGTACCTATAAGGCTGATGTCTCTGATT 900  
 QY 368 GlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIlePro 387  
 Db 901 GCGTTTATTGGAAGTGTGATATACGAAGGCAATGATCTCAATCAACTTATCATACCA 960  
 QY 388 AspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGlu 407  
 Db 961 GATCTCATGCGGGAAGATGTTCAATTTGTATGCTTGGATCTGGTGACCCAGAGCTTGAA 1020  
 QY 408 AspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPhe 427  
 Db 1021 GATGTGATGAGATCTACAGAGTGCATCTTCAAGGATAAAATTTGCTGGATGGGTGGATT 1080  
 QY 428 SerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArg 447  
 Db 1081 AGTGTTCAGTTTCCACCGCAATACTCGCGGCTGCGATATATGTTAATGCCATCCAGA 1140  
 QY 448 PheGluProCysGlyLeuAenGlnLeuTyrAlaMetGlnTyrGlyThrValProValVal 467  
 Db 1141 TTCGAACCTTGTGTTCTCAATCAGCTATATGCTATGCTGATGGCACAGTCTCTGTGTC 1200  
 QY 468 HisAlaThrGlyGlyLeuArgAspThrValGluAenPheAsnProPheGlyGluAenGly 487  
 Db 1201 CATGCAACTGGGGGCTTACAGATACCGTGGAGAACTTCAACCCCTTTCGGTGAGATGGA 1260  
 QY 488 GluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAenMetPheValAspIle 507  
 Db 1261 GAGCAGGGTACAGGGTGGGCAATTCGACCCCTTAACCAACAAACATGTT-GTGGACATT 1319  
 QY 508 AlaAenCysAenIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAenGluAla 527  
 Db 1320 CGCAACTGCAATATCTACATACAGGGAACACAAAGTCTCTCTGGGAAGGCTTAATGAAGC 1379  
 QY 528 ArgHisValLysArgLeuHisValGlyProCysArg 539  
 Db 1380 AGGCATGTCAAAGACTTCAAGTGGGACCATGCCGC 1415

RESULT 10

US-10-437-963-51322  
 ; Sequence 51322, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 51322  
 ; LENGTH: 2812  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:

OTHER INFORMATION: Clone ID: PAT\_MRT4530\_53725C.1  
 US-10-437-963-51322

Alignment Scores:  
 Pred. No.: 4,36e-293 Length: 2812  
 Score: 2511.50 Matches: 476  
 Percent Similarity: 85.9% Conservative: 31  
 Best Local Similarity: 80.7% Mismatches: 32  
 Query Match: 86.8% Indels: 52  
 DB: 7 Gaps: 3

US-10-628-525A-21 (1-539) x US-10-437-963-51322 (1-2812)

QY 1 CysValAlaGluLeuSerArgGlu-----8  
 Db 238 TCGTGGCGGAGCTGAGCAGGACGGTGGTCCGGCGCAGCGCCGCTGGCACCGGGCGCG 297

QY 8 -----8  
 Db 298 CTGGTGAAGCAGCGGTCCTGCCGACCTTCTCGTCCGACGTCGACGCCACCGCGGCC 357

QY 9 -----AspLeuGly-----11  
 Db 358 AGCAGTCCGCCGCGCGCGCGCGCGCGCGCGCGCTTCCGCGACTCCGCGCGTGGGGAG 417

QY 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAsnThrValValAla 29  
 Db 418 ATCGACCGCGATCTAGAGGTCTTCCAGAAAGTTCATCAGCAAAACAATTTTGTGGCT 477

QY 30 SerGluGlnAspSerGluIleValValGlyLysGluGlnAlaArgAlaLysValThrGln 49  
 Db 478 AGTGAGCAGGAGCTCGAGATCATGGATGTGAAGGAGCAAGCTCAAGCTAAAGTAAACAGC 537

QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69  
 Db 538 AGCGTGTCTTTGTAACCGGTGAAGCTTCTCTTATGCAAGTCAAGTCAAGTGGAGTATAG 597

QY 70 ValCysGlySerLeuProValAlaLeuAlaAargGlyHisArgValMetValMet 89  
 Db 598 GTTGTGGTTCCTACTGCAATTCCTCTTCTCGTGGTGCATCGTGTGATGGTTGTAATG 657

QY 90 ProArgTyrLeuAenGlyThrSerAspLysAsnTyrAlaAenAlaPheTyrThrGluLys 109  
 Db 658 CCGAGATACATGACCGGGCTTGAACAAAATTTTGCAACGCCATTTTACACTGAGAG 717

QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129  
 Db 718 CACATTAAAGATTCCATGCTTTCGCGGAGAACATGAAGTTACTTTTTTCCAGGATATAG 777

QY 130 AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGluAenLeuTyr 149  
 Db 778 GATTCGTGATGGGTGTTTGTGATCATCTCCATATCATAGAGCTCGAAATTTGTAT 837

QY 150 GlyAspLysPheGlyAlaPheGlyAspAenGlnPheArgTyrThrLeuLeuCysTyrAla 169  
 Db 838 GGAGATAATTTTGGTGTCTTTTCGCGATATCAGTTTCAGATACACACTCTCTGCTATGCG 897

QY 170 AlaCysGluAlaProLeuIleLeuGluLeuGlyTyrIleTyrGlyGlnAenCysMet 189  
 Db 898 GCGTGTGAAGCCCATTAATCTTGAATCGGAGGATATATCTATGAGACAGAAATGCATG 957

QY 190 PheValValAenAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyrArg 209  
 Db 958 TTGTGTGAATGATGGATGCCAGTCTGTGGCAGTCTCTTCTGTCGCAAAATATAGA 1017

QY 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAenLeuAlaHisGln 229  
 Db 1018 CCATATGGTGTTCAGGGATGCCGCGAGTCTTGTTCATACATAATCTAGCACATCAG 1077

QY 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrGlyAla 249  
 Db 1078 GGTGTGGAGCCTGCCAGTACATATCTGACCTGGGATGGCCACCTGAATGGTATGGAGCA 1137

QY 250 LeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGlyGluAlaVal 269  
Db 1138 TTGAATGGGGTGTTCAGAGTGGGCAAGGGCGCATGCCCTTGCACAAAGGGGTGAGGCAGTC 1197  
QY 270 AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr 289  
Db 1198 AATTTTTTAAAGCGCAGTTGTGACAGCAGATCGAATTTGACTGTTCAGCCAGGGGTAT 1257  
QY 290 SerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArg 309  
Db 1258 TCATGGGAGGTGCACACTGCTGAAGGTGGGCAAGGCCTCAATGAGCTCTTAAGCTCCCGG 1317  
QY 310 LysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThr 329  
Db 1318 AAGAGTGTATTGAATGGAATTTGTAATGGAATGACATTAAATGATGGAAACCCCATCCACA 1377  
QY 330 AspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLys 349  
Db 1378 GACAAAGTTTCCCTTATCATATTCTGTGTGACCTGTCCGGAAAGGCCAAGTGTA 1437  
QY 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe 369  
Db 1438 GCTGAATTCGAGAAGGAGCTGGGTTTACCTATAGGCCCGCATGTGCTCTGATTGGCTTT 1497  
QY 370 IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeu 389  
Db 1498 ATTGGAAGATTGGACTATCAAAAGGCATTGATCTAATTAACCTTGCCATTCCAGATCTC 1557  
QY 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrp 409  
Db 1558 ATCGGGGACAAATTCATTCGTCATCTTGATCTGGTACCCAGGTTTTGAAGGATGG 1617  
QY 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerVal 429  
Db 1618 ATGAGATCCACAGAAATCAGGGTACAGGATAAATTTCTGTGATGGGTTCGATTAGTGT 1677  
QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449  
Db 1678 CCAGTTTCCACCGAATACTCAGAGTTCGGATATATTTGTATGATGCCATCCAGATTCCGA 1737  
QY 450 ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValHisAla 469  
Db 1738 CCTGTGGCTCAATCAGCTATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 1797  
QY 470 ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln 489  
Db 1798 ACTGGAGGCTCAGAGATACAGTGGAGAAATTTAAACCCGTTTCTGAGAAAGGAGAGCAG 1857  
QY 490 GlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsn 509  
Db 1858 GSTACAGGGTGGGCATTTCTGCCCACTAACCAATTTGAAAAATGCT-GTGGGCATTTGGCGAT 1916  
QY 510 CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529  
Db 1917 GGCATTTTCACATACAGGACACAAAGTCTCTTGGAGGGTCTAATGAAGCGAGGCAT 1976  
QY 530 ValLysArgLeuHisValGlyProCysArg 539  
Db 1977 GTCAAGCGACTTATACATGGGACCATGCCGC 2006

RESULT 11

US-10-739-930-5458  
; Sequence 5458, Application US/10739930  
; Publication No. US20040216190A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; FILE REFERENCE: 38-21(53377) B  
; CURRENT APPLICATION NUMBER: US/10739,930  
; NUMBER OF SEQ ID NOS: 11088  
; SEQ ID NO 5458

; LENGTH: 2747  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; OTHER INFORMATION: Clone ID: TRIAB-23APR03-CLUSTER93\_1  
US-10-739-930-5458  
Alignment Scores:  
Pred. No.: 3,96e-288 Length: 2747  
Score: 2470.50 Matches: 465  
Percent Similarity: 91.8% Conservative: 29  
Best Local Similarity: 86.4% Mismatches: 41  
Query Match: 85.4% Indels: 4  
DB: 8 Gaps: 2  
US-10-628-525A-21 (1-539) x US-10-739-930-5458 (1-2747)  
QY 2 ValAlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGlySer 21  
Db 538 GTGGGGAACTCGCG---CCCGACCTCCTGCTC-----GAAGGGATTGCTGAGGATTCC 588  
QY 22 IleAspAsnThrValValValAlaSerGluGlnAspSerGluIleValValGlyLysGlu 41  
Db 589 ATCGACAGCATATAATTGTGGCTGCAAGTGACGAGATTCTCAGATCATGGATGCGAATGAG 648  
QY 42 GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61  
Db 649 CAACCTCAAGTAAAGTTACACGTAGCATGCTGTTGTGACTGGTGAAGCTGCTCCTTAT 708  
QY 62 AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaArg 81  
Db 709 GCAAAGTCAGGGGGGCTGGGAGATGTTGTGGTTCGTTACCAATTGCTTGTGCTCGT 768  
QY 82 GlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr 101  
Db 769 GGTACCCGTGTAGTGTGTAATGCCAAGATACTTGAATGGGTCTCTGATAAAACTAT 828  
QY 102 AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu 121  
Db 829 GCAAAGGCATTATACACTGGGAAGCACATTAAAGTTCCATGCTTTGGGGGATCAGATGAA 888  
QY 122 ValThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSer 141  
Db 889 GTGACCTTTTTTCATGATATAGACACAACGTCGATTTGGGTGTTGTGCGATCATCCGTCA 948  
QY 142 TyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161  
Db 949 TATCATAGACCAGGAAGTTTATATGGAGATAATTTTGGTCTCTTTGGTGAATCATGTTTC 1008  
QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGly 181  
Db 1009 AGATACACACTCCTTTTGTCTATGCTGATGCGAGGCCCCCACTAATCCTTGAATTTGGGAGA 1068  
QY 182 TyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValPro 201  
Db 1069 TATATTATGGACAGAAATTCATGTTTGTGTGACGATTTGGCATGCGACCTTTGTGCCA 1128  
QY 202 ValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeu 221  
Db 1129 GTCTTTCTTGTGTCAAAATATAGCATACGGGTGTTTACAGAGATTCCCGCAGACCCCTT 1188  
QY 222 ValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGly 241  
Db 1189 GTTATACATAATTTAGCACATCAGGGTGTGGAGCCCTGCAAGTACATATCTTGATCTGGGA 1248  
QY 242 LeuProProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHis 261  
Db 1249 TTGCCACCTGAAATGGTATGGAGCTTTAGAAATGGGTATTTCCAGATGGGCAAGGAGCAT 1308  
QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArg 281  
Db 1309 GCCCTTGACAAGGGTGAGGCGATTAACTTTTGAAGAGGAGCAGTCTGTGACAGCAGATCGA 1368





QY 82 GlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr 101  
DB 261 GGTCAACGAGTGATGGTGTAAATGCAAGATACCTTAAATGGGTCTCTGTGATAAAACCTAT 320  
QY 102 AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu 121  
DB 321 GCAAAGGCATATACACTCGCAAGCACATTAAGATTCCATGCTTTGGGGGATCATGAA 380  
QY 122 ValThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSer 141  
DB 381 GTGACCTTTTTCATAGTATAGATAGACAAACGTCGATTGGGTGTGTTCGATCATCCGTC 440  
QY 142 TyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161  
DB 441 TATCACAGACGAGGATATATATGGAGATAAATTTGGTGTCTTTGGTGATTAATTCAGTTTC 500  
QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuLysLeuGluGlyGly 181  
DB 501 AGATACACACTCTTTGCTATGCTGATGCGAGGCCCACTAATCTTGAATTGGAGGA 560  
QY 182 TyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValPro 201  
DB 561 TATATTTATGACAGAATTGCTATGTTGTGAACGATTGGCATGCCAGCTTGTGCCA 620  
QY 202 ValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeu 221  
DB 621 GTCTCTTCTGTCGAAATATAGACCATACGGTGTTCACAGAGATCCCGCAGCACCTTT 680  
QY 222 ValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGly 241  
DB 681 GTTATACATAATTAGCACATCAGGTGTGGAGCTGCAGTACATATCTGTATCTGGGA 740  
QY 242 LeuProProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHis 261  
DB 741 TTGCCTCCTGAATGGTATGAGCTTTAGAAATGGTATTTCCAGAAATGGCAAGGAGCAT 800  
QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArg 281  
DB 801 GCCCTTGACAGGGGTGAGGAGTAACTTTTGAAGAGGACAGTGTGTGACAGCAGATCGG 860  
QY 282 IleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGly 301  
DB 861 ATTGTGACCTCAGTCAGGTATTCTATGGAGGTCAACTCTGTAAGTGGACAGGCG 920  
QY 302 LeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsp 321  
DB 921 CTCATAGCTCTTAAAGTCCCGAAAGGTGATTGAATGGAATTTGAAATGGAATTGAC 980  
QY 322 IleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp 341  
DB 981 ATTAATGATTGGAAACCCCAACACAGACAAAGTGTCTCCCTCATCATATTCTGTGATGAC 1040  
QY 342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg 361  
DB 1041 CTCTCTGGAAGGCCAAATGAAGCTGAATTCAGAGAGATGGTTTACTCTGTAAGG 1100  
QY 362 ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381  
DB 1101 GAGGATGTTCTCTGATTGGCTTTATTTGAAGACTGGATTACCAGAAAGGCATTGATCTC 1160  
QY 382 IleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer 401  
DB 1161 ATTAATGATGGCCATTTTGAAGCTGGATGAGATCTACCGAGTGGAGGACGTGCAATTTGTCTGTTGGATCT 1220  
QY 402 GlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPhe 421  
DB 1221 GGGATCCCAATTTTGAAGCTGGATGAGATCTACCGAGTGGAGGATTCACAGGATAAATTC 1280  
QY 422 ArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle 441  
DB 1281 CGTGGATGGTGTGGAATTAAGTGTCCAGTTTCCACAGATAACTCCAGGTTGGATATA 1340  
QY 442 LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461

DB 1341 TTGTTAATGCATCGACATTTGAACCTTGGGTCTTAATCAGCTATATGCTATGCAATAT 1400  
QY 462 GlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsn 481  
DB 1401 GGTACAGTCTCTGTAGTTTCATGGAACTGGGGGCCCTCCGAGACACAGTCGAGACCTTCAAC 1460  
QY 482 ProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGlu 501  
DB 1461 CCTTTGGTCAAAAGAGAGAGGGGTACAGGGTGGGGCTTCTCACCCTTAACCGTGAC 1520  
QY 502 AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu 521  
DB 1521 AAGATGTT-GTGGCATTTGCAACCGCATGTGCACATTTCAGGGAGCACAAAGCGCTCTG 1579  
QY 522 GlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCys 538  
DB 1580 GGAGGGCTCATGAAGCGAGCATGACGAAAGACCATACGTGGGACCATGC 1630  
RESULT 13  
US-10-618-624-1  
; Sequence 1, Application US/10818624  
; Publication No. US20040204579A1  
; GENERAL INFORMATION:  
; APPLICANT: Block, Martina  
; Lorz, Horst  
; Lutticke, Stephanie  
; Walter, Lennart  
; Proberg, Claus  
; Kossmann, Jens  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES  
; FROM WHEAT WHICH ARE INVOLVED IN STARCH  
; SYNTHESIS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: James F. Haley, Jr., c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/818,624  
; FILING DATE: 05-Apr-2004  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/952,677  
; FILING DATE: 14-Sep-2001  
; APPLICATION NUMBER: 09/196,390  
; FILING DATE: 19-Nov-1998  
; APPLICATION NUMBER: DE 196 21 588.9  
; FILING DATE: 29-MAY-1996  
; APPLICATION NUMBER: DE 196 36 917.7  
; FILING DATE: 11-SEP-1996  
; APPLICATION NUMBER: PCT/EP97/02793  
; FILING DATE: 28-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley, Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: AGREVO-9  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2239 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: *Triticum aestivum* L.  
 STRAIN: cv. Florida  
 HAPLOTYPE: ca. 21 d Caryopses  
 IMMEDIATE SOURCE:  
 LIBRARY: cDNA library in pBluescript sk (-)  
 CLONE: TaSSS  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 3..2017  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-10-818-624-1

Alignment Scores:  
 Pred. No.: 8,97e-288 Length: 2239  
 Score: 2466.50 Matches: 464  
 Percent Similarity: 91.8% Conservative: 29  
 Best Local Similarity: 86.4% Mismatches: 41  
 Query Match: 85.3% Indels: 4  
 DB: 8 Gaps: 2

US-10-628-525a-21 (1-539) x US-10-818-624-1 (1-2239)

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QY      2 ValAlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyLeuAlaGluGlySer 21
DB      30 GTGGGGGAACCTCGCG---CCGACCTCTCGTCTC-----GAAGGGGATTCCTGAGGATTC 80

QY      22 IleAspAsnThrValValAlaLaserGluGlnAspSerGluLeuValValGlyLysGlu 41
DB      81 ATCGACAGCATAAATTGTGGCTCGAAGTGCAGGAGGATTCCTGAGATCATGATGCGATGAG 140

QY      42 GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61
DB      141 CAACCTCAAGCTAAAGTTACAGCTAGCATCGTGTGTGTGCTGACTGCTGGAAGCTGCTCTTAT 200

QY      62 AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaLarg 81
DB      201 GCAAGTCAAGGGGGTGTGGAGATGTTGTGTGTTCTTACCAATTGCTCTCTGCTGCTGT 260

QY      82 GlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr 101
DB      261 GGTCAACCGAGTGTGTTGTATATGCAAGATCACTTAATGGTCTCTCATTAATAACTAT 320

QY      102 AlaAsnAlaPheTyrThrGluLysHisIleAraGileProCysPheGlyGlyGluHisGlu 121
DB      321 GCAAAAGGCATTATACACTCGGAAGCACATTAAGATTCCATGCTTTGGGGGATCACATGAA 380

QY      122 ValThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSer 141
DB      381 GTGACCTTTTTCATGAGTATAGACAACACGTCGATTTGGGTGTTGTGTCATCATCGTCA 440

QY      142 TyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161
DB      441 TATCAGACACCGAAGATTATATGGAGATTAATTTGGTGTCTTTGGTGTATATCATGTTTC 500

QY      162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuLeuLeuGlyGly 181
DB      501 AGATACACACTCTTTGCTATGCTGATCGAGGCGCCCACTAATCTTGAATTGGGAGGA 560

QY      182 TyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHisAlaSerLeuValPro 201
DB      561 TATATTATGGACAGAAATTGATGTTGTGTGAGCATTTGGCATGCCAGCTTTGTGCCA 620

QY      202 ValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeu 221
DB      621 GTCTCTCTGCTGCAAAATATAGACCATACGAGTGTATACAGAGATTCCTCCGACGACCTT 680

QY      222 ValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGly 241
DB      681 GTTATACATAATTTAGCACATCAGGCTGTGGAGCTTGAAGTACATATCTGATCTGGGA 740

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QY      242 LeuProProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHis 261
DB      741 TTGCTCTCTGAAATGGTATGGAGCTTTAGAAATGGGTATTTCCAGAAATGGGAGGAGCAT 800

QY      262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyValAlaValThrAlaAspArg 281
DB      801 GCCCTTGACAAGGGTGAGGAGCTTAACCTTTTGAAGAGGAGCAGTTCTGACAGCAGATCG 860

QY      282 IleValThrValSerLysGlyTyrSerTyrGluValThrThrAlaGluGlyGlnGly 301
DB      861 ATTGTGACCGTCACTCAGGCTTATTCATGGAGGTCACTAATCTGCTGAGGCTGACAGGCG 920

QY      302 LeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp 321
DB      921 CTCATAGAGCTCTTAAGCTCCCGAAAAAGTATTGAATGGAATGTAATGGAATTGAC 980

QY      322 IleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp 341
DB      981 ATTAATGATTGGAACCCACACACAGTGTCTCCCTCATCATTTATCTGTGATGAC 1040

QY      342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg 361
DB      1041 CTCCTCGAAAGGCCAAATGTAAAGCTGAATTCGCAAGAGAGTTGGGTTTACCTGTAAAG 1100

QY      362 ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381
DB      1101 GAGGATGTTCTCTCATTTGGCTTTATTTGAAGACTGGATTACCAAGAGCATTTGATCTC 1160

QY      382 IleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer 401
DB      1161 ATTAATGAGCCATTCACAGAGCTCATGGGAGGAGCTGCAATTTGTCATGCTTGGATCT 1220

QY      402 GlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPhe 421
DB      1221 GGGGATCCAAATTTTGAAGGCTGGATGAGATCTACCGAGTCGAGTTTACAAGGATAAATTC 1280

QY      422 ArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle 441
DB      1281 CTGTGATGGTGGATTTAGTGTTCAGTTTCCCACAGAAATTAACGAGTTGCGGATATA 1340

QY      442 LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461
DB      1341 TTGTTAATGCCATCGAGATTGAACTTGGCTTCTTAATCAGCTATATCTATGCAATAT 1400

QY      462 GlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsn 481
DB      1401 GGTACAGTTCCTGTAGTTTCATGGAATCTGGGGGCTCCGAGACACAGTCGAGACCTTCAAC 1460

QY      482 ProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGlu 501
DB      1461 CTTTTTGTGCAAAAGGAGGAGGAGGTACAGGGTGGCGTCTTCCCGCTAACCGTGGAC 1520

QY      502 AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu 521
DB      1521 AAGATGTT-GTGGGCAATTGCGAACCCGATGTCGACATTCAGGGAGACACAAGCGGCTGT 1579

QY      522 GlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCys 538
DB      1580 GGAGGGGCTCATGAAGCGGAGCATGCAAAAGACCATACGTGGGACCATGTC 1630

RESULT 14
US-10-284-668-9
; Sequence 9, Application US/10284668
; Publication NO. US20030106100A1
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; Springer, Franziska
; Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17

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QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449
DB 1604 CAGTTTCTCATAGGTAACAGCAGATCGCATACTATTGATGCCCTCAGATTCGAA 1663
QY 450 ProCysGlyLeuAsnGlnLeuTyAlaMetGlnTyThrValProValValHisAla 469
DB 1664 CCGTGTGGCTTAAACCAATTGTATGCAATGAGATATGGCACCACCTATTGTTTCATAGC 1723
QY 470 ThrGlyGlyLeuArgAspThrValGluAsnProPheGlyGluAsnGly---Glu 488
DB 1724 ACGGGGGGCTTAAGAGACACAGTGAAGGATTTAATCCATATGCTCAAGAAGGAATAGGT 1783
QY 489 GlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAla 508
DB 1784 GAAGGTACCGGTGGACATTTCTCTCTAAAGAGTGAAGTGGTGGTGGTGGTGGTGGTGGT 1843
QY 509 AsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArg 528
DB 1844 CT-GGCAATCGGACTTATACAGAACATAAGTCATCTGGGAGGGATTGATGAGGAGAGG 1902
QY 529 HisValIysArgLeuHisValGlyProCys 538
DB 1903 TATGGAAGGACTATTCTCTGGGAAATGC 1932

RESULT 15
US-10-284-668-3
; Sequence 3, Application US/10284668
; Publication No. US20030106100A1
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; Springer, Franziska
; Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/284,668
; FILING DATE: 29-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,567
; FILING DATE: 24-JUL-1997
; APPLICATION NUMBER: PCT/EP95/04415
; FILING DATE: 09-NOV-1995
; APPLICATION NUMBER: DE P 44 41 408.0
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agrevo-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1758 base pairs
; TYPE: nucleotide
; STRANDEDNESS: unknown
; TOPOLOGY: linear
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; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Solanum tuberosum
; STRAIN: cv. Berolina
; TISSUE TYPE: tuber tissue
; IMMEDIATE SOURCE:
; LIBRARY: cDNA-library in pBluescriptSKII+
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1377
; OTHER INFORMATION: /function= "Polymerization of
; starch"
; /product= "Starch synthase"
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-284-668-3

Alignment Scores:
Pred. No.: 2,48e-188 Length: 1758
Score: 1645.50 Matches: 304
Percent Similarity: 81.7% Conservatives: 63
Best local Similarity: 67.7% Mismatches: 70
Query Match: 56.9% Indels: 13
DB: 5 Gaps: 5

US-10-628-525A-21 (1-539) x US-10-284-668-3 (1-1758)
QY 95 GlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIlePro 114
DB 1 GGCACGAGC-----AATGCTGTGACCTTGATGTGGGGCCACTGTCCAT 45
QY 115 CysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrp 134
DB 46 TGCTTTGTGTATGTCACAGAAAGTAGCCTTCTACCAATGAATACAGGCGAGGTGTTGATTGG 105
QY 135 ValPheValAspHisProSerTyrHisArgProGlyLysAsnLeuTyrGlyAspLysPheGly 154
DB 106 GTATTTGTGGACCACTCTTCTTACCGCAGACCTGGAACGCCATATGGTGATATTATGGT 165
QY 155 AlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaPro 174
DB 166 GCATTTGGTGATTAATCAGTTTCGCTTCTTCTTCTCAGCGCAGCATGTGAAGGCCCA 225
QY 175 LeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAsp 194
DB 226 TTGGTCTTCCACTGGGAGGGTTCACTTATGAGAGAAAGTCTTGTTCCTCGCTAATGAT 285
QY 195 TrpHisAlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyr 214
DB 286 TGCAACGCTGCTTGGTTCTTACTTTTAGGGCCAAAGTATCGTTCCTTATGTTGTATTAC 345
QY 215 LysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAla 234
DB 346 AAGGATGCTCGTAGTATTGTGCAATACACAACTTGACATCAGGAGTGGAGCTGCA 405
QY 235 SerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGlyTrpValPhe 254
DB 406 GTAACCTACAATAATTTGGGTTTGGCTCCACAATGTTATGGAGCAGTGAATGGATATT 465
QY 255 ProGluTrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274
DB 466 CCCACATGGCCAAAGGGCGCATGGCTGCACACTGGTGAACAGTGAACGTTTGAAGGG 525
QY 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThr 294
DB 526 GCATAGCAGATTGCTGATCGGATACAGTACAGTTAGCCAGGAGTACTCATGGGAAATAACA 585
QY 295 ThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsn 314
DB 586 ACTCCTGAAGGGGGGATATGGGCTACATGAGCTGTTGAGCAGTAGACAGCTGTTCTTTAT 645
QY 315 GlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIlePro 334
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Db 646 GGAATTACTAATGAAATAGATGTTAAATGATGGAAACCGTCGACAGATGAGCATATCGCT 705
Qy 335 CyHisTyrSerValAspAspLeuSer-----GlyLysAlaLysCysLysGlyAlaLeu 352
Db 706 TCGCATTAATCCATCAATGACCTCTCCCCCTCGAAGGTTTCAGTCGACAGATGATCTG 765
Qy 353 GlnLysGlnLeuGlyLeuProLleArgProAspValProLeuLeGlyPheIleGlyArg 372
Db 766 CAAGAAGNACTGGGCGCTTCCAATTCGACCGCGATGTCCACTGATGGATTTATTTGGAAGG 825
Qy 373 LeuAspTyrGlnLysGlyIleAspLeuLeGlnLeuLeIleProAspLeuMetArgGlu 392
Db 826 CTGACCTACCAAGAGGTGTGACATAATCTGTGACCAATTCAGAACCTATATGCGAAT 885
Qy 393 AspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSer 412
Db 886 GATGTCCAAAGTTGTAATGCTTGGATCTGGTGAGNAACAATATGAGACTGATGAGACAT 945
Qy 413 ThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPheSerValProValSer 432
Db 946 ACAGAAATCTTTTAAAGACAAATTTTCGTCTGGGTTGGATTTAATGTTCCAGTTCT 1005
Qy 433 HisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGly 452
Db 1006 CATAGGATAACAGCAGATGCGACATATCTATGATGCCCTCAAGATTGGAACCGTGTGGC 1065
Qy 453 LeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGly 472
Db 1066 TTAACCAATGTATGCAATGAGATATGACCATACCTATTGTTCTATAGCAGCGGGGC 1125
Qy 473 LeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGlu---GlnGlyThr 491
Db 1126 CTAAGACACACAGTGAAGGATTTTAATCCATATGCTCAAGAAGGAAAGGTGAAGGTACC 1185
Qy 492 GlyTyrAlaPheAlaProLeuThrThrGluAsnMetPhe-----ValAspIleAlaAsn 509
Db 1186 GGGTGACATTTCTCTCTAACGAGTGAAGATGTTGTTGATACACTGAAGCTGGCGAT- 1244
Qy 510 CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529
Db 1245 CAGGACTTATAC-----AGAACATAAGTCACTCTTGGAGGGATGTATGAGAGAGGTAT 1298
Qy 530 ValLysArgLeuHisValGlyProCys 538
Db 1299 GCGAAGGGACTATTCTCGGGAATGC 1325
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## RESULT 16

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US-10-425-114-30782
; Sequence 30782, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 30782
; LENGTH: 1294
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73078D02_FLI
US-10-425-114-30782
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## Alignment Scores:

## RESULT 17

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US-10-425-114-3524
; Sequence 3524, Application US/10425114
; Publication No. US20040034888A1
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Pred. No.: 2,14e-170 Length: 1294
Score: 1496.00 Matches: 284
Percent Similarity: 99.6% Conservative: 0
Best Local Similarity: 99.6% Mismatches: 1
Query Match: 51.7% Indels: 1
DB: Gaps: 0

US-10-628-525A-21 (1-539) x US-10-425-114-30782 (1-1294)

Qy 255 ProGluTyrAlaArgArgHisAlaLeuAspLysGlyGluAlaValaAsnPheLeuLysGly 274
Db 2 CTTGAATGGCGAGGAGGATGCCCTTGACAAGGGTGAGCAGTTAATTTTTTGAAGGT 61
Qy 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrGluValThr 294
Db 62 GCAGTTGTGACAGCAGATCGATCGTCTGCTCAGTAAGGGTTATTTCATGCGAGGTCCACA 121
Qy 295 ThrAlaGlnGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsn 314
Db 122 ACTGCTGAAGGTGGACAGGGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAAC 181
Qy 315 GlyIleValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCysIlePro 334
Db 182 GGAATTTGTAATGGAATTGACATTAAATGATTGGAACCTGCCACACAAATGTTATCCCC 241
Qy 335 CysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLys 354
Db 242 TGTCAATTATCTGTTGATGACCTCTCTGGAAAGGCCAAATGTAAGGTGCTATTCAGAAAG 301
Qy 355 GluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAsp 374
Db 302 GAGCTGGGTTTACCTATAAGGCTGATGTTCTCTCTGATTTGGCTTTATTTGAAGATTGGAT 361
Qy 375 TyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspVal 394
Db 362 TATCAGAAAGGCATTTGATCTCACTTATCTACACAGATCTCATGCGGGAAGATGTT 421
Qy 395 GlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGlu 414
Db 422 CAATTTGTCATGCTTGGATCTGTCACCCAGAGCTTGAAGATTGGATGAGATCTACAGAG 481
Qy 415 SerIlePheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArg 434
Db 482 TCGATCTTCAAGGATAAATTTCTGTTGATGGGTTGGATTTAGTGTTCAGTTTCCACCGA 541
Qy 435 IleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsn 454
Db 542 ATAACCTGCCCGGCTGCGATATATTGTTAATGCCATCCAGATTCGAACCTTGTGTGCTCAAT 601
Qy 455 GlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArg 474
Db 602 CAGCTATATGCTATGTCAGTATGCGACAGTTCTCTGTTGTCATGCAACTGGGGGCTTAGA 661
Qy 475 AspThrValGluAsnPheAsnProPheGlyGluAsnGlyGlnGlnGlyThrGlyTyrPala 494
Db 662 GATACCGTGGAGAACTTCAACCTTTTCGGTGAAGATGGAGAGCAGGGGTACAGGGTGGCA 721
Qy 495 PheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIle 514
Db 722 TTCGCAACCTTACCCACAGAAACATGTT-GTGACATTCGCAACTGCAATATCTACATA 780
Qy 515 GlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHis 534
Db 781 CAGGGAACACAAATCTCTCTGGGAGGGCTAATGAAGCGAGGATGTCATAAGACTTCAC 840
Qy 535 ValGlyProCysArg 539
Db 841 GTGGGACCATGCCGC 855
```

```
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 3524
; LENGTH: 1300
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700268092_FLI
US-10-425-114-3524

Alignment Scores:
Pred. No.: 6,64e-166 Length: 1300
Score: 1459.00 Matches: 278
Percent Similarity: 99.6% Conservative: 0
Best Local Similarity: 99.6% Mismatches: 1
Query Match: 50.4% Indels: 1
DB: 7 Gaps: 0

US-10-628-525A-21 (1-539) x US-10-425-114-3524 (1-1300)

QY 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAsp 280
DB 3 CATGCCCTTGACACAGGCTGAGCGAGTTAATTTTGAAGAGTGCAGTTGTGACAGAGAT 62
QY 281 ArgIleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGln 300
DB 63 CGAATCGTGACTGTCTAGTAAGGTTATTTCATGGAGGTCACAACTGCTGAAGTGGACAG 122
QY 301 GlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320
DB 123 GGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGGTATTAACCGGAATTGTAAATGGAATT 182
QY 321 AspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340
DB 183 GACATTATGATTGGNACCCTGCCACAGACAAATGTATCCCTGTCTATTCTGTGTAT 242
QY 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIle 360
DB 243 GACCTCTCTGGAAGGCCAAATGTAAGGTGCATTGACAGAGAGCTGGGTTTACCTATA 302
QY 361 ArgProAspValProLeuIleGlyPheIleGlyArgGluAspTyrGlnLysGlyIleAsp 380
DB 303 AGGCTGTAGTTCCCTCTGATTGGCTTTATTTGAAGAGATTGGATTATCAGAAAGGCATTGAT 362
QY 381 LeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400
DB 363 CTCATTCACTTATCATACAGATCTCATGCGGAGAGATGTTCAATTTGTCTATGCTTGA 422
QY 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys 420
DB 423 TCTGGTGACCCAGAGCTTCAAGATTGGATGAGATCTACAGATCGCATCTTCAAGGATAA 482
QY 421 PheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440
DB 483 TTTCGTGGATGGGTGGATTTAGTTAGTTGTTCAGTTTCCACCGAATAACTCCCGGCTGCGAT 542
QY 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460
DB 543 ATATTGTTAATGCCATCCAGATTGACACTTGTGGTCTCAATCAGCTATATGCTATGCGAG 602
QY 461 TyrGlyThrValProValValHisAlaThrGlyLeuArgAspThrValGluAsnPhe 480
```

```
DB 603 TATGGCACAGTTCTCTGTTCATGCAACTGGGGCCTTTAGAGATACCGTGGAGAACTTC 662
QY 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThr 500
DB 663 AACCCCTTTCCGGTGAGAAATGGAGAGCAGGGTACAGGGTGGGCATTTCGACCCCTTAACACA 722
QY 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520
DB 723 GAAACATAGTTT-GTGGACATTGGAACTGCATATCTACATACAGGGAACACAAAGTCTTC 781
QY 521 LeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
DB 782 CTGGGAAGGCTTAATGAAGCGAGGCATGTCAAAAGACTTCACGTGGGACCATGCCGC 838

RESULT 18
US-10-424-599-73305
; Sequence 73305, Application US/10424599
; Publication NO. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 73305
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3720C.1
US-10-424-599-73305

Alignment Scores:
Pred. No.: 2,01e-153 Length: 1158
Score: 1355.50 Matches: 251
Percent Similarity: 86.0% Conservative: 44
Best Local Similarity: 73.2% Mismatches: 47
Query Match: 46.9% Indels: 2
DB: 7 Gaps: 1

US-10-628-525A-21 (1-539) x US-10-424-599-73305 (1-1158)

QY 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216
DB 2 GCCAGCCTAGTTCCCAATACTTTTGGCAGCGAAGTATCGTCCACATGGGGGTATATAAGGAT 61
QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236
DB 62 GCACGTAGTATTTTGGTGATACATAATATAGCACACCCAGGGAGTGGAACTTCAATATTA 121
QY 237 TyrProAspLeuGlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGlu 256
DB 122 TATAGCAATTTGGGCTACCTCCAGATGGTATGGAGCACTGGGATGGGTGTTCCCTACG 181
QY 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276
DB 182 TGGGCAAGGACACATGCTCTTGACACGGGAGAAGCTGTCAACTTTCTAAAGGTGCTGTT 241
QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296
DB 242 GTTACATCTGACCGGATTTGTACAGTAAGCAAGGCTATTCTCGGAGATAACGACTAGT 301
QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle 316
DB 302 GAAAGTGGATGGTCTACATGATTTTATAGCACTCGNAAAAGTATTCTCAGTGGGATC 361
QY 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336
```



Db 362 ACAATGGAATTGATGTCACGTGAATGGACCCGTCATGTGTGATAAACATATTGCTTCCAAC 421  
Qy TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
Db TATTCTGCTGATGACCTTTTCGGGAGCCGAATGCAAGATTTCGTTGCAGAGGAATTG 481  
Qy GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
Db GGTCTTCAGTGAAGCCCTGATGTGTCATGATGATGATGATGATGATGATGATGATGATGAT 541  
Qy LysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPhe 396  
Db AAGGTATTGACCTGATTCGTTGGCAATGCCAGCTCATGAGACCTGATGTTTCACTTT 601  
Qy ValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIle 416  
Db GTTATGCTAGCTTCAGGAACCCCTATTATTGAGACTGGATGAGACCAACAGATCAGCT 661  
Qy PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436  
Db TATAAAGATAAATTTTCGGGGTGGGTGGGATTCATGTTCCAAATATCTCATAAAATAACT 721  
Qy AlaGlyCysAspIleLeuMetProSerArgPheGluValHisAlaThrGlyGlyLeuArgAspThr 456  
Db GCAGGCTGTGATATCTGTTAATGCCATCTGCATTGAGCCCTGCGGACTGAATCAGTTG 781  
Qy TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
Db TATGCAATGAGATGATGAACCTATACCTGTGATGTTCACTGAAACTGGGGGCTAAGAGATACT 841  
Qy ValGluAsnPheAsnProPheGlyGluAsnGlyGlu---GlnGlyThrGlyTyrAlaPhe 495  
Db GTTCATAATTATAATCCCTATCTACTAGAGAAAGCAAGCTGAAAGCACTGGGTGGACATTT 901  
Qy AlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGln 515  
Db TCTCCACTGCAAGGATACATGTTAGCGGCTCTAGATA-TGCCATTCCAAACATATAA 960  
Qy GlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisVal 535  
Db TGAACACACAGCTTCTTGGGAGGGTGTGATGATAAGAGGCGATGACAGAGATTACACATG 1020  
Qy 536 GlyProCys 538  
Db 1021 GGTAAATGC 1029

## RESULT 19

US-10-425-114-8227  
; Sequence 8227, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 8227  
; LENGTH: 1860  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700741124\_FLI  
US-10-425-114-8227

Alignment Scores:

Pred. No.: 3.5e-132 Length: 1860

Score: 1183.00 Matches: 264  
Percent Similarity: 62.2% Conservative: 67  
Best Local Similarity: 49.6% Mismatches: 167  
Query Match: 40.9% Indels: 36  
DB: 7 Gaps: 11

US-10-628-525A-21 (1-539) x US-10-425-114-8227 (1-1860)

Qy 15 GluGlyIleAlaGluGlySerIleAspAsnThrValValValAlaLaserGluGlnAspSer 34  
Db 31 GAAGCTTTGAGTGAATCAAGT-----ACAAGGAGGTTGCTAATGAAGGCGCAAT 81  
Qy 35 GluIleValValGlyLysGluGln-----AlaArgAlaLysValThrGlnSerIle 51  
Db 82 GTGGAGAGTAAAGGTGAACACCCACCCGCTGGCTGGGGCCCAATGTC---ATGAATGTC 138  
Qy 52 ValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCys 71  
Db 139 ATATTGGTTGCACGACGAATGTCTCCCTTCGTCANAAACAGGTGCTCTTGGAGATGTTGCT 198  
Qy 72 GlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValValMetProArg 91  
Db 199 GGATCATTTACCTAAGCCTTTGGCTAGCGTGGACACAGAGTTATGGTTGTAGTACCTCGG 258  
Qy 92 TyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIle 111  
Db 259 TAT-----AGTCATTATGCTGACGCACAAGATATAGGAGTATGGAAA 300  
Qy 112 ArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSer 131  
Db 301 CGATACAAAGTAGATGCTGAGGACATGGAAGTAACATATTTCACCTCTTATATTGATGGT 360  
Qy 132 ValAspTyrValPheValAspHisProSerTyr---HisArgProGlyAsnLeuTyrGly 150  
Db 361 GTTGACTTCTGTTTATTGACAGTCCAACTTCGCCCATTTACAGATTAACATATATGGG 420  
Qy 151 AspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAla 170  
Db 421 -----GGAAACCGAGAGGATATTCCTAAACGCGATGCTGTTGTTTTCAGGCGAGCT 471  
Qy 171 CysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGln---AsnCysMet 189  
Db 472 GCTGAGGTTCTCTGGCATGTTCTTGTGGTGGAGTTTGTCTATGGAGATGGAATTTGGCC 531  
Qy 190 PheValValAsnAspTyrHisAlaSerLeuValProValLeuLeuAlaLysTyrArg 209  
Db 532 TTCATCGCAATGATTGGCATACTGCTTGTGCGCAGTGTATCTGAAGCATATTATTCGT 591  
Qy 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGln 229  
Db 592 GACCATGGTTTAAATGAAGTACACAAGATCTGTTCTTGTGATTTCATAACATAGCACACCAG 651  
Qy 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAla 249  
Db 652 GGACGGGGCCCATTTGATGATTTTCGCTACACAGATTTTACCTGAACACATACATAGACCTT 711  
Qy 250 LeuGluTyrValPheProGluTyrAlaArgHisAlaLeuAspLysGlyGluAlaVal 269  
Db 712 TTCAAATTATATGACCCGGTT-----GGAGGTGAGCACTTC 747  
Qy 270 AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr 289  
Db 748 AATATCTTTTCGCTGGTTTAAAGGCGAGCTGACCGGATTTGCTACTGTGAGTCATGGATAT 807  
Qy 290 SerTyrGluValThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArg 309  
Db 808 GCATGGAGATTAAAACTTCTGAAGGTGGTTGGGGTTTGCATGGGATCATATAATGAGAAT 867  
Qy 310 LysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTyrAsnProAlaThr 329  
Db 868 GACTGGAATTGAGAGGAATTGTGAATGGAATTGACCCAAAGATTGGAAACCCCAAGATT 927  
Qy 330 AspLysCysIlePro-----CysHisTyrSerValAspAspLeu---SerGly 344



Db 1896 AAGCGTCAGTCGAAAGCCGCTTGCAAAAGGAGCTCGGTTTGCCTGTCCTGAGGATGTT 1955  
Qy 365 ProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeu 384  
Db 1956 CCGTTACTTGGATTCAITGGAAGGCTGGATCAACAGAAAGGCAITGATCTCATAGCCGAA 2015  
Qy 385 IleIleProAspLeuMetArgGluAspValGlnPheValMetLeuLysSerGlyAspPro 404  
Db 2016 GCAATTCCTTCGATAGTGGCCGCGATGTGCAGCTAGTCAITGTTGGGAACCTGGGAAGCCG 2075  
Qy 405 GluLeuGluAspTyrPheMetArgSerThrGlnSerIlePheLysAspLysPheArgGlyTyr 424  
Db 2076 GACTTAGAGATATGCTTAGCCAGCTTTGAGTCCCAACACCGTGACAAAGTCAGAGGATGG 2135  
Qy 425 ValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMet 444  
Db 2136 GTTGGCTTTTGGTCAAGATGGCTCACCGGATACAGCAGGTGCAGACATATTCTGTATG 2195  
Qy 445 ProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrVal 464  
Db 2196 CCATCAAGATTGAGCCATGTTGGATTGAATCAACTATGTCATGAATTAACGGAACAATT 2255  
Qy 465 ProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGly 484  
Db 2256 CCAGTTGTACATGCTGTGCGTGGATTGAGGATACAGTGAAGCCTTTTATCCATTGAA 2315  
Qy 485 GluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPhe 504  
Db 2316 GAGTCG-----GGCCTTGGGTGGACATTTTGACAGTGCAGAACTAACAAGTTAATA 2366  
Qy 505 ValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAla 524  
Db 2367 AATGCATTAGGAACACTGCTT-GTTCACCTTCAGGCAGTATAAGCAGAGCTGGGAAGGGCT 2425  
Qy 525 AsnGluAlaArgHisValLysArgLeuHisValGly 536  
Db 2426 CCAACCGCGAGGATGA-CGCAGGATCTTAGTTGGG 2460

RESULT 21  
US-10-628-525-10  
; Sequence 10, Application US/10628525  
; Publication No. US20040185114A1  
; GENERAL INFORMATION:  
; APPLICANT: Keeling, Peter  
; Guan, Hanping  
; TITLE OF INVENTION: Search Encapsulation  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/628,525  
; FILING DATE: 28-Jul-2003  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/941,445  
; FILING DATE: 30-SEP-1997  
; APPLICATION NUMBER: US 60/026,855  
; FILING DATE: 30-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winner, Ellen P  
; REGISTRATION NUMBER: 28,547  
; REFERENCE/DOCKET NUMBER: 89-97  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2097 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: Not Relevant  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHEetical: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Zea mays  
; FEATURES:  
; NAME/KEY: CDS  
; LOCATION: 1..2097  
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-628-525-10  
  
Alignment Scores:  
Pred. No.: 9.82e-126 Length: 2097  
Score: 1130.50 Matches: 254  
Percent Similarity: 57.2% Conservative: 64  
Best Local Similarity: 45.7% Mismatches: 159  
Query Match: 39.1% Indels: 80  
DB: Gaps: 11  
  
US-10-628-525A-21 (1-539) x US-10-628-525-10 (1-2097)  
Qy 3 AlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGlySerIle 22  
Db 565 GCTCCTTATGACAGGAGGAT-----AATGAACCTGGCCCTTTGGCTGGGCCCTAATGTG 618  
Qy 23 AspAsnThrValValAlaLaserGluGlnAspSerGluIleValValGlyLysGluGln 42  
Db 619 ATGAACGTCGTCGTGTGGCTTCT----- 642  
Qy 43 AlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluLaserProTyrAla 62  
Db 643 -----GAATGTGCTCTTCTTCGC 660  
Qy 63 LysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAAsrGly 82  
Db 661 AAGACAGGTGGCCCTGGAGATGTCGTGGGTGCTTTGCTTAAGGCTCTGGCGAGAGGA 720  
Qy 83 HisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAla 102  
Db 721 CACCGTGTATGTCGTGTATACCAATAT-----GGAGATATGCT 762  
Qy 103 AsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluVal 122  
Db 763 GAAGCCCGGATTTAGGTGTAAAGGACGTTACAAGGTAGCTGCACAGGATTCAGAAGTT 822  
Qy 123 ThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSerTyr 142  
Db 823 ACTTATTTTCACTCTTACATTTGATGAGTGTGATTTTGTATTCGTAGAAGCCCTCCCTTC 882  
Qy 143 ---HisArgProGlyAsnLeuTyrGlyAspLysPhePheAlaPheGlyAspAsnGlnPhe 161  
Db 883 CGGCACCGGCACAAATATATTTATGG-----GGAAAGATGATGATATTTGAAG 933  
Qy 162 ArgTyrThrLeuLeuCysTyrAlaLysGluAlaProLeuIleLeuGluGlyGly 181  
Db 934 CGCATGATTTTGTCTGCAAGCGCGCTGTGAGTTCCATGTTATGCTCCATGTCGCGGT 993  
Qy 182 TyrIleTyrGlyGln---AsnCysMetPheValValAsnAspTyrHisAlaserLeuVal 200  
Db 994 ACTGCTATGTTGATGGCAACTTAGTTTCAATGCTTAATGATGGCATACCCGACTTCTG 1053  
Qy 201 ProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
Db 1054 CTGTCTATCTAAGGCCTATTACCGGGCAATGTTTGATCGCATGCTGCTCTG 1113  
Qy 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaserThrTyrProAspLeu 240

```

Db 1114 CTGTGATACACACATTCTCATCAGGCTCGTGGCCCTGTAGACGACTTCGTCATTTT 1173
QY 241 GlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArg 260
Db 1174 GACTTGGCTT-----GAA 1185
QY 261 HisAlaLeuAspLys-----GlyGluAlaValAsnPheLeu 272
Db 1186 CACTACATCGACACTTCAACTGATGATGACCACTTGGTGGGATCACAGCACTGTTTTT 1245
QY 273 LysGlyAlaValAlaValAlaAspArgIleValThrValSerLysGlyTyrSerTrpGlu 292
Db 1246 GCTGCGGGCTGAGACGCGCAGACCGGTGTGACCGTTAGCAATGGCTACATGTGGAG 1305
QY 293 ValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerVal 312
Db 1306 CTGAAGACTTCGGAAGCGGTGGGCTCCAGCATCATATAAACAGAACGACTGGAAG 1365
QY 313 LeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys 332
Db 1366 CTGACGGGCATCGTGAACGGCATCGACATGACGAGTGAACCCCGCTGTGGAC----- 1419
QY 333 IleProCysHisTyrSerValAspAspLeu-----Ser 343
Db 1420 -----GTGCACCTCCACTCCGACGACTACACCACTACACGTTCCGAGCGCTGGACACC 1473
QY 344 GlyLysAlaLysCysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363
Db 1474 GGCAGCGCGCATGTCAGCGCGCTGTCAGCGCGCAGCTGGCGCTGCGCGCACGAC 1533
QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuGln 383
Db 1534 GTGCCACTCATCGGGTTCATCGGGCGGTGGACCAACAGAGCGCTGGACATCATCGCC 1593
QY 384 LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403
Db 1594 GACCGCATCACTGGATCGCGGGCAGAGCTGCAGCTGTGATGCTGGCAGCGGGCGG 1653
QY 404 ProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423
Db 1654 GCCGACCTGGAGGACATGCTGGCGCGGTTCGAGTCGGAGCACAGCACAAAGTGGCGCG 1713
QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeu 443
Db 1714 TGGTGGGGTTCCTCGTGGCCCTGGCGCACCGCATCACGGCGGGCGCGACATCCTGCTG 1773
QY 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463
Db 1774 ATGCCCTCGGGTTCAGCGCGTGGCGGTGMAACCACTCTACGCCATGGCGTACGGGAC 1833
QY 464 ValProValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPhe 483
Db 1834 GTGCCGCTGTGCACCGCTGGGGGGCTCCGGGACACGCTGGCGCGCTTCGACCCGCTTC 1893
QY 484 GlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMet 503
Db 1894 AACGACACC-----GGGCTCGGGTGGACGTTTCGACCGCGCGAGCGCAACCGGATG 1944
QY 504 PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523
Db 1945 ATCGACCGCTCTCGCACTGCCT-CACCACTACCGGAACACTACAGGAGCTGGCGCGC 2003
QY 524 AlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
Db 2004 CTGACGGCGCGGGCATGGCCGAGGACCTCAGCTGGGACCGCGCGC 2051

```

RESULT 22

US-10-336-753-48

; Sequence 48, Application US/10336753

; Publication No. US20030226176A1

; GENERAL INFORMATION:

; APPLICANT: Guan, Hauping

```

; APPLICANT: Keeling, Peter L.
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; FILE OF INVENTION: HOSTS
; FILE REFERENCE: 2461-52
; CURRENT APPLICATION NUMBER: US/10/336,753
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US/09/402,254
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/06660
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/042,939
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 2423
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (join(1..2094, 2098..2103, 2107..2304, 2308..2421))
US-10-336-753-48

```

Alignment Scores:

```

Pred. No.: 1,22e-125 Length: 2423
Score: 1130.50 Matches: 254
Percent Similarity: 57.2% Conservative: 64
Best Local Similarity: 45.7% Mismatches: 159
Query Match: 39.1% Indels: 80
DB: 6 Gaps: 11

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US-10-628-525A-21 (1-539) x US-10-336-753-48 (1-2423)

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QY 3 AlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGlySerIle 22
Db 565 GCTCCTTATGACAGCGAGGAT-----AATGAACCTGGCCCTTGGCTGGGCTAATGTG 618
QY 23 AspAsnThrValValValAlaSerGluGlnAspSerGluIleValValGlyLysGluGln 42
Db 619 ATGAACGTCGTCGTGGTGGCTTCT-----642
QY 43 AlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAla 62
Db 643 -----GAATGTGCTCCTTCTGCG 660
QY 63 LysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGly 82
Db 661 AAGACAGGTGGCTTGGAGATGCTGGGTGGCTTTGCCCTAAGGCTCTGGCGAGGAGGA 720
QY 83 HisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAla 102
Db 721 CACCGTGTATGTCGTGATACCAAGATAT-----GGAGAGTATGCG 762
QY 103 AsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluVal 122
Db 763 GAAGCCCGGATTTAGGTGTAAGGAGACGTTACAAGGTAGCTGGACAGATTTCAGAAGTT 822
QY 123 ThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSerTyr 142
Db 823 ACTTATTTTCACTCTTACATTCATGAGTGTGATTTGTATTCGTAGAACCCCTCCCTTC 882
QY 143 ---HisArgProGlyAsnLeuTyrGlyAspLysPheGlyValPheGlyAspAsnGlnPhe 161
Db 883 CGGCACCGGCACAATAATATTTATGGG-----GGAGAAAGATTGGATATTTTGAAG 933
QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGly 181
Db 934 CGCATGATTTTCTCTGCAAGCGCGCTGTGAGTTCCATGTTATGCTCCATGTCGCGGT 993
QY 182 TyrIleTyrGlyGln---AsnCysMetPheValValAsnAspTrpHisAlaSerLeuVal 200
Db 994 ACTGTCTATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1053

```

QY 201 ProValLeuLeuAlaAlaValTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
 Db 1054 CCTGCTATCTAAAGGGCTATTACCGGACAAGGTTTGATGTCAGATGCTCGCTCTGTG 1113  
 QY 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240  
 Db 1114 CTTGTGATACACAACTTGTCTATCAGGCTCGTGGCCCTGTAGACGACTTCGTCAATTTT 1173  
 QY 241 GlyLeuProGluThrTyrGlyAlaLeuGluThrValPheProGluThrAlaArgArg 260  
 Db 1174 GACTTGCT-----GAA 1185  
 QY 261 HisAlaLeuAspLys-----GlyGluAlaValAsnPheLeu 272  
 Db 1186 CACTATATGACCACTTCAAACTGTATGACAACATTCGTGGGGATCATCACAAAGTTT 1245  
 QY 273 LysGlyAlaValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGlu 292  
 Db 1246 GCTGCGGGCTGAAGACGCGACCGGGTGTGACCTTAGCAATGGCTACATGTGGAG 1305  
 QY 293 ValThrThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerVal 312  
 Db 1306 CTGAAGACTTCGAAGCGGCTGGGGCTCCACGACATATAAACACGACGACTGGAAG 1365  
 QY 313 LeuAsnGlyIleValaGlnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys 332  
 Db 1366 CTGAGGACATCGTGAACGCGATCGACATGAGCGAGTGAACCCCGCTGTGGAC----- 1419  
 QY 333 IleProCysHisTyrSerValAspAspLeu-----Ser 343  
 Db 1420 -----GTGCACCTCCACTCCGACGACTACACCACTACAGCTTCGAGCGCTGGACACC 1473  
 QY 344 GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363  
 Db 1474 GGCAAGCGGAGTGAAGCGCGCCCTGCAGCGCAGCTGGGCTCGAGGTCGCGGACGAC 1533  
 QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 393  
 Db 1534 GTCCCACTGATCGGGTTTCATCGCGCGCTGACACACGAGGCGGTGGACATCATCGCC 1593  
 QY 384 LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403  
 Db 1594 GACCGCATCCACTGGATCGCGGGCGAGGCTGACGCTGTGATGCTGGCGACCGGCGG 1653  
 QY 404 ProGluLeuLeuAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423  
 Db 1654 GCGGACCTGGAGGACATGCTGCGCGGCTTCGAGTCGAGGCACACGACGACGCGCGG 1713  
 QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443  
 Db 1714 TGGGTGGGGTTCTCGGTGCCCCCTGGCGGCACCGCATCACGCGCGCGCGGACATCTCTG 1773  
 QY 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463  
 Db 1774 ATGCCGTGCGGTTTGAGCGCTGCGGGCTGAACACGCTTACGCCATGGCGTACGGGACC 1833  
 QY 464 ValProValHisAlaThrGlyLeuArgAspThrValGluAsnPheAsnProPhe 483  
 Db 1834 GTGCCGTGTGTGACCGCGTGGGGGGCTCCGGGACACGCGTGGCGCTTCGACCGCTTC 1893  
 QY 484 GlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMet 503  
 Db 1894 AACGACACC-----GGGCTCGGGTGGACGCTTCGACCGCGCGGAGCGAACCGGATG 1944  
 QY 504 PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523  
 Db 1945 ATGACGCGCTCTCGCACTGCTCT-CACACGATACCGGAACCTACAGGAGCTGGCGGC 2003  
 QY 524 AlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
 Db 2004 CTGACGGCGCGCGGATGCGCGAGGACCTCAGCTGGGACCGACCGCGC 2051

RESULT 23

US-10-109-048-1144  
 ; Sequence 1144, Application US/10109048  
 ; Publication No. US20040107461A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COMMURI, PADMA  
 ; APPLICANT: KEELING, PETER L.  
 ; APPLICANT: RAMIREZ, NONA  
 ; APPLICANT: MCKEAN, ANGELA  
 ; APPLICANT: GAO, ZHONG  
 ; APPLICANT: GUAN, HANPING  
 ; TITLE OF INVENTION: GLUCAN CHAIN LENGTH DOMAINS  
 ; FILE REFERENCE: 2461-76  
 ; CURRENT APPLICATION NUMBER: US/10/109, 048  
 ; CURRENT FILING DATE: 2003-03-04  
 ; PRIOR APPLICATION NUMBER: 60/279, 720  
 ; PRIOR FILING DATE: 2001-03-30  
 ; NUMBER OF SEQ ID NOS: 1154  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1144  
 ; LENGTH: 2480  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 US-10-109-048-1144

Alignment Scores:  
 Pred. No.: 1,27e-125 Length: 2480  
 Score: 1130.50 Matches: 254  
 Percent Similarity: 57.2% Conservative: 64  
 Best Local Similarity: 45.7% Mismatches: 159  
 Query Match: 39.1% Indels: 80  
 DB: Gaps: 11

US-10-628-525A-21 (1-539) x US-10-109-048-1144 (1-2480)

QY 3 AlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGlySerIle 22  
 Db 622 GCTCTTATGACAGCGGAGGAT-----AATGAACCTTGGCCCTTGGCTGGCCCAATGTG 675  
 QY 23 AspAsnThrValValValAlaSerGluGlnAspSerGluIleValValGlyLysGluGln 42  
 Db 676 ATGAAGCTCGTGTGGTGGCTTCT----- 699  
 QY 43 AlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAla 62  
 Db 700 -----GAATGTGCTCTTCTTCG 717  
 QY 63 LysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGly 82  
 Db 718 AAGACAGGTGGCTTGGAGATGCTGGGGTCTTTTCCCTAAGGCTCTGGCGAGGAGGA 777  
 QY 83 HisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAla 102  
 Db 778 CACCGTGTATGCTGTGTATACCAAGATAT-----GGAGAGTATGCC 819  
 QY 103 AsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluVal 122  
 Db 820 GAAGCCCGGATTTAGGTGTAAGGACGCTTCAAGGTAGCTGGACAGGATTCAGAAGTT 879  
 QY 123 ThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSerTyr 142  
 Db 880 ACTTATTTTCACTCTTACATTGATGAGTTGATTTTGTATTCGTAGAACCCCTCCCTTC 939  
 QY 143 ---HisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161  
 Db 940 CGGACCGGACCAATAATATTTATGG-----GGAGAAAGATTGGATATTTTGAAG 990  
 QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGly 181  
 Db 991 CGCATGATTTTGTCTGCAAGCGCGCTGTGGTTCATGCTGCTCCATGTCGCGGT 1050  
 QY 182 TyrIleTyrGlyGln-----AsnCysMetPheValValAsnAspTrpHisAlaSerLeuVal 200  
 Db 1051 ACTGTCTATGGTATGGCAACTTAGTTTTCATGCTAATGATGGCATACCGCACTTCTG 1110

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QY 201 ProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220
Db 1111 CCTGCTATCTAAAGCCCTATTACCGGCAATGTTGATCGCATATGCTCGCTCTGTG 1170
QY 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240
Db 1171 CTTGTGATACACAACTTGTCTCATAGGCTCGTGGCCCTGTAGACACTTCGTCAATTT 1230
QY 241 GlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArg 260
Db 1231 GACTTGCCT-----GAA 1242
QY 261 HisAlaLeuAspLys-----GlyGluAlaValAsnPheLeu 272
Db 1243 CACTACTCGACCTTCAAACTGTATGACAATTTGGTGGGATCACAGCAAGTCTTTT 1302
QY 273 LysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGlu 292
Db 1303 GCTGCGGGCTGAAGACGGCAGACCGGGTGTGACCGTTAGCAATGGCTACATGTGGAG 1362
QY 293 ValThrThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerVal 312
Db 1363 CTGAAGACTTCGAAGCGGGTGGGGCTCCACGACATCAATAACCAAGACGACTGGAAG 1422
QY 313 LeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys 332
Db 1423 CTGACGGGATCGTGAACGGCATCGACATGAGCGAGTGAACCCCGCTGTGGAC----- 1476
QY 333 IleProCysHisTyrSerValAspAspLeu-----Ser 343
Db 1477 -----GTGCACCTCCACTCCGACGACTACACCACTACACGTTTCGAGCGCTGGACACC 1530
QY 344 GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363
Db 1531 GGCAGCGCGAGTGCAGGCGCGCTGCAGCGCGAGCTGGCGCTGCAGGTCCGCGACGAC 1590
QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 383
Db 1591 GTGCCACTGATCGGGTTCATCGGGCGGCTGGACCAACAGAGCGCGTGACATCATCGCC 1650
QY 384 LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403
Db 1651 GACGCGATCCACTGATCGCGGCGAGGAGCTGCAGCTGTGATGCTGGCGACCGGCGG 1710
QY 404 ProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423
Db 1711 GCCGACCTGGAGGACATGCTGCGCGCGGTTTCGAGTTCGAGCACAGCGACGAGGTGCGCG 1770
QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443
Db 1771 TGGGTGGGGTCTTCGGTGGCCCTTGGCGCACCGCATCACGCGGCGCGGACATCTCGCTG 1830
QY 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463
Db 1831 ATGCGGTCGCGGTTCGAGCGCGTGGGGCTGAACAGCTCTACGCCATGGCGTACGGGACC 1890
QY 464 ValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPhe 483
Db 1891 GTGCCCGTGTGCACGCGTGGGGGGCTCCGGGACACGCGTGGCGCGCTTCGACCGCTTC 1950
QY 484 GlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMet 503
Db 1951 AACGACACC-----GGGTCGGGTGGAGCGTTGCACCGCGCGGAGCGCAACCGGATG 2001
QY 504 PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523
Db 2002 ATCGACGCGCTCTCGCACTGCCT-CACACAGTACCGGAACTACAGGAGAGCTGGCGCG 2060
QY 524 AlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
Db 2061 CTGCGAGGCGCGCGGATCGCGGAGGACCTGAGCTGGGACCAACCGCGCG 2108
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## RESULT 24

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US-10-425-115-149880
; Sequence 149880, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 149880
; LENGTH: 2813
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_69215C.1
US-10-425-115-149880
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## Alignment Scores:

Pred. No.:	6-21e-125	Length:	2813
Score:	1125.50	Matches:	254
Percent Similarity:	57.0%	Conservative:	63
Best Local Similarity:	45.7%	Mismatches:	160
Query Match:	38.9%	Indels:	38.80
DB:	8	Gaps:	11

US-10-628-525A-21 (1-539) x US-10-425-115-149880 (1-2813)

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QY 3 AlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGlySerIle 22
Db 692 GCTCTTATGATGACAGGAGGAT-----AATGAACCTGGCCCTTTGGCTGGCGCTAATGTG 745
QY 23 AspAsnThrValValValAlaSerGluGlnAspSerGluIleValValGlyLysGluGln 42
Db 746 ATGAACGTCGTCGTGGTGGCTTCT----- 769
QY 43 AlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAla 62
Db 770 -----GAATGTGCTCTCTTCTGC 787
QY 63 LysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaArgGly 82
Db 788 AAGACAGGTGGCTTCGAGATGTCGTGGGTGCTTTGCCCTAAGGCTCTGCGAGGAGGA 847
QY 83 HisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAla 102
Db 848 CACCGTGTATGTCGTGATACCAAGATAT-----GGAGAGTATGCC 889
QY 103 AsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluVal 122
Db 890 GAGCCCGGGATTTAGGTGTAGGAGACGTTTACAGGTAGCTGGACAGAGTTCAGAAGTT 949
QY 123 ThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSerTyr 142
Db 950 ACTTATTTTCACTCTTACATTCATGAGTGTATTTTGTATTCGTAGAACCCCTCCCTTC 1009
QY 143 ---HisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161
Db 1010 CGGCACCGGCACAATAATATTTATGGG-----GGAAAGATTGATATTTTGAAG 1060
QY 162 ArgTyrThrLeuLeuCystyrAlaAlaCysGluAlaProLeuIleLeuGluGlyGly 181
Db 1061 CGCATGATTTTGTCTGCAAGCGCGCTGTGAGTTCCATGTTATGTCATGTCGCGGT 1120
QY 182 TyrIleTyrGlyGln---AsnCysMetPheValAsnAspTrpHisAlaSerLeuVal 200
Db 1121 ACTGTCTATGTTGATGGCAACTTAGTTTTCATTGCTTAATGATTGGCATACCGCACTTCTG 1180
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QY 201 ProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220
Db 1181 CCTGCTATCTAAAGCGCTATTACCGGACAATGGTTGAGTGTGCTGCTGCTG 1240
QY 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240
Db 1241 CTTGTGTATACAAACATTGCTCATCAGGGTGTGGCCCTGTAGACGACTTGGTCAATTTT 1300
QY 241 GlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArg 260
Db 1301 GACTTGCT-----GAA 1312
QY 261 HisAlaLeuAspLys-----GlyGluAlaValAsnPheLeu 272
Db 1313 CACTATCTGACCACTTCAAACTGTATGACAACATTTGGTGGGATCAGCAACTTTT 1372
QY 273 LysGlyAlaValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrGlu 292
Db 1373 GCTGCGGGCTGAAGACGCGGAGCGGTGGTACCGTTAGCAATGGCTACATGTGGAG 1432
QY 293 ValThrThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerVal 312
Db 1433 CTGAAGACTTCGGAAGCGGGTGGGCTCCACGACATCATAAACCAAGACGACTGGAAG 1492
QY 313 LeuAsnGlyIleValAlaGlnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys 332
Db 1493 CTGAGGGCATCTGAACGGCATTCGATAGCGAGTGAACCCCGCTGTGGAC----- 1546
QY 333 IleProCysHisTyrSerValAspLeu-----Ser 343
Db 1547 -----GTGCACCTCCACTCCGACGACTACACCACTACAGTTCGAGACGCTGGACAC 1600
QY 344 GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363
Db 1601 GGCAGCGCGAGTCAAGCGCGCTCGCAGCGCGAGCTGGCGCTCGCAGGTCCGCGACGAC 1660
QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 383
Db 1661 GTGCCACTGATCGGGTTTCATCGCGCGCTGGACCCAGCAAGCGCGTGGGACATCATCGCC 1720
QY 384 LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403
Db 1721 GACCGCATCCACTGGATCGCGGGCAGGAGTGCAGCTGTGATGCTGGCACCAGCGCGG 1780
QY 404 ProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423
Db 1781 GCCGACCTGGAGGACATGCTGCGCGGTTCGAGTCGCGAGCACAGCGACAGGTGCGCGG 1840
QY 424 TrpValGlyPheSerValProValSerHisArgIleThrIleGlyCysAspIleLeuLeu 443
Db 1841 TGGTGGGGTTCTCGGTGCCCTCGCGCACCGCATCACGCGCGCGCGCGGACATCTGCTG 1900
QY 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463
Db 1901 ATGCCGTGCGGGTTCGAGCGCTGCGGGCTGACAGCTCTACGCCATGGCGTACGGGACC 1960
QY 464 ValProValValHisAlaThrGlyLysArgAspThrValGluAsnPheAsnProPhe 483
Db 1961 GTGCCGTGTGTGCACGCGTGGGGGGCTCCGGGACACGCGTGGCGGCGCGGACATCTG 2020
QY 484 GlyGluAsnGlyGlnGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMet 503
Db 2021 AACGACACC-----GGGCTCGGGTGGACGCTTCGACCGCGCGGAGCGCAACCGGATG 2071
QY 504 PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523
Db 2072 ATCAGCGCGCTCTCGCACTGCCT-CACCAGCTACCGGAACCTACAGAGAGCTGGCGCG 2130
QY 524 AlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
Db 2131 CCTGCAGCGCGCGGATGCGCGGACGCTCAGCTGGGACCGCGCGC 2178
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RESULT 25

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US-10-437-963-80144
; Sequence 80144, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 80144
; LENGTH: 3260
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURES:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_79798C.1
US-10-437-963-80144

Alignment Scores:
Pred. No.: 7,26e-124 Length: 3260
Score: 1117.50 Matches: 245
Percent Similarity: 60.7% Conservative: 85
Best Local Similarity: 45.0% Mismatches: 168
Query Match: 38.6% Indels: 47
DB: 7 Gaps: 12

US-10-628-525A-21 (1-539) x US-10-437-963-80144 (1-3260)

QY 3 AlaGluLeuSerArg---GluAspLeuGlyLeuGluProGluGlyIleAlaGluGlySer 21
Db 770 GCACAACTAAGTCAATAAGTGAATGGGA-----CAGTCAGTTGCTGAGGGCACA 820
QY 22 IleAspAsnThrValValValAlaSerGluGlnAspSerGluIleValValGlyLysGlu 41
Db 821 AGTGATGATCCCATCTGCTTCCAGCTCT-----GTAGATCTTATC----- 859
QY 42 GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61
Db 860 -----AATATCATATGTTAGTCGCGGAGGTGCTCTCTGG 895
QY 62 AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaArg 81
Db 896 TCCAAACACAGGTGGGCTTGGAGATGTTGCTGGAGCTTTGCCAAGGCTTTGGCTAGGAGA 955
QY 82 GlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr 101
Db 956 GGTCAACCGTGTATGTTAGTGTAGTGCCTATGTTAT-----AAAACTAC 997
QY 102 AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu 121
Db 998 GCAGAACCTCAACAGCTAGAGAGCCAGAGATACACAGTTGCCAGGCGAGATATGGAG 1057
QY 122 ValThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSer 141
Db 1058 GTAAATTTATATCATCATACATAGATGCTGTGGATTGTTGTTTTCATTGCAATCTATC 1117
QY 142 TyrHisArgProGlyAsn---LeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGln 160
Db 1118 TTCCACCACTGTGAGAATGACATTTATGTC-----GGAGACCGAACAGACATCTTA 1168
QY 161 PheArgTyrThrLeuLeuCysTyrValAlaCysGluAlaProLeuIleLeuGluGly 180
Db 1169 AACCGGATGGTTTGTGTGCAAGCGGCTATAGAGTTCCATGCTATGTTCTCTGTTGGT 1228
QY 181 GlyTyrIleTyrGlyGln---AsnCysMetPheValValAsnAspTrpHisAlaSerLeu 199
```

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Db 1229 GGCCTACTGCTACGGTGATGGAATCTTGTTGCTTCCAAATGATGGCATACTGCACCTA 1288
      ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Qy 200 ValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSer 219
      ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 1289 CTGCCTGTTTATTGAAGGCATACTACTCATGATCAATGGTTTCATGATATATGCCGTTCT 1348
      ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Qy 220 IleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAsp 239
      ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 1349 GTCTTGCTATACATATAGACATCAGGCTCGTGCCCATTAGACTACCTTCAGTTAT 1408
      ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Qy 240 LeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArg 259
      ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 1409 CTGGATTTGCCAGTTCATTACATGGATCTTTTCAAACTTTATGACCCA----- 1456
      ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Qy 260 ArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValThrAla 279
      ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 1457 -----TTTGGGGGTGATCACCTAAACATATTTGCAGCTGGTATTAAAGCTGCT 1504
      ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Qy 280 AspArgIleValThrValSerLysGlyTyrSerTyrGluValThrAlaGluGlyGly 299
      ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
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Qy 300 GlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGly 319
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Qy 320 IleAspIleAsnAspTyrAsnProAlaThrAspLysCysIlePro-----Cys 335
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Qy 336 HisTyrSerValAspAspLeu---SerGlyLysAlaLysCysLysGlyAlaLeuGlnLys 354
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Qy 355 GluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAsp 374
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Qy 395 GlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGlu 414
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Db 1865 CAGTTAATAATGTTGGGCACTGGACGGCAAGACCTCGAAGATACATTGAGGAGGCTTGAG 1924
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Qy 415 SerIlePheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArg 434
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Qy 455 GlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArg 474
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Qy 475 AspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAla 494
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Db 2275 TTGGGATAATGTC 2286
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; Sequence 7, Application US/10284668
; Publication No. US20030106100A1
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; Springer, Franziska
; Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/284,668
; FILING DATE: 29-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,567
; FILING DATE: 24-JUL-1997
; APPLICATION NUMBER: PCT/EP95/04415
; FILING DATE: 09-NOV-1995
; APPLICATION NUMBER: DE P 44 41 408.0
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agrevo-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2793 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Solanum tuberosum
; STRAIN: cv Desiree
; TISSUE TYPE: leaf tissue
; IMMEDIATE SOURCE:
; LIBRARY: cDNA-library in Lambda ZAPII
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 242..2542
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-284-668-7

Alignment Scores:
Pred. No.: 5,368-123 Length: 2793
Score: 1109.50 Matches: 240
Percent Similarity: 61.2% Conservative: 65
Best Local Similarity: 48.2% Mismatches: 162
Query Match: 38.4% Indels: 32
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US-10-628-525A-21 (1-539) x US-10-284-668-7 (1-2793)
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 QY 108 GluLysHisIleArgIleProCysPheGlyGlyLysGluValThrPheHisGlu 127  
 Db 1250 GAT-----GGTCAGAGTGTGAAGTGAATTTTCCAAAGCT 1285  
 QY 128 TyrArgAspSerValAspTyrValPheValAsp---HisProSerTyrHisArgProGly 146  
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 QY 147 AsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeu 166  
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 QY 187 ---AsnCysMetPheValValAsnAspTyrPheAlaSerLeuValProValLeuLeuAla 205  
 Db 1457 GGAATTTAGTGTTCATGTAATGATGGCATACTGCTTTATGCGCAGTATATCTGAAA 1516  
 QY 206 AlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsn 225  
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 QY 226 LeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGlu 245  
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 QY 246 TrpTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeuAspLys 265  
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 Db 1673 GGTGAGCATTTCAACATTTTGGCGCTGGTCTAAAGACACACATCGTGTAGTTACAGTT 1732  
 QY 286 SerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeu 305  
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 QY 306 LeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrp 325  
 Db 1793 ATTAATGAGAACATTTGGAATTTACAGGGTATTTGTAATGGGATGTATCAAAAGAGTGG 1852  
 QY 326 AsnProAlaThrAspLysCysIlePro-----CysHisTyrSerValAspAsp 341  
 Db 1853 AACCTGAGTTGACGCTTCACTACAGTCAGATGGTTACATGAACCTACTCTTGGACAGC 1912  
 QY 342 Leu---SerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIle 360  
 Db 1913 CTACAGACTGGCAAGCCTCAATGTAAGCTGCATTCGAGAAGCACTTGGTTTACCAGTT 1972  
 QY 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380  
 Db 1973 CGTGATGATGCTCCACTGATCGGTTCATGGAGGCTTGACCCACAAAGGGTGTGTAT 2032  
 QY 381 LeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
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Db 2093 ACGGGAGGCGCTGACCTTGAACAGATGCTAAAGGCAATTTTGAGTGTCAACACAATGATAAA 2152  
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 Db 2153 ATTAGAGGATGGGTGGTCTCTCTGTGAAGACTTCTCATCGTATAACTGCTGTGGTGCAGAC 2212  
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 Db 2384 AGCCAGCTGATCCACGCATTTAGGAAATTTGCTTACTGAC--TTATCGTGAGTACAAAAAGAG 2442  
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 ; Sequence 25, Application US/10044543  
 ; Publication No. US20030135883A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Singletary, George  
 ; APPLICANT: Zhou, Lan  
 ; TITLE OF INVENTION: No. US20030135883A1el Starch Synthese Polynucleotides  
 ; TITLE OF INVENTION: and Their Use in the Production of New Starches  
 ; FILE REFERENCE: 1144D  
 ; CURRENT APPLICATION NUMBER: US/10/044,543  
 ; CURRENT FILING DATE: 2002-01-11  
 ; PRIOR APPLICATION NUMBER: 09/388,743  
 ; PRIOR FILING DATE: 1999-09-02  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 25  
 ; LENGTH: 2418  
 ; TYPE: DNA  
 ; ORGANISM: Typha latifolia  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1) ... (2418)  
 US-10-044-543-25  
 Alignment Scores:  
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 Percent Similarity: 59.7% Conservative: 78  
 Best Local Similarity: 45.2% Mismatches: 176  
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 QY 35 GluIleValValGlyLysGluGln-----AlaArgAlaLysValThr 48  
 Db 619 GATTTGAATCTCTGGGGAAGAAATAGGTTCTCTTCTTTTGGCTGGGCAAAATGTC--- 675  
 QY 49 GlnSerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGly 69  
 Db 676 ATGAACATCATAGTAGTTCTGTCAGAAATGTCTCTCTTGTGTCACAAACAGGTGGCTTGA 735



538 AACGTGATCGTGGTGGCTGTAATGTTCTCCATGGTGGCAAAACAGGTGGTCTTGGAGAT 597  
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90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAlaAlaPheTyrThrGluLys 109  
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700 CGGAATACTACAAGCTCGAGGACAGACCTAGAGTGAATATTTCCATGCAATTTATT 759  
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149 TyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyr 168  
820 TATGGG-----GGAAGTAGCGAGGAAATCATGAAGCGCATGATTTGTTTTCGAAG 870  
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871 GTTGTCTGTGAGTTCCTTGGCAGCTTCATGCGGTGTGTGTCTACGGAGATGGAAAT 930  
188 CysMetPheValValAsnAspTyrHisAlaSerLeuValProValLeuLeuAlaAlaLys 207  
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1051 CACAGGGCCGTGGTCTCTAGATGAATTCCTGATCATGACTGGCTGCTGAACACTACCTT 1110  
248 GlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeuAspLysGlyGlu 267  
1111 CAACATTTCCAGCTGACGATCCGTC-----GGTGGCGAG 1146  
268 AlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLys 287  
1147 CACGCCAACATCTTTGCGCGGGTCTGAAGATGGCAGCGGTGGTGTGACTGTGACGCGC 1206  
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1207 GGTACTGTGGAGCTGAAGACAGTGAAGGCGGCTGGGGCCCTCCACGACATCATCCGT 1266  
308 SerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTyrAsnPro 327  
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328 AlaThrAspLysCysIlePro-----CysHisTyrSerValAspLeu--- 342  
1327 AAGGTGGACCTGCACCTCGCGTGGCGGCTACACCAACTACTCTCCCTCGAGACACTCGAC 1386  
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403 AspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPheArg 422  
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423 GlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeu 442  
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1687 GTGATGCTTCCCGCTTCGAGCCCTCGGGCTGAACCCAGCTCTACGCGATGGCGTACGGC 1746  
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1837 -----GACCGCGCGGAGGCCAACAGCTGATCGA-GGCGCTCAGGCACCTGCCTCGA 1886  
521 -----LeuGlyArgAlaAsnGluAlaArgHisValLysArg 532  
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; Sequence 1143, Application US/10109048  
; Publication No. US20040107461A1  
; GENERAL INFORMATION:  
; APPLICANT: COMMURI, PADMA  
; APPLICANT: KEELING, PETER L.  
; APPLICANT: RAMIREZ, NONA  
; APPLICANT: MCKEAN, ANGELA  
; APPLICANT: GAO, ZHONG  
; APPLICANT: GUAN, HANPING  
; TITLE OF INVENTION: GLUCAN CHAIN LENGTH DOMAINS  
; FILE REFERENCE: 2461-76  
; CURRENT APPLICATION NUMBER: US/10/109,048  
; CURRENT FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: 60/279,720  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 1154  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1143  
; LENGTH: 2865  
; TYPE: DNA  
; ORGANISM: Zea mays  
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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 2, 2006, 01:09:48 ; Search time 1683.07 Seconds
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Title: US-10-628-525A-21
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Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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-TRANS=human40.cdi -LIST=150 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
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15: /SID55/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description
-----
1 2861 98.9 2970 11 US-11-096-568A-26590 Sequence 26590, A
2 2467.5 85.3 2662 14 US-11-144-630-11 Sequence 11, Appl
```



137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
1259 GTTGATCATCTCCATATACAGACCTGGAAATTTATATGGAGATAAGTTTGGTGTCTTT 1318  
157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
1319 GGTGATTAATCAGTTTCAGATACACACTCTCTTTGGCTATGCTGATGGAGGCTCTTTGATC 1378  
177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis 196  
1379 CTTGAAATGGGAGGATATATTTATGGACAGAAATGGCATGTTTGTGTCAATGATGGCAT 1438  
197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
1439 GCCAGTCTAGTGGCAGCTCTCTTCTGCTGCAAAATATAGACCATATGGTGTATTAAAGAC 1498  
217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
1499 TCCGCGAGCATCTTGTAAATACATAATTTAGCATCAGGTGTAGAGCTTGCAGCACCA 1558  
237 TyrProAspLeuGlyLeuProProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256  
1559 TATCTTGACCTTGGTTGGCCACCTGAATGGTATGGAGCTCTGGAGTGGGTATTCCTGAA 1618  
257 TrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
1619 TGGCGGAGGAGGATGCGCTTGCACAGGGTGAGGAGTAAATTTTGAAGGTGCAGTT 1678  
277 ValThrAlaAspArgIleValThrValSerIleGlyTyrSerTyrGluValThrAla 296  
1679 GTGACAGCATCGAATCGTGACTGTCTGTAAGGGTTATTCTGGGAGGTCACAACTGCT 1738  
297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316  
1739 GAAGTGGACAGGGCCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAAGGAAAT 1798  
317 ValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHis 336  
1799 GTAAATGGAATTCACATTAATGATGGAACTTGAACCTGCCACAGCAAAATGATCCCTGTGAT 1858  
337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
1859 TATCTGTTGATGACCTCTCTGAAAGGCCAAATGTAAAGGTGATTTGCAGAGAGAGCTG 1918  
357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
1919 GGTTTACCTATAGGCTGATGTTCTCTGATTTGGCTTTATTTGGAAGTTGGATTATCAG 1978  
377 LysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPhe 396  
1979 AAAGGCATTGATCTCAATCACTTATCATACAGATCTCATCGGGAAGATGTTCAATTT 2038  
397 ValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIle 416  
2039 GTCAATGCTTGATCTGTGTGACCCAGAGCTTGAAGATTGGAGATGAGATCTACAGAGTCGATC 2098  
417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436  
2099 TTCAAGGATAAATTCGTGATGGTTGGATTAGTTGTTCCAGTTTCCCAACCGAATAACT 2158  
437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456  
2159 GCCGGCTCGCATATATGTTAAATGCCATCCAGATTCGAACCTTGTGGTCTCAATCAGCTA 2218  
457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyLeuArgAspThr 476  
2219 TATGCTATGAGATGAGCAAGTTCCTGTTGTCATGCAACTGGGGGCTCTTAGAGATACC 2278  
477 ValGluAsnPheAsnProPheGlyGluAsnGlyGlnGlyThrGlyTyrAlaPheAla 496  
2279 GTGGAGNACTTCAACCTTTTGGTGAGATGGAGAGCGAGGTACAGGGTGGGCATTCGCA 2338

497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
2339 CCCCTAACCAACAGAAACATGTTTGTGGACATTCGGAACATGCAATATCTCATACAGGGA 2398  
517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536  
2399 ACACAAGTCTCTCTGGGAAGGGCTTAATGAAGCGAGGCATGTCAAAAGAACTTCACGTGGGA 2458  
537 ProCysArg 539  
2459 CCATGCCGC 2467  
RESULT 2  
US-11-144-630-11  
; Sequence 11, Application US/11144630  
; Publication No. US20060010517A1  
; GENERAL INFORMATION:  
; APPLICANT: KALEEN, ZHONGYILI  
; APPLICANT: MORELL, MATTHEW  
; APPLICANT: RAHMAN, SADEOUR  
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION IN PLANTS  
; FILE REFERENCE: 054270/0126  
; CURRENT APPLICATION NUMBER: US/11/144,630  
; CURRENT FILING DATE: 2005-06-06  
; PRIOR APPLICATION NUMBER: US/09/508,377  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: AU PP 2509  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: PCT/AU98/00743  
; PRIOR FILING DATE: 1998-09-11  
; PRIOR APPLICATION NUMBER: AU PP 9108  
; PRIOR FILING DATE: 1997-09-12  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 2662  
; TYPE: DNA  
; ORGANISM: Triticum tauschii  
US-11-144-630-11  
Alignment Scores:  
Pred. No.: 1,42e-257 Length: 2662  
Score: 2467.50 Matches: 464  
Percent Similarity: 91.8% Conservative: 30  
Best Local Similarity: 86.2% Mismatches: 41  
Query Match: 85.3% Indels: 4  
DB: 14 Gaps: 2  
US-10-628-525A-21 (1-539) x US-11-144-630-11 (1-2662)  
QY 2 ValAlaGluLeuSerArgGluAspLeuGluProGluGlyIleAlaGluGlySer 21  
DB 539 GTGGGGGGAATTCGG---CCCAGCTCTCTGCTC-----GAAGGGATTGCTGAGGATTC 589  
QY 22 IleAspAsnThrValValValAlaSerGluGlnAspSerGluIleValGlyLysGlu 41  
DB 590 ATCGACAGCATTAATTTGGCTGCAAGTCAGCAGGATTCTTGAGATCATGGATGCGAATGAG 649  
QY 42 GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61  
DB 650 CAACCTTCAAGCTAAAGTTACACGTAGCATCGTGTGTTGTGACTGTGTAAGCTGCTCTTAT 709  
QY 62 AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaArg 81  
DB 710 GCMAAGTCAAGGGGGCTGGAGATGTTTGTGTTTCTGTTACCAATGCTCTTGTCTCTCGT 769  
QY 82 GlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr 101  
DB 770 GGTCAACCGTGTGATGTTGTTAATGCCAAGATACTTGAATGGGTCCTCTGATAAAACTAT 829  
QY 102 AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu 121  
DB 830 GCAAGGCAATTTACACTCTGGGAAGCACATTAAGATTCCATGCTTTGGGGGATCACATGAA 889













Db 652 GCGCTGTTAGGTTCCATGGCAGCTTCCATGCGCGGTGTCCTTATGGGGATGGAAT 711  
Qy 188 CysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLys 207  
Db 712 CTGGTGTATTGCAATGATGGCAGCGCACTCTGCTGCTATCTGAAGCATAT 771  
Qy 208 TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla 227  
Db 772 TACAGGACCATGGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 831  
Qy 228 HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyr 247  
Db 832 CACAGGCGCGTGGCCCTGTAGATGAATTCCTGTTACCGAGTGGCTTGAGCACTACTG 891  
Qy 248 GlyAlaLeuGluTyrValPheProGluTyrAlaArgHisAlaLeuAspLysGlyGlu 267  
Db 892 -----GNACCTTCAGACTGTACGACCCCGTGGGTGGTGA 927  
Qy 268 AlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLys 287  
Db 928 CACGCCCACTACTTCGCGCGCGGCTGAAGATGCGGACAGGTTGTGTTGAGGCC 987  
Qy 288 GlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuSer 307  
Db 988 GGGTACTGTGGAGCTGAAGAGCGTGGAGGCGGCTGGGGGCTTCACGACATCATACGG 1047  
Qy 308 SerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnPro 327  
Db 1048 CAGAACGACTGGGAAGACCCCGCGCATGCTCAACGGCATCGAACATGGAGTGGACCCC 1107  
Qy 328 AlaThrAspLysCysIlePro-----CysHisTyrSerValAspLeu--- 342  
Db 1108 GAGGTGAGCCCGCCACTTCAAGTCGGACGGCTACACCAACTTCTCCCTGAGGACGCTGAC 1167  
Qy 343 SerGlyValAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgPro 362  
Db 1168 TCCGGCAGCGGAGTGCAGAGGCGCTCGACGGAGCTGGGCGCTGGAGTGGAGTCAATC 1227  
Qy 363 AspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIle 382  
Db 1228 GAGGTGCGGTGCTCGCTTCATCGCGCGCTGAGCGGCGAGGCGGTGGAGTCAATC 1287  
Qy 383 GlnLeuIlePheProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGly 402  
Db 1288 GCGGACGCGCATGCGCTGGATCGTGAGCGAGCGTGCAGCTGCTGATGCTGGGACCGGG 1347  
Qy 403 AspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArg 422  
Db 1348 CGCCACGACTGGAGAGCATGCTGCAGCACTTCGAGCGGGAGCACCACGACAGGTGGCG 1407  
Qy 423 GlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeu 442  
Db 1408 GGGTGGTGGGTCTTCGTCGCGCTGGCGGACCGGATCAGCGCGGGGCGGAGCGCTC 1467  
Qy 443 LeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGly 462  
Db 1468 CTATGCCCTCCCGTTCGTCGCGTGGCGCTGAACAGCTCTACGCCATGGCTACGGC 1527  
Qy 463 ThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnPro 482  
Db 1528 ACCGTCCCGTGTGACGCGCTGGCGGCGCTCAGGGACACCGTGGCGCGCTTCGACCCC 1587  
Qy 483 PheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsn 502  
Db 1588 TTCACCACTCC-----GGGCTGGGTGGACGCTTCGACCGCGCGCGGCGGACAG 1638  
Qy 503 MetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGly 522  
Db 1639 CTGATCGAGCGCTCGGCGACTGCTCT-CGCGACCTACCGAGACTTCAGAGGAGCTGGAG 1697  
Qy 523 ArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
Db -----

Db 1698 GGCCCTCCAGGAGCGCGCATGTGCGAGGACTTTCAGCTGGGAGCACGCCGC 1748

## RESULT 7

US-11-096-568A-18030  
; Sequence 18030, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096, 568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 18030  
; LENGTH: 2410  
; TYPE: DNA  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(2410)  
; OTHER INFORMATION: Ceres Seq. ID no. 12362462  
US-11-096-568A-18030

## Alignment Scores:

Pred. No.:	1,05e-78	Length:	2410
Score:	823.00	Matches:	188
Percent Similarity:	55.1%	Conservative:	94
Best Local Similarity:	36.7%	Mismatches:	168
Query Match:	28.4%	Indels:	62
DB:	11	Gaps:	13

US-10-628-525A-21 (1-539) x US-11-096-568A-18030 (1-2410)

Qy 34 SerGluIleValValGlyLysGluGlnAla-----43

Db 407 AGTAAGATCAGGTGGCTAAAGAGAGCTACAGATAATGAATTCATCCAAAGACTACG 466

Qy 44 -----ArgAlaLysValThr-----GlnSerIleValPheValThrGlyGlu 57

Db 467 GGNATCGGGACCTTATGTATGTTCTGCTGGATGACTATTGTATTGTTGCACTGAA 526

Qy 58 AlaSerProTyrAlaLysSerGlyLeuGlyAspValCysGlySerLeuProValAla 77

Db 527 GTGCACCCATGGTGCAAACTGGTGCTCGGTGATGTTGTAGGAGGACTGCCCCAGCT 586

Qy 78 LeuAlaAlaArgGlyHisArgValMetValMetProArgTyrLeuAsnGlyThrSer 97

Db 587 TTGGCTGCTATGGGACACCGTGTCAATAGCTCCTCGTTAT-----631

Qy 98 AspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGly 117

Db 632 ---GATCATATACAGATGATCGGATACAGTGTCTGTTGAGGATAAATATTGTTGAC 688

Qy 118 GlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPheVal 137

Db 689 ACGGTAGAAACTGTTGCTGCTCTTCCACTGCTACAAAGAGGAGTTGATCGTGTGTTTGT 748

Qy 138 AspHisProSerTyr-----HisArgProGlyAsnLeuTyrGlyAsp 151

Db 749 GATCATCTTATGTTCTTCAAAAGGTATGGGCAAGACTGGAGCAAAATTTGATGTCCT 808

Qy 152 LysPheGlyAla---PheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAla 170

Db 809 ACTACTGGAGACTGACTATCGAGATAACAGTTGAGGTTCTGCTTGTGCTTGTGCTGCT 868

Qy 171 CysGluAlaProLeuIleLeuGluLeuGlyGly-----TyrIle-----TyrGly 185

Db 869 TTGGAGGCTCCAAAGAGTTCTCAATTTCAACAATTTCTGAATATTCTCTCGACCATATGG 928

Qy 186 GlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAla 205

Db 929 GAAGATGTTGCTCTGAGCCAATGATTGGCACACTGCTATTGTCATGTTATTTGAAG 988

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QY 206 AlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsn 225
Db 989 AGCATGTATAGCCAAATGGAATTTATAAATGCTTAAGTTGCTTCTTCGCATACATAAT 1048
QY 226 LeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGlu 245
Db 1049 ATTGCCTATCAAGGTAGATTGCGCGAGCAGACTTCGATCTTCTTAATCTACCTGACACT 1108
QY 246 TrpTyrGlyAlaLeuGluTrpVal-----PheProGluTrpAlaArg 259
Db 1109 TTCCTTGCCATCATTTGATTTTATTGATGACATGTTTAAGCCTTTT----- 1153
QY 260 ArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAla 279
Db 1154 -----CTAGGGAGAAAGCTTAAGTATGATGAGCGGAGTCAATGAGACT 1198
QY 280 AspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla----GluGly 298
Db 1199 GATCTGTTTCTTAACAGTCAGTCACATTTATGTCAGGAACCTCACATCTCGGCCAGATAG 1258
QY 299 GlyGlnGlyLeuAsnGluLeuLeuSerArgLysSerValLeuAsnGlyIleValAsn 318
Db 1259 GGTGTGTGAGTTGGATGGTGTCTCTCGCACCA--AAGCCTCTAGAAATTGGAATCGTTAT 1315
QY 319 GlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSer 338
Db 1316 GGCATGGATGTTTGAATGGATCTCTCAACAGATAGTACATCAGCGTGAATATGAT 1375
QY 339 ValAspAspLeuSer---GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGly 357
Db 1376 GCAACAACAGCTAACTGMAAGCAAGGCTCTCAATAAAGAGAGTTTTGCAACAGAGAAGTCG 1435
QY 358 LeuProIleArgProAspValProIleGlyPheIleGlyArgLeuAspTyrGlnLys 377
Db 1436 TTGCTGTGTGACTCGAGCATCTCTGTATAGTTTTCTGTCGGCGCTCTCGAAGACAGAA 1495
QY 378 GlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheVal 397
Db 1496 GGGTCGACATACTCATTCACCCATTCAGAGTTCTGGGGGAGATGTCAGATAATC 1555
QY 398 MetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePhe 417
Db 1556 GTTCTTGGCAGCGGAAAGAGAGATGGAGGAGGAACCTAAACGAGCTGGAAGTGAATAT 1615
QY 418 LysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAla 437
Db 1616 CCMAACAACGCTAGAGGCGCATACGAAATTCATATGTTCCATTTGGCACACATGATGTTGC 1675
QY 438 GlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyr 457
Db 1676 GGGGCTGACTTCATTATCGTCCACAGCAGGTTTGAGCCATGTGGTCTCATTCAGGTGCNA 1735
QY 458 AlaMetGlnTyrGlyThrValProValValHisAlaThrGlyLeuArgAspThrVal 477
Db 1736 GGGATGAGATATGAGTGAATCTATCTGTTTCATCTCCACTGGAGGACTTGTGCACACGGTT 1795
QY 478 GluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaPro 497
Db 1796 GAG-----GAGGCGCTCACCGGATTCACATCATGGTTCT 1828
QY 498 LeuThrThrGluAsnMetPheValAspIleAlaAsn 509
Db 1829 TTCATGTGCGATGTGGAACCTGTAGACCCAGCCGAC 1864
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## RESULT 8

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US-11-231-599-37
; Sequence 37, Application US/11231599
; Publication No. US20060035379A1
; GENERAL INFORMATION:
; APPLICANT: Morrell, Matthew
; APPLICANT: Li, Zhongyi
; APPLICANT: Rahman, Sadequr
```

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; APPLICANT: Appels, Rudolph
; TITLE OF INVENTION: GENES ENCODING WHEAT STARCH SYNTHASES AND USES
; FILE OF INVENTION: THERSFOR
```

```
; CURRENT APPLICATION NUMBER: US/11/231,599
; CURRENT FILING DATE: 2005-09-21
```

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; PRIOR APPLICATION NUMBER: US/10/018,418
; PRIOR FILING DATE: 2002-05-09
```

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; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patent in version 3.1
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; SEQ ID NO 37
; LENGTH: 9024
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; TYPE: DNA
; ORGANISM: Triticum sp.
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US-11-231-599-37
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## Alignment Scores:

Pred. No.:	6,75e-61	Length:	9024
Score:	666.00	Matches:	151
Percent Similarity:	59.6%	Conservative:	48
Best Local Similarity:	45.2%	Mismatches:	119
Query Match:	23.0%	Indels:	18
DB:	11	Gaps:	4

US-10-628-525A-21 (1-539) x US-11-231-599-37 (1-9024)

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QY 211 TyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGly 230
Db 7241 TATTCATCTTCTCGGTACTCGGTTCGGCTAAATCTTCTTCTTCATGTTGCATG-CAGGGC 7299
QY 231 ValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrGlyAlaLeu 250
Db 7300 CGTGGCCCTGTAGATGAATTCCTGTTCCCGGTTGCTCGACACTACTCTG----- 7350
QY 251 GluTrpValPheProGluTrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsn 270
Db 7351 -----GAACACTTCAGATGTACGACCCCGTGGTGGTGAACACGCGCAAC 7395
QY 271 PheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSer 290
Db 7396 TACTTCGCGCGCGCTCGAAGATGCGGACACGAGTTGCTGTGAGCCCGCGGTACTCTG 7455
QY 291 TrpGluValThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLys 310
Db 7456 TGGGAGCTGAACAGCGTCGAGGGCGGCTGGGGGCTTCAGACATCATACGCGCAGACGAC 7515
QY 311 SerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAsp 330
Db 7516 TGGAGACCCGCGGCATCGTCAACGCGCATCGACACATCGAGTGGAAACCCCGAGGTGGAC 7575
QY 331 LysCysIlePro-----CysHisTyrSerValAspAspLeu---SerGlyLys 345
Db 7576 GCCCACTCAAGTCGAGCGGTACACCAACTTCTCCCTGAGGACGCTGAGACTCCCGGCAAG 7635
QY 346 AlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValPro 365
Db 7636 CGGCAGTCAAGGAGCGCTCGACGCGGAGCTGGGCTCGAGTCCGCGCCGACGTCGCG 7695
QY 366 LeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIle 385
Db 7696 CTGCTCGGCTTTCATCGGCGCTCGACGCGGAGAGGGCGGTGGAGATCATCTCGCGACGCC 7755
QY 386 IleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGlu 405
Db 7756 ATGCCCTGGATCGGACGAGCATGTCAGTGTGGTGTGCTGGCGGCGCGCGCCACGAC 7815
QY 406 LeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpVal 425
Db 7816 CTGGAGACATGCTCGGCACTTCGAGCGGGAGCACACAGGTGCGCGGTGGGTG 7875
QY 426 GlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetPro 445
Db 7876 GGGTTCTCGTGGCGCTGGCGCACCGGATCATCGGCGGGGGGCGGACGCGCTCTCTCATGCC 7935
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QY 446 SerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValPro 465  
 Db 7936 TCCGGGTTCGAGCGGTGGGGCTGAACAGCTCTACGCCATGGCTACGGCACCGTCCCC 7995  
 QY 466 ValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGlu 485  
 Db 7996 GTCTGACCGCGGTGGGGCTCAGGACACCGTGGCGGCTTCGACCCCTTCAACAC 8055  
 QY 486 AsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPheVal 505  
 Db 8056 TCC-----GGGCTCGGTGACGTTTCGACCGCGCGGCGGCGCAGCTCGAG 8106  
 QY 506 AspilealaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsn 525  
 Db 8107 GCGCTCGGGCACTGCCT-CCGCACCTACCGAGACTTCAAGGAGAGCTGGAGGCGCTCCA 8165  
 QY 526 GluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
 Db 8166 GGAGCGCGGATGTCGAGGACTTCAGCTGGGAGCAGCGCGC 8207

## RESULT 9

US-10-504-599A-15

; Sequence 15, Application US/10504599A

; Publication No. US20050272033A1

; GENERAL INFORMATION:

; APPLICANT: YAMAKAWA, HIROHITO

; APPLICANT: SUZUKI, ERIKO

; APPLICANT: MIYATAKE, KIYOKO

; APPLICANT: HAYAKAWA, KATSUYUKI

; TITLE OF INVENTION: WHEAT DETECTING METHOD

; FILE REFERENCE: 8036-1018

; CURRENT APPLICATION NUMBER: US/10/504,599A

; CURRENT FILING DATE: 2004-08-16

; PRIOR APPLICATION NUMBER: PCT/JP02/09983

; PRIOR FILING DATE: 2002-09-26

; PRIOR APPLICATION NUMBER: JP 2002-39040

; PRIOR FILING DATE: 2002-02-15

; PRIOR APPLICATION NUMBER: JP 2002-132119

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 15

; LENGTH: 2886

; TYPE: DNA

; ORGANISM: Triticum aestivum

US-10-504-599A-15

## Alignment Scores:

Pred. No.: 2,81e-52 Length: 2886  
 Score: 581.00 Matches: 208  
 Percent Similarity: 36.2% Conservative: 103  
 Best Local Similarity: 24.2% Mismatches: 191  
 Query Match: 20.1% Indels: 362  
 DB: 8 Gaps: 21

US-10-628-525A-21 (1-539) x US-10-504-599A-15 (1-2886)

QY 11 GlyLeuGluProGluGlyIleAlaGluGlySerIleAspAsnThrValValValAlaSer 30  
 Db 97 GCGTGAGGCCCGCGAGCCCGCGGATGGCGCTCTCGGCATGAGGACCGCGGAGCTAGC 156  
 QY 31 -----GluGlnAspSerGluIleValValGlyLysGluGlnAlaArgAlaLysVal 47  
 Db 157 GCGGCCCAACGCAAGCCGGAAGCGCAGCCGCGGAGCCCGCGGCTCTCCATGGTG 216  
 QY 48 ThrGln-----SerIleValPheValThrGlyGluAlaSerPro 60  
 Db 217 GTGCGGCCCAACCGCGAGCGCGCATGAACCTCGTGTCTCGCGCGCGAGATGGCGCC 276  
 QY 61 TyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAla--- 79  
 Db 277 TGGAGCAGACCGCGGCTCTCGCGAGCTCTCGGGGGGCTCTCCCGCAGCCATGGCCGTA 336

QY 79 ----- 79  
 Db 337 AGCTAGACAGCACCACCTGTCTTCTCATATGTTTCATCTTGCAGTTGCAGCATCCCTGCC 396  
 QY 80 -----AlaArgGlyHisArgValMetValValMetPro 90  
 Db 397 GTTACACGGGTGTGTGTCGTCAGGCCAACCGGCCCATGGTTCATCTCCCG 456  
 QY 91 ArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHis 110  
 Db 457 CGCTAC-----GACCACTACAGGACCGCTGGGACACCAAG-CGTGCT 497  
 QY 111 IleArg----- 112  
 Db 498 CTCGAGGTACTTGAACCTTACCGCAACTTTAACGATCAAAATTCGCATGCTCTGCAC 557  
 QY 113 -----IleProCysPheGlyGly 118  
 Db 558 ATTTCTCAGGATCTTACTGACTGACTAATCGGATCTCGCAGATCAAGGTCGTTGACAAG 617  
 QY 119 GluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAsp 138  
 Db 618 TAGCAGAGGTGAGGTACTTCCACTGCTACAAGCGCGGGGTGACCGCGTGTTCGTCGAC 677  
 QY 139 HisProSerTyrHisArgProGlyAsn----- 147  
 Db 678 CACCCGTGCTTCT-GGAGNAGGTGACCGATCGTCTGTGGACCGATCAAGTAGTCTCT 736  
 QY 147 ----- 147  
 Db 737 TCGTCGTCTCAACCTTGTATAGCATGGTGTGATGATTTCAGTTGTTTCTGCTGTGCAAT 796  
 QY 148 -----LeuTyrGlyAspLysPheGlyAla---Phe 156  
 Db 797 TTCCAGGTCCGGGCAAGACCAAGGAGAAGATCTACGGGCCCGCAGCCGCGCATAC 856  
 QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
 Db 857 GAGGACACCCAGCAGCGCTTCTGCGCAGCGCGGTGAGNAGTGCAGGATC 916  
 QY 177 LeuGluLeu-----GlyGlyTyr----- 182  
 Db 917 CTGAACCTCGACAAATAACCCCTACTTTTCTGGGCCCTACGGTAAGATCAAGATCAAGCAC 976  
 QY 182 ----- 182  
 Db 977 GCCTACTGTTCAAGCTAGAGTGTGTAACTCTGAACCTCTGAAGAACTTGATATTTCTT 1036  
 QY 182 ----- 182  
 Db 1037 GAGAGAGCTGGATGATCACCATTTTTGTATCTGGGTGCGCTGCTGCTCCCTGTTG 1096  
 QY 183 -----IleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuVal 200  
 Db 1097 CGCGCGCGCA-GGGGAGGACGTGTGTGTCGTCGCAATGACTGGCACAACGGGCTCTG 1155  
 QY 201 ProValLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
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 QY 220 ----- 220  
 Db 1216 CATCTTCTTCAAACTATATATCTCTCTGCATTCATGATGATGATATCTTGCTCTTC 1275  
 QY 220 ----- 220  
 Db 1276 ATTTCTGAACAGGCATATCAATTTTGGGTTCATCTTGGCTGAATTTTACATTCGAAC 1335  
 QY 221 -----LeuValIleHisAsnLeuAlaHisGlnGlyValGluPro 233  
 Db 1336 TCATTTTCATGGCAGGTGGCATTTCTGCATCTCAACATCTCTGTACAGGGCCGCTTCTCC 1395

QY 234 AlaSerThrTyrProAspLeuGlyLeuProGluTyrTrpGlyAlaLeuGluTrpVal 253  
DB 1396 TTCGACGACTTCGCGAGCTCAACCTGCCGACAGGTTCAAGTCGCTTGCATTCATC 1455  
QY 254 PheProGluTrpAlaAlaArgHisAlaLeuAspLys-----GlyGluAlaValAsn 270  
DB 1456 -----GACGCTACGACAAAGCCGCTGAGGGCGCAAGATCAAC 1494  
QY 271 PheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSer 290  
DB 1495 TGGATGAAGCCGGAGATCTGACGGCGACAAAGGTGCTGACGGTAGCCCTTACTACGG 1554  
QY 291 TrpGluValThrThrAlaGluGly----GlyGlnGlyLeuAsnGluLeuSerSerArg 309  
DB 1555 GAGGAGCTCATCTCTGCGAAGCCAGGGGCTGGAGCTGACAAACATCATG-----CGC 1608  
QY 310 LysSerValLeuAsnGlyIleValIleAspIleAsnAspTrpAsnProLalaThr 329  
DB 1609 CTCACTGGGATCACCGGCATCGTCAACGCGATGATGTAGCGAGTGGGACCCCAAG 1668  
QY 330 AspLysCysIleProCysHisTyr----- 337  
DB 1669 GACAAGTTCTCGCGCTCAACTACGACATCACACCGTGACCAACACAAAGATTTCT 1728  
QY 338 -----SerVal-As 340  
DB 1729 TCCTCTTCTTCGGTGATCGTGGTTCTGGGTGGTTCTCACAGACGGCAAGTGACA 1788  
QY 340 pAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuProLil 360  
DB 1789 GCGGTGGAGGAGGAGCGCTGAACAAGGAGCGCTGACGGCGAGGTGGGCTGCGGT 1848  
QY 360 eArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAs 380  
DB 1849 GGACCGAAGGTGCGCTGCGTTCATCGCAGGTGGAGGACGACGAGGCGCCCA 1908  
QY 380 pLeuIleGlnLeuIleProAspLeuMetArg---GluAspValGlnPheValMetLe 399  
DB 1909 CGTGATGTCGCGGCATCCCGAGATCTGAGGAGGAGGAGCTCCAGATCGTTCTCT 1968  
QY 399 u----- 399  
DB 1969 GGTATCATCATGACCGCCGCAACCGACCGCCATTGCTGAAACTTCGATCAAGCAGACCTA 2028  
QY 400 -----GlySerGlyAspProGluLeuGluAspTrpMetArgS 412  
DB 2029 AGAATGATCGAATGATTCGAGGGGACCGGGAAGAAGAGTTTCGAGCGGCTACTCAAGA 2088  
QY 412 erThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerValProValS 432  
DB 2089 GCATTGAGGAGAAATTCGAGCAGAGGTGAGGGCGGTGTGAGTTCAAGCGCGCGCTGG 2148  
QY 432 erHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysG 452  
DB 2149 CTCACCATGATGCGCGCGCGCGAGTGTCTGCGGTCAACGACGCGCTTCGAGCGCTGG 2208  
QY 452 LysLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrVal----- 464  
DB 2209 GCCTCATCATGCTCCAGGGGATGCGCTACGGAACGGTAAACTTTTCTTTCGCCAAGTC 2268  
QY 465 -----P 465  
DB 2269 CTTACTTCTGAGCAATCATGACCATGCCATGACCGAAGTTTCTTCCAAATTTTCAGC 2328  
QY 465 roValValHisAla---ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheG 484  
DB 2329 CGTGGCGGTGCGGTCTCACCGCGGCTGTGTCACACAGCATCGT----- 2372  
QY 484 LysGluAsnGlyGlnGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMetP 504  
DB 2373 -----GAGGGCAAGACCGGTTCCACATGGCGCGCTCAGTGTGCGATGT-AAGT 2420  
QY 504 heValAspIleAlaAsn----- 509

DB 2421 TCATCAATCTCTTCAATAAATTTTCATCTTGTTCATCTCTGGAGGCTCAGGCAGATCATC 2480  
QY 510 -----CysAsnIleTyrIleGlnGlyThrGlnV 519  
DB 2481 AAACGGGTTTCCTTTTTCCTCTTGTGGCGACATGCAACGCTGTGGGA-GCCGGCCGACGTG 2539  
QY 519 alLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536  
DB 2540 AAGAAAGGTGGTGACCACTCTGAAGCGCGCCGCTCAAGGTCGTGCGCACGCCGCGC 2592  
RESULT 10  
US-11-231-599-9  
; Sequence 9, Application US/11231599  
; Publication No. US20060035379A1  
; GENERAL INFORMATION:  
; APPLICANT: Morrell, Matthew  
; APPLICANT: Li, Zhongyi  
; APPLICANT: Rahman, Sadequr  
; APPLICANT: Appels, Rudolph  
; TITLE OF INVENTION: GENES ENCODING WHEAT STARCH SYNTHASES AND USES  
; FILE OF INVENTION: THEREFOR  
; FILE REFERENCE: 72715Supplemental  
; CURRENT APPLICATION NUMBER: US/11/231,599  
; PRIOR FILING DATE: 2005-09-21  
; PRIOR APPLICATION NUMBER: US/10/018,418  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 3621  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3177)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1520)..(1520)  
; OTHER INFORMATION: n can be a or g or c or t, and the encoded amino acid  
; OTHER INFORMATION: cannot be a  
; OTHER INFORMATION: assigned with certainty.  
US-11-231-599-9  
Alignment Scores:  
Pred. No.: 9,48e-40 Length: 3621  
Score: 467.00 Matches: 154  
Percent Similarity: 44.2% Conservative: 90  
Best Local Similarity: 27.9% Mismatches: 183  
Query Match: 16.1% Indels: 126  
DB: 11 Gaps: 20  
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QY 42 GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61  
DB 1811 CAATTGAAACAGAGAAATACATG-CGTATTATCCACATTGCCGTTGAGATGCCCGCGTT 1869  
QY 62 AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaArg 81  
DB 1870 GCAAGGTTGGAGGCTTTGGGGATGTTGTACAACTCTTCACGTCTTCACGTGCCATTCAAGATCTA 1929  
QY 82 GlyHisArgValMetValValMetProArgTyr-----LeuAsnGlyThrSerAspLys 99  
DB 1930 GGACATACTGTGAGGTATTCTCCGGAAGTACGACTGTTCGAACCAAGCAGTGTCAAG 1989  
QY 100 Asn-----TyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
DB 1990 GATTTACATTATATCAAAAGTTTCTTGGGGTGTACAGAAATTAAGATATGGGTGGA 2049  
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136



Db 3725 GATTTACATTTATATCAAAAGTTTTCTTGGGGTGGTACAGAAATAAAAGTATGGTTGCA 3784  
Qy 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136  
Db 3785 CGAGTCGAGACCTGACCGTTTACTTCTCCGGAACCTCAAAATGGGATGTTGGCGTT--- 3841  
Qy 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
Db 3842 -----GGATGTGTATATGGA----- 3856  
Qy 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
Db 3857 AGCAATGATGACCGCAGATTTGGGTTCTTCTGTCAATCTGCTCTAGAGTTTATCCTCCAG 3916  
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196  
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Qy 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
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Qy 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
Db 4016 ACTCGGGTGTATTTACCATCCACAATCTTGAA----- 4048  
Qy 237 TyrProAspLeuGlyLeuProGluTyrTrpTyrGlyAlaLeuGluTyrValPheProGlu 256  
Db 4049 -----TTTGGAGCA----- 4057  
Qy 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
Db 4058 -----CATATATTGGTAAAGCAATG 4078  
Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
Db 4079 ACATAGTGTGATAAAGCCCAACTGTTCTCTACATATTCAAGGCGATG----- 4129  
Qy 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle 316  
Db 4130 ---GCAGGCCATGGC-----GCCATTGTCTCTCATCGTGAGAAATTTACGGCAAT 4177  
Qy 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
Db 4178 CTCATAGGAATGATCCAGATATCTGGGATCGGTACACTGACAAATTTATCCGGTCCCT 4237  
Qy 337 TyrSerValAspAsp---LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGlu 355  
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Db 4415 GTGGTTTTCGTTGCTGCTCAGCTCCAGATCATCGAATACAAAGGCGATTTTTCAGATTGGCC 4474  
Qy 414 GluSer-----IlePheLysAspLysPheArgGlyTrpValGlyPheSerValPro 430  
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Qy 431 ValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetSerArgPheGluPro 450  
Db 4535 CTTTCTCACTGATATACGCTGGCTCGGACTTCATAATTTGTCCTTCATCTCGAAGCC 4594  
Qy 451 CysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThr 470  
Db 4595 TGTGGCTTAACACAACACTTGTGCCATGCGTTATGGATCGATCCCTATATAGTTCCGAAACT 4654

Qy 471 GlyGlyLeuArgAspThrValGluAsnPhe----- 480  
Db 4655 GGAGGACTTTCCAGCACACAGCTCTTCGACGCTAGACAATATAAGACCGGCTCGGTCTCTT 4714  
Qy 481 -----AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAla 496  
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RESULT 12  
US-11-231-599-38  
; Sequence 38, Application US/11231599  
; Publication No. US20060035379A1  
; GENERAL INFORMATION:  
; APPLICANT: Morrell, Matthew  
; APPLICANT: Li, Zhongyi  
; APPLICANT: Rahman, Sadequr  
; APPLICANT: Appels, Rudolph  
; TITLE OF INVENTION: GENES ENCODING WHEAT STARCH SYNTHASES AND USES  
; FILE REFERENCE: 72715Supplemental  
; CURRENT APPLICATION NUMBER: US/11/231,599  
; CURRENT FILING DATE: 2005-09-21  
; PRIOR APPLICATION NUMBER: US/10/018,418  
; PRIOR FILING DATE: 2002-05-09  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 11611  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
US-11-231-599-38  
Alignment Scores:  
Pred. No.: 3,02e-14 Length: 11611  
Score: 238.50 Matches: 108  
Percent Similarity: 36.4% Conservative: 56  
Best Local Similarity: 24.0% Mismatches: 131  
Query Match: 8.2% Indels: 156  
DB: 11 Gaps: 18  
US-10-628-525A-21 (1-539) x US-11-231-599-38 (1-11611)  
Qy 163 TyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyTyr 182  
Db 9024 TTTACTACTAGCTTATTTGGTGCATTTGGTTCCTTCTCTACTC-----TAC 9071  
Qy 183 IleTyrGlyGlnAsnCysMetPheValVal----- 192  
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Qy 193 -----AsnAspTrpHis 196  
Db 9132 TTAATAAAACTTGCATCTGTATTTCACGTGACAGCATATAATACATTGCCATGTTGGTCA 9191  
Qy 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 9192 AGTCTCCGTCGCTGGCTATATAGGACACTATTCCAATCCAGATG---GCAAGC 9248  
Qy 217 SerArgSerIleLeuValIleHisAsnLeu-----AlaHisGlnGlyValGluPro 233  
Db 9249 ACTCGGGTGTATTATACCATCCACAATCTTGAATTTGGAGCACAATTAT---ATTGTTAA 9305  
Qy 234 AlaSerThrTyrProAspLeuGlyLeuProGluTyrTrpTyrGlyAlaLeuGluTrp--- 252  
Db 9306 GCAATGACATACTGTGATAAAGCCACAATGT---GAGTGCCTTACTGTCTTGTAAATTTTA 9364  
Qy 253 ValPheProGluTrpAlaArgArg-----HisAlaLeuAspLysGlyGluAlaValAsn 270  
Db 9365 ATCTTCTGTTGGCGCACAGAAATCTTCCACATTTTACAGAAATCATGTTCTTGTGTTT 9424  
Qy 271 PheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSer 290  
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311	Ser	Val	Leu	Asn	Gly	Ile	Val	Asn	Gly	Ile	Asp	Ile	Asn	Asp	Trp	Asn	Pro	Ala	Thr	Asp	330
9518	GAGA	AA	TTC	TAC	CGC	CA	TTC	CA	TG	GA	TT	GA	TTC	CA	GAT	AT	CT	GG	AT	CT	9577
331	Lys	Cys	Ile	Pro	-----	Cys	His	-----	---	---	---	---	---	---	---	---	---	---	---	---	336
9578	AA	TTT	AT	CCG	TAC	CG	TAC	AG	AT	TTT	TTT	CC	CA	GAT	GCA	AG	TAT	AT	TAC	CA	9637
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9638	GAT	AG	TTT	TAT	TG	CTT	AA	CT	AT	TG	TTT	CT	ACT	TAC	TAC	TTC	AGG	TCC	TT	AT	9697
340	pAsp	Leu	Ser	Gly	Ile	Val	Ala	Lys	Cys	Ile	Val	Leu	Gln	Lys	Glu	Leu	Gly	Leu	Pro	Ile	360
9698	TG	TT	GC	AA	GG	CA	AG	GAG	CT	CA	AA	AA	GG	CG	CTT	GC	CA	GCA	AG	TTT	9755
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9756	CA	AA	CT	GA	TG	CT	CT	TAT	TG	CG	AT	CA	TCC	CG	TCT	GA	CA	CC	CA	AG	9814
380	pLeu	Ile	Gln	Leu	Ile	Ile	Pro	Asp	Leu	Met	Arg	Glu	Asp	Val	Gln	-----	---	---	---	---	395
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401	rGly	---	Asp	Pro	Glu	Leu	Glu	---	Asp	Trp	Met	Arg	Ser	Thr	Glu	Ser	-----	---	---	---	416
9995	AG	CT	CA	GAT	CA	TG	CA	AT	AC	AG	CG	CA	TAT	TTT	TG	CA	AT	TG	CG	CA	10054
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444	tPro	Ser	Arg	pPhe	Glu	Pro	Cys	Gly	Leu	Asn	Gln	Leu	Tyr	Ala	Met	Gln	Tyr	Gly	Thr	Val	464
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1032 TCATCTCTTGCACCCCTGTGCCTTAACACAACTTTGTGCCATGCGTTATGGATCGATCCCT 103

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APPLICANT: Dotson, Stanton B  
APPLICANT: Duff, Stephen M  
APPLICANT: Sisson, Pamela J  
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE NUCLEIC ACID MOLECULES FROM CYANOBACTERIA  
TITLE OF INVENTION: US5 THEREFOR  
FILE REFERENCE: 38-21 (52176) A  
CURRENT FILING DATE: 2003-01-03  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 11  
LENGTH: 1269  
TYPE: DNA  
ORGANISM: Nostoc punctiforme  
FEATURE:  
NAME/KEY: gene  
LOCATION: (1)..(1269)  
OTHER INFORMATION:  
US-10-336-263A-11

Alignment Scores:  
Pred. No.: 4.13e-06 Length: 1269  
Score: 152.50 Matches: 74  
Percent Similarity: 39.0% Conservative: 49  
Best Local Similarity: 23.5% Mismatches: 95  
Query Match: 5.3% Indels: 97  
DB: 8 Gaps: 14

US-10-628-525A-21 (1-539) x US-10-336-263A-11 (1-1269)

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QY 249 AlaLeuGluTrpValPheProGluTrpAlaArgArgHieAlaLeuAspLysGlyGluAla 268  
Db 442 ACTATAGAAATATTCCTCTGATTGCTAGTCAGCGATTGCGAGTAGAA----- 489

QY 269 ValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGly 288  
Db 490 -----AAACAGGTGTTAGAAACAGCAGCAGCGAATTGTA----- 522

QY 289 TyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuSerSer 308  
Db 523 -----CGCACGAGTCGCAAGACAGCACATCGATCGCTAGTTCCACT 570

QY 309 ArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAla 328  
Db 571 GAA-----GGCAATATCGATATT----- 588

QY 329 ThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCys 348  
Db 589 -----ATCCCTGTGTGTACAGATATTTCAGCGTTT----- 618

QY 349 LysGlyAlaLeuGlnLysGluLeuGly-----LeuProIleArgProAspValPro 365  
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QY 366 LeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp---LeuIleGlnLeu 384  
Db 676 GTTGATTATTATGTAGGGGTTTGACCAACGCAAGGTATAGAAACCCCTAGTCGTGCA 735

QY 385 IleIleProAspLeuMetArgGlu-----AppValGlnPheValMetLeuGlySerGly 402  
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QY 470 ThrGlyGlyLeuArgAspThrValGluAsn----- 479  
Db 1018 GTCGGTGAGCTTCAATTCTAGTGTAAATGAACAACTGGTTTATTAGCACCACCACAA 1077

QY 480 -----PheAsnPro----- 482  
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RESULT 15  
US-11-082-389-41  
; Sequence 41, Application US/11082389  
; Publication No. US20050244935A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schoder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
; TITLE OF INVENTION: TRANSPORT  
; FILE REFERENCE: BGI-131PCPN  
; CURRENT APPLICATION NUMBER: US/11/082,389  
; CURRENT FILING DATE: 2005-03-16  
; PRIOR APPLICATION NUMBER: US 09/603024  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 60/143262  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: US 60/151281  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19930487.4  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19930489.0  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931549.3  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931550.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932134.5  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19941379.7  
; PRIOR FILING DATE: 1999-08-31  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 446  
; SEQ ID NO 41  
; LENGTH: 1293  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (101)..(1270)  
; OTHER INFORMATION: RXN02062  
US-11-082-389-41

Alignment Scores:  
Pred. No.: 5.43e-06 Length: 1293  
Score: 151.50 Matches: 77  
Percent Similarity: 36.3% Conservative: 42



Best Local Similarity: 23.5% Mismatches: 100  
Query Match: 5.2% Indels: 109  
DB: 13 Gaps: 18

US-10-628-525A-21 (1-539) x US-11-082-389-41 (1-1293)

```
QY 212 GlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyVal 231
DB 221 GGTGCACCTCGGATATGGAGGAGTTTCGTC-----CACGGCGTC 262
QY 232 GluProAla-----SerThrTyrPro----- 238
DB 263 GATCTGCTTGGAAAGCGGAACCTCGGATTAAGACACTGTCCACGGTTTACGCATG 322
QY 239 -----AspLeuGlyLeuProGluTyrPyrGlyAlaLeuGlu 251
DB 323 GCAGAACTGCACAAACAGCTGGATGCTGCTCACTCACACACTTGGTATGCAGGTC 382
QY 252 -----TrpValPheProGluTyrPalaArgArgHisAlaLeuAsp 264
DB 383 GGCACCTTGCAGTCTCTCCACGGCAATTCCTCACGTGCTACCGCGCACTCTTTGGAG 442
QY 265 -----LysGlyGluAlaValAsn-----Phe 271
DB 443 CCAGATCGCCATCGAAGCTGACACTTGGCGGTGATACGACGTGCTCTCTGCTCT 502
QY 272 LeuLysGlyAlaValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrp 291
DB 503 GAAAAAATGCCATGGAATACGCTGACGCGCTCATCTGCTGCG----- 547
QY 292 GluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSer 311
DB 548 -----GCTCGCATGAAGATTCCATCTCTGCTGCTGCTACCTCCCTCGC 586
QY 312 Val-----LeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnPro 327
DB 587 ATCAGCGCGACACGCGTGTGCTCTCACGGCATCGACACTGATGTTGGCAGCT 646
QY 328 AlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLys 347
DB 647 CGCCCG-----ACTTTCATGAC----- 664
QY 348 CysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIle 367
DB 665 GCGGAAGATTCCTACTCTCCCTCCCTAGGC-----GTTGACCCACAGCGGCCCATCGTC 718
QY 368 GlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp---LeuIleGlnLeuIleIle 386
DB 719 GCATTTGTCGCCCGCATCCCCGCAAAAGGGGTGAGCACCTCATCAGGCGAGCG 778
QY 387 ProAspLeuMetArgGluAspValGlnPheValMet---LeuGlySerGlyAsp---Pro 404
DB 779 -----CTTTTCAGCAGTCCGTGAGCTGTGCTCTGTGCGCGCGCCAGACACCC 832
QY 405 GluLeu-----GluAspTrpMetArgSerThrGluSerIle 416
DB 833 GAAATCGCAGCTCGCACCCACCGCTGTTGGAAGAACTCCAGGCAAGCGCGAAGCAT 892
QY 417 Phe-----LysAspLysPheArgGlyTrpValGlyPheSerVal 429
DB 893 TTCTGGGTTCCAGACATGCTGGCGCAGGACAAATCCAA----- 931
QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449
DB 932 -----GAGATTCTCACCGCTGCTGACACCTTCTGTGTGCGCCATTCATTACGAG 979
QY 450 ProCysGlyLeuAsnGlnIleuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469
DB 980 CCACTGGGCATCTGTAACCTTGGAAAGCAATGGCTGCAACACCGCACTGTGTCATCCGAC 1039
QY 470 ThrGlyGlyLeuArgAspThrVal 477
DB 1040 GTTGGAGGCATCCTCGAGGTGTT 1063
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## RESULT 16

US-11-082-389-43  
; Sequence 43, Application US/11082389  
; Publication No. US20050244935A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
; FILE REFERENCE: BGI-131CPCN  
; CURRENT FILING DATE: 2005-03-16  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 09/603024  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: US 60/141031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 60/143262  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: US 60/151281  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19930487.4  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19930489.0  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931549.3  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931550.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932134.5  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19941379.7  
; PRIOR FILING DATE: 1999-08-31  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 446  
; SEQ ID NO 43  
; LENGTH: 1293  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (101)..(1270)  
; OTHER INFORMATION: FRXA02062  
US-11-082-389-43

## Alignment Scores:

Pred. No.:	5,43e-06	Length:	1293
Score:	151.50	Matches:	77
Percent Similarity:	36.3%	Conservative:	42
Best Local Similarity:	23.5%	Mismatches:	100
Query Match:	5.2%	Indels:	109
DB:	13	Gaps:	18

US-10-628-525A-21 (1-539) x US-11-082-389-43 (1-1293)

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QY 212 GlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyVal 231
DB 221 GGTGCACCTCGGATATGGAGGAGTTTCGTC-----CACGGCGTC 262
QY 232 GluProAla-----SerThrTyrPro----- 238
DB 263 GATCTGCTTGGAAAGCGGAACCTCGGATTAAGACACTGTCCACCGTTTACGCATG 322
QY 239 -----AspLeuGlyLeuProGluTyrPyrGlyAlaLeuGlu 251
DB 323 GCAGAACTGCACAAACAGCTGGATGCTGCTCACTCACACACTTGGTATGCAGGTC 382
QY 252 -----TrpValPheProGluTyrPalaArgArgHisAlaLeuAsp 264
```

```
Db 383 GGCCACCTTTCAGCTCGTCTCCACGGCAATTCCTCAGCTGGCTACCGCGCACTCTTTGGAG 442
QY 265 -----LysGlyGluAlaValAsn-----Phe 271
Db 443 CCAGATCGCCCATGGAAGCGTGAGCAGCTTGGCGGTGGATACGACGTGCTCCTCGTCT 502
QY 272 LeuLysGlyAlaValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrp 291
Db 503 GAAAAAATGCCATGGAATACGTCAGCGGTCACTCGCTGTGTCG----- 547
QY 292 GluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSer 311
Db 548 -----GCTCGCATGAAAGATTCATCCTCGCTCGTACCCCTCG 586
QY 312 Val-----LeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnPro 327
Db 587 ATCGAGCCGGACACCTGCGTGTGTCCTCAAGCGCATCGACACTGAGTTGGCGACCT 646
QY 328 AlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLys 347
Db 647 CGCCCG-----ACTTCGATGAC----- 664
QY 348 CysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIle 367
Db 665 GCGGAAGATTCGCTACTCGCTCCCTAGGC-----GTTGACCCACAGCGGCCCATCGTC 718
QY 368 GlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp---LeuIleGlnLeuIleIle 386
Db 719 GCATTTGTGCGCGCATACCCGCCAAAAGCGTGCAGCCTGCTGTGCGCGCGGACACCCCC 832
QY 387 ProAspLeuMetArgGluAspValGlnPheValMet---LeuGlySerGlyAsp---Pro 404
Db 779 -----CTTTTCGACGAGTCCGTCGACGTTGTGCTGTGCGCGCGGACACCCCC 892
QY 405 GluLeu-----GluAspTrpMetArgSerThrGluSerIle 416
Db 833 GAAATCGCAGCTCGCACCCACCGCCCTGTGTGGAAGAACTCCAGGCAAGCGCGAAGGCATT 892
QY 417 Phe-----LysAspLysPheArgGlyTrpValGlyPheSerVal 429
Db 893 TTCTGGGTTTCAGACATGTCGGCAGGACAAATCCAA----- 931
QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449
Db 932 -----GAGATTCTCCCGCTGCTGACACCTCGTGTGCCCATCCATTACGAG 979
QY 450 ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469
Db 980 CCACTGGGCATCGTGAATCTGGAAGCAATGGCTGCAACACCGCAGTTGTGCGCATCCGAC 1039
QY 470 ThrGlyGlyLeuArgAspThrVal 477
Db 1040 GTTGGAGGCATCCCTGAGGTGTT 1063
```

```
RESULT 17
US-10-336-263A-1
; Sequence 1, Application US/10336263A
; Publication No. US20050251882A1
; GENERAL INFORMATION:
; APPLICANT: D'Ordine, Robert L
; APPLICANT: Dotson, Stanton B
; APPLICANT: Duff, Stephen M
; APPLICANT: Sisson, Pamela J
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE NUCLEIC ACID MOLECULES FROM CYANOBACTE
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 38-21 (52176) A
; CURRENT APPLICATION NUMBER: US/10/336,263A
; CURRENT FILING DATE: 2003-01-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1278
; TYPE: DNA
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; ORGANISM: Anabaena sp.
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1278)
; OTHER INFORMATION:
US-10-336-263A-1

Alignment Scores:
Pred. No.: 7,8e-06 Length: 1278
Score: 150.00 Matches: 92
Percent Similarity: 38.8% Conservative: 63
Best Local Similarity: 23.1% Mismatches: 131
Query Match: 5.2% Indels: 114
DB: 8 Gaps: 21
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US-10-628-525A-21 (1-539) x US-10-336-263A-1 (1-1278)

```
QY 163 TyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle-LeuGluLeuGlyGlyTy 182
Db 270 TTACCGGAATTGT-----TGCCGAATTCACACGCTTCCAAAAGGCCCAAGGTTA 320
QY 182 rIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProVa 202
Db 321 TAACTATCAA-----CTCATTACACAAAATTACTGTTGTCATCTTGGTGGGAAT 371
QY 202 lLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuVa 222
Db 372 GCAACTG-----AAAAAGCAACAACCCCTTGTGT 401
QY 222 lIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLe 242
Db 402 GGTGCATACATACCCTCATTTAGGACCAATCAATATCAACGATCGCAGATATA----- 456
QY 242 uProProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAla---ArgArgHi 261
Db 457 -----CCCGCCATTGCGGAATCAGCGATT 479
QY 261 sAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspAr 281
Db 480 AGCTATAGAAA-----AAAGCTTGTTTAGAGAGGTAGACAC 515
QY 281 gIleValThrValSerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGlnGln 301
Db 516 AGTAGTT-----GCCACACGCCCCCAAGACAGCAACA 548
QY 301 yLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAs 321
Db 549 TATGCGCGCCCTGGTT---TCTAAGAAGGGACGCATAGAGATGATTCTCTTGGCGGACTGA 605
QY 321 pIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAs 341
Db 606 CATTAACTACTTC----- 618
QY 341 pLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleAr 361
Db 619 -----GGAACAATTTGAA---AAGTCGCGCTCACGGGAAAAAATCGGA-----ATTGA 662
QY 361 gProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp-- 380
Db 663 GCCTGATGCCAAGATGGTATTTTATAGTAGTCTTTGTATCCCGGTAAAGGCGATAGAAAC 722
QY 381 -LeuIleGlnLeuIleIleProAspLeuMetArg-----GluAspValGlnPheValMe 398
Db 723 CTTAGTCAGAGCGGTGTGCTCACTCTAGGTTGAGAGGTGAAGCAAACTCCAGTTAGTAAT 782
QY 398 tLeuGlySerGlyAspProGluLeuGluAspTrpMet-----ArgSerThrGluSe 415
Db 783 TGGTGTGTAGCCGCTCCTGGTCAAAGTGTATGGCAGAGAGCGCATCGCATTCGGAATAT 842
QY 415 rIlePheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgI 435
Db 843 TGTGGCTGAACTAGAAGTGAACGATGGCACCACTTCGCTGCTGCGCTAGATCATGAAT 902
```

```
Qy 435 eThr-----AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCys 451
Db 903 CCTCCCTTACTACTACGCTGGCGTGTGTTGGCTGTTGCCAGTCACTACGAACTT 962
Qy 451 sGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrG1 471
Db 963 TGGTTTGTGCTATTGAAGGATGGCTAGCMAAATCCCGTAATCCCGTAATGTAGG 1022
Qy 471 yGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGly 491
Db 1023 TGGATTGCAATTACAGTAGTT-----CCAGAAGTCAC 1055
Qy 491 xGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPhe-----ValAsp----- 506
Db 1056 AGGT---TTACTTGCACCTCCACAGATGAGTCACTTGTGCTACGCCATAGACCGCAT 1112
Qy 507 -IleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnG1 526
Db 1113 ATTAGCCAAACC-AACTTG-----GGCAGATC 1138
Qy 526 uAlaArgHisVallys-----ArgLeuHisValGlyProCys 538
Db 1139 AGCTAGGCACAGCGCGCCGCGAGCTGGAAACCACTTTCAGCTGGCGCGGTGT 1193

RESULT 18
US-10-336-263A-9
; Sequence 9, Application US/10336263A
; Publication No. US20050251882A1
; GENERAL INFORMATION:
; APPLICANT: D'Ordine, Robert L
; APPLICANT: Dotson, Stanton B
; APPLICANT: Duff, Stephen M
; APPLICANT: Sisson, Pamela J
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE NUCLEIC ACID MOLECULES FROM CYANOBACTER
; FILE REFERENCE: 38-21 (52176) A
; CURRENT APPLICATION NUMBER: US/10/336, 263A
; CURRENT FILING DATE: 2003-01-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Nostoc punctiforme
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1272)
; OTHER INFORMATION:
US-10-336-263A-9

Alignment Scores:
Pred. No.: 2.39e-05 Length: 1272
Score: 145.50 Matches: 74
Percent Similarity: 40.2% Conservative: 53
Best Local Similarity: 23.4% Mismatches: 96
Query Match: 5.0% Indels: 93
DB: 8 Gaps: 15

US-10-628-525A-21 (1-539) x US-10-336-263A-9 (1-1272)

Qy 181 GlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHisAlaSerLeuVal 200
Db 316 GGGTTTCTTACTTACC-----TTAATTCAACCAACTACTGTTATCATCTTGGGTG 366
Qy 201 ProValLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220
Db 367 GGTATGGAATG-----AAAAACAGCAATCCCTG 396
Qy 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240
Db 397 ATTCAGGTACAT-----ACTTACCATTCTTTA 423
Qy 241 GlyLeuProProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrPalaArgArg 260
```

```
Db 424 GGAGCCGTTAAA-----TACAGAAGTATTGGTGTATGTTCCCGTAATTGCAGCCACGGA 477
Qy 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAsp 280
Db 478 TTAGCTGTAGAA-----AAAGCCCTGCTTGGAAATATATAGAC 513
Qy 281 ArgIleValThrValSerLysGlyTyrSerTyrGluValThrAlaGluGlyGln 300
Db 514 TGTGTAGTT-----GCNACCAGTCCCAAGAACAAGAA 546
Qy 301 GlyLeuAsnGlnLeuSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320
Db 547 CACATCGCGGTACTCGTTTCTAGCAAAAGGGAACATT----- 582
Qy 321 AspIleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340
Db 583 -----GAATGATTCCTGTGGCACTGACTACTGAC 612
Qy 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIle 360
Db 613 AAATTTGGGGGAATTCAGCGAAT-----GCGGCGCAGAGAAAGTTGGCA-----ATT 660
Qy 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380
Db 661 GCCCAGATGCCAAATAGTTCTATGTTGGTGGCTTTGACCGCGCAAGGAATTTGAA 720
Qy 381 ---LeuIleGlnLeuIleIleProAspLeuMetArg-----GluAspValGlnPheVal 397
Db 721 ACCTTGTGAAGCTGTGTGCCAAGTCTAGTTTAAAGGGGTGAAGCTAACCTCCAGCTAGTA 780
Qy 398 MetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePhe 417
Db 781 ATTGGCGGTGGTAGCGCTCCGCTCAGAGTGAT-----GCAATAGAA 822
Qy 418 LysAspLys-----PheArg 422
Db 823 CGCGATCGCATTCGTAGCATCGTGAATCGGATTAGAAAATTTGTACACCTTTTGGC 882
Qy 423 GlyTyrValGlyPheSerVal---ProValSerHisArgIleThrAlaGlyCysAspIle 441
Db 883 GGTGCGCTAGATGAATACTGTCTCCCTCTCTACTAC-----GCCGCGCTGATGTC 933
Qy 442 LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461
Db 934 TGGTAGTCCCCAGCCATTATGAACCTTTTGGTTAGTTGCTATTGAGGCAATGGCTAGT 993
Qy 462 GlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrVal 477
Db 994 CAGACTCCAGCTGCTAGCTAGTGTGATGTTGGTGGGTTCAGTTTACTGTT 1041

RESULT 19
US-10-336-263A-3
; Sequence 3, Application US/10336263A
; Publication No. US20050251882A1
; GENERAL INFORMATION:
; APPLICANT: D'Ordine, Robert L
; APPLICANT: Dotson, Stanton B
; APPLICANT: Duff, Stephen M
; APPLICANT: Sisson, Pamela J
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE NUCLEIC ACID MOLECULES FROM CYANOBACTER
; FILE REFERENCE: 38-21 (52176) A
; CURRENT APPLICATION NUMBER: US/10/336, 263A
; CURRENT FILING DATE: 2003-01-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Anabaena sp.
; FEATURE:
; NAME/KEY: gene
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/ LOCATION: (1)..(1269)  
/ OTHER INFORMATION:  
US-10-336-263A-3

Alignment Scores:  
Pred. No.: 0.000107  
Score: 139.50  
Percent Similarity: 40.7%  
Best Local Similarity: 24.7%  
Query Match: 4.8%  
DB: 8  
Gaps: 14

Length: 1269  
Matches: 74  
Conservative: 48  
Mismatch: 107  
Indels: 71  
Gaps: 14

US-10-628-525A-21 (1-539) x US-10-336-263A-3 (1-1269)

QY	227	AlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrP	246
DB	382	GCATCCAGGAAGCAACAAAGTTCTATCTCTTTAGGACAGTCAG	435
QY	247	TyrGlyAlaLeuGluTyrPheProGluTyrPheProGluTyrPheProGluTyrP	266
DB	436	TACAAATCTATAGATACGATCTCTTTGGTTGCTACTAAAGTTTATCGGTAGAA	489
QY	267	GluAlaValAsnPheLeuGlyGlyAlaValThrAlaAspArgLeValThrValSer	286
DB	490	-----AAACAAGTATTAGAAACAGCAGCAAGAAATCGTT-----	522
QY	287	LysGlyTyrSerTyrGluValThrAlaGluGlyGlnGlyLeuAsnGluLeuLeu	306
DB	523	-----GCTACCAAGTCTCAAGAACAGCAACATATGCGTGTAGTT	564
QY	307	SerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAsp	326
DB	565	TCTACTAAA-----GGTTACATTTGATATC-----	588
QY	327	ProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGly	346
DB	589	-----GTTCTCGGTGACAGATATTCACCGCTTTGGTTCAATGTCT	630
QY	347	LysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspVal	366
DB	631	-----AGCAAGCCGACAGAGAGAGAAATAGGA-----ATTGATCAAGAA	678
QY	367	IleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp-----Leu	385
DB	679	GTCTGTATGATGAGCGCTTTGATCAACGTAAGGATAGAAACCTTAGTACGT	738
QY	386	IleProAspLeuMetArgGlu-----AspValGlnPheValMetLeuGlySer	403
DB	739	AATGAGTCTCAATTTGGTGCACAGCAATAAACTCAAACTAATTTATTTGGT	798
QY	404	ProGluLeuGluAspTyrMetArg-----SerThrGluSerIlePheLysAsp	419
DB	799	CCTGGTATAGCGATGGCAGAGCGCGATCGCATTTGAGGCCATTTGCAAGAA	858
QY	420	-----LysPheArgGlyTyrValGlyPheSerValProValSerHisArg	434
DB	859	ATGACGGAATGACTAGTTTCCAGGC-----CGCTCAGCCAGATGCTCTCC	912
QY	435	IleThrAlaGlyCysAspIleLeuMetProSerArgPheGluProCysGlyLeu	454
DB	913	TACTACGCTGCGCGTATGTTGCGGTGTTGCCAGTCACTATGAACCTTTTGG	972
QY	455	GlnLeuTyrAlaMetClnTyrGlyThrValProValValHisAlaThrGlyLeu	474
DB	973	GCAATTTGAAGCAATGGCAAGTGGTACACTGTAGTACCGCAGGATGTTGGT	1032
QY	475	AspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyTyrP	494
DB	1033	TTTACGGTAGTTTCC-----GAGAAACCGTTTATTG	1065
QY	495	PheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIle	514
DB	1066	GPACCACCA-----AAAGATATTGCTGCGTTCAACATTGCAATT	1104

RESULT 20

US-11-098-686-9230  
; Sequence 9230, Application US/11098686  
; Publication No. US20060024696A1  
; GENERAL INFORMATION:

; APPLICANT: Kapur, Vivek and Gebhart, Connie J.  
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES  
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING  
; FILE REFERENCE: 09531-128001  
; CURRENT APPLICATION NUMBER: US/11/098,686  
; PRIOR FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US03/31318  
; PRIOR FILING DATE: 2003-10-01  
; PRIOR FILING DATE: 2002-10-04  
; NUMBER OF SEQ ID NOS: 11433  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9230  
; LENGTH: 1341  
; TYPE: DNA  
; ORGANISM: Lawsonia intracellularis  
US-11-098-686-9230

Alignment Scores:  
Pred. No.: 0.000355  
Score: 135.00  
Percent Similarity: 33.9%  
Best Local Similarity: 19.8%  
Query Match: 4.7%  
DB: 14  
Gaps: 23

US-10-628-525A-21 (1-539) x US-11-098-686-9230 (1-1341)

QY	57	GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuPro	76
DB	25	GAATTCCTCCATTTTA---AGTGGAGATTAGGAACAGCATGTTATGGAATGACT	81
QY	77	AlaLeuAlaAlaArgGlyHisArgValMetValMetProArgTyrLeuAsnGly	96
DB	82	GCTCTATTTCGATCAGGAGCCAAATTTGCTTTATTTCTCTCCGA-----	126
QY	97	SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIlePro	114
DB	127	-----TCAGAACACAGCTCAGCTATGTCGACAAATAAACATTTTCTTAA	177
QY	115	-----CysPheGlyGlyGluHisGluValThrPhePheHisGluTyr	128
DB	178	CGTTCTGCTGCTGATGTTGTATTATACAAACAACTTGGTTACTTCACTCA	237
QY	129	ArgAspSerValAspTyrVal-----PheValAspHisPro-----Ser	143
DB	238	TTTCAAGAAATC---TGAAGAAACCTTTTCTATCCGTCCTTATTAAAGCA	294
QY	144	ArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnP	163
DB	295	---CCATATGTTCTCTTAGTCAACACTTTCTGCTTATTTACTTACTCAG	351
QY	164	Thr-----LeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGlu	178
DB	352	ACTGAACACAAATGAAATTTCTACAGTTAGTTTCAGCATGTGCTTTACT	405
QY	179	LeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrp	198
DB	406	TCTGTGTGA-----TATGGTCCACACTTAATGGAAGATATTCGTTAT	459
QY	199	LeuValProValLeuAlaAlaLysTyr-----LeuLeuLeuLeuLeuLeu	208
DB	460	GCTGCACAAATAGCTATGAGAAATATGATGATTTATTCATGCTCCTG	519
QY	209	ArgProTyrGlyValTyr-----LysAspSerArgSerIleLeuValIle	224
DB	520	TACCTGCTGGAATCATAGCTAAAAAATAGTAATAAACCACTTATTAT	579

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225 QY -----AsnLeuAlaHis 228
580 Db GCTACAGAAATTGATCGATGGTGAAGTCACTCACTAATCAAGATATTCTAAATATAGAAAG 639
229 QY GlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGly 248
640 Db GTTGGTCTTGAGCGTGTGATCATATTATTGCTGTCAGC----- 678
249 QY AlaLeuGluTyrValPheProGluTyrPalaArgHisAlaLeuAspLys----- 265
679 Db -----CACTATCTGTAATCTTATTATGAATAATATCATATT 717
266 QY -----GlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThr 284
718 Db CCAGGAGAAAAATTAGTGTGTTTCATAATGCTGTACTTCCAGCA----- 762
285 QY ValSerLysGlyTyrSerThrGluValThrAlaGluGlyGlnGlyLeuAsnGlu 304
763 Db -----TCTGGAATTATACATGCGCAG-----AAAAA 789
305 QY LeuLeuSerArgLysSerValLeuAsnGlyIleValAlaAsnGlyIleAspIleAsnAsp 324
790 Db AGAAATTCARACAAAGATGATGACTC----- 816
325 QY TrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGly 344
816 Db ----- 816
345 QY LysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspVal 364
816 Db ----- 816
365 QY ProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGly-----IleAsp 380
817 Db -----TTCTTGAAGAGTTACACATCAAAAGCCCTCGACACTTTTAAAT 864
381 QY LeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400
865 Db GCTGCATATCTGTTTCAAAAAATTA-----CAAAATGTATGTTTATCATGGCTGGT 918
401 QY SerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLys 420
919 Db AGCGGGGAT---ATGTTACCTCAATGATCCGTAAGAGTAGCTTCATTACGCCCTTGGGAGT 975
421 QY PheArgGlyTyrValGlyPhe-----SerValProValSerHisArgIleThrAlaGly 438
976 Db CGTTTCCACTTACTGGCTTTTACATAACCAAGTTGAACAT---ATATATTCTT 1032
439 QY CysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAla 458
1033 Db AGCAATGTATATGTTATGCTAGTATTCTGAACCATTTTGAATTTACCCACTTGAAGCT 1092
459 QY MetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGlu 478
1093 Db ATAAGACATGGAACACCTGTAAATTATATCAAAAAAATCCGGAGTTAGTGAAGTATTAAAG 1152
479 QY Asn 479
1153 Db AGT 1155

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RESULT 21

```

US-11-098-686-8739
; Sequence 8739, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kepur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318

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; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8739
; LENGTH: 1457619
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-11-098-686-8739

Alignment Scores:
Pred. No.: 2.55 Length: 1457619
Score: 135.00 Matches: 95
Percent Similarity: 33.9% Conservative: 68
Best Local Similarity: 19.8% Mismatches: 156
Query Match: 4.7% Indels: 162
DB: 14 Gaps: 23

US-10-628-525A-21 (1-539) x US-11-098-686-8739 (1-1457619)

QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76
Db 413509 GAATTTCTCCATATTTA---AGTGAGGATTAGGAACAGCATGTTATGGAATGACCTCAG 413565
QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96
Db 413566 GCTCTTATTCGATCAGAGCCAAATTTCTTTTATTTCTCTCGA----- 413610
QY 97 SerAspLysAsnTyrAlaAlaAlaPheTyrThrGluLysHisIleArgIlePro----- 114
Db 413611 -----TCGAACACAGCTCAGCTATGTCGAACAAATAAACATATTTTCTCTAAATA 413661
QY 115 -----CysPheGlyGlyGluHisGluValThrPhePheHisGluTyr 128
Db 413662 CGTTCGTGCTGATGTTGTATTATACAAACATAAAACACTGGTACTTCTCATCAACAA 413721
QY 129 ArgAspSerValAspTrpVal-----PheValAspHisPro-----SerTyrHis 143
Db 413722 TTTCAGAAATC---TGAAGAAAAACTTTCTATCCGCTTATTAAGCAACACTTCAT 413778
QY 144 ArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyr 163
Db 413779 ---CCATATGTTTCTTCTAGTCAACACTTTCTGCTTATTATTCTACTCAGAAATCATTTA 413835
QY 164 Thr-----LeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGlu 178
Db 413836 ACTGAACACAAGAAATCTCTACAGTTAGTTACAGCATGCTTTTACTCTCTCTGT----- 413889
QY 179 LeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSer 198
Db 413890 TCTGGTGGG-----TATGTCACACTTAATGAAGAGATGTTCCGTTATAGCCAAAGCT 413943
QY 199 LeuValProValLeuLeuAlaLysTyr----- 208
Db 413944 GCTGCACAAATAGCTATGGAAGAAATGTATGATTATTATTCATGTCATGCTGCATGACA 414003
QY 209 ArgProTyrGlyValTyr-----LysAspSerArgSerIleLeuValIleHis----- 224
Db 414004 TACCTCTGGAATCATAGCTAAAAAATTTAGTAAATTAACCACTTATGCCCCATGTTTCAT 414063
QY 225 -----AsnLeuAlaHis 228
Db 414064 GCTACAGAAATTTGATCGATGGTGAAGTCACTCACTAATCAAGATATTCTAAATATAGAAAG 414123
QY 229 GlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGly 248
Db 414124 GTTGGTCTTGAGCGTGTGATCATATTATTGCTGTCAGC----- 414162
QY 249 AlaLeuGluTyrValPheProGluTyrPalaArgHisAlaLeuAspLys----- 265
Db 414163 -----CACTATCTGTAATCTTATTATGAATAATATCATATT 414201

```

QY 266 ---GlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThr 284  
 Db 414202 CCAGGAGAAAATAGTGTGTCATATGCTGTACTTCCAGCA----- 414246  
 QY 285 valSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlnGlyLeuAsnGlu 304  
 Db 414247 ---TCTGGAAATATATACATGGCAG-----AAAAAA 414273  
 QY 305 LeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAsp 324  
 Db 414274 AGAAATTCAAACAAAAGATGTACTTC----- 414300  
 QY 325 TrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGly 344  
 Db 414300 ----- 414300  
 QY 345 LysAlaLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspVal 364  
 Db 414300 ----- 414300  
 QY 365 ProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGly-----IleAsp 380  
 Db 414301 -----TTCCTTGGAGAGTTACACATCAAAAAGCCCTGAACACTTTATAAAT 414348  
 QY 381 LeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
 Db 414349 GCTGCATATCTGTTCAAAAAATTA-----CAAATGTATGTTTATCATGCTGT 414402  
 QY 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys 420  
 Db 414403 AGCGGGGAT---ATGTTACCCTCAATGATCCGTAAAGTAGCTTCATTAGCCCTTGGGAGT 414459  
 QY 421 PheArgGlyTrpValGlyPhe-----SerValProValSerHisArgIleThrAlaGly 438  
 Db 414460 CQTTTCCACTTACTGGCTTTTACATAACCAACCAAGTTGAACAT---ATATATTCTCTT 414516  
 QY 439 CysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyra 458  
 Db 414517 ACCAATGTATATGTTATGCTAGTATTTCTGAAACCAATTTGGAAATTACACCCTTGAAGCT 414576  
 QY 459 MetGlnTyrGlyThrValProValValHisAlaThrGlyLeuArgAspThrValGlu 478  
 Db 414577 ATAAGACATGGAACACCTGTATATTATATCAAAACCAATCCGGAGTTAGTGAAGTATTAAAG 414636  
 QY 479 Asn 479  
 Db 414637 AGT 414639

RESULT 22  
 US-10-336-263A-7  
 ; Sequence 7, Application US/10336263A  
 ; Publication No. US20050251882A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: D'Ordine, Robert L  
 ; APPLICANT: Dotson, Stanton B  
 ; APPLICANT: Duff, Stephen M  
 ; APPLICANT: Sisson, Pamela J  
 ; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE NUCLEIC ACID MOLECULES FROM CYANOBACTERIA  
 ; FILE REFERENCE: 38-21 (52176) A  
 ; CURRENT APPLICATION NUMBER: US/10/336,263A  
 ; NUMBER OF SEQ ID NOS: 58  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 1443  
 ; TYPE: DNA  
 ; ORGANISM: Nostoc punctiforme  
 ; FEATURE:  
 ; NAME/KEY: gene  
 ; LOCATION: (1)..(1443)  
 ; OTHER INFORMATION:  
 US-10-336-263A-7

Alignment Scores:  
 Pred. No.: 0.00695 Length: 1443  
 Score: 123.50 Matches: 73  
 Percent Similarity: 39.1% Conservative: 47  
 Best Local Similarity: 23.8% Mismatches: 93  
 Query Match: 4.3% Indels: 95  
 DB: 8 Gaps: 15  
 US-10-628-525A-21 (1-539) x US-10-336-263A-7 (1-1443)  
 QY 215 LysAspSerArgSerIleLeuValIleHisAsn-----LeuAlaHisGlnGly 230  
 Db 364 CGAACAGGCGCGCTATACCTTGATTCACACTAATCTTGGCTTCTGCTGGGTAGGA 423  
 QY 231 ValGluProAlaSerThrTyrProAspLeuGlyLeuProPro-----GluTrp 246  
 Db 424 TTAGAACTTAATCTCGA-----TTGGGACTACCCCAAGTTTCATACCTCATCTCT 474  
 QY 247 TyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGly 266  
 Db 475 ATAGTGTCAGTTTAAATAC-----CGCAATATGGAAATATCCG 510  
 QY 267 GluAlaValAsnPheLeuLysGlyAlaVal-----ValThrAlaAspArg 281  
 Db 511 CGCAGATTTCTGCAATTCGTAATTTGTGGAGAGGGCAATTTTAGAACACAGCAGATTAT 570  
 QY 282 IleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlnGly 301  
 Db 571 GTAATATCC-----ACTAGCCCTCAAGAACGGGAAGAT 603  
 QY 302 LeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp 321  
 Db 604 TTACGTCTAGTTAATTTCCACATCGTCGTATT----- 636  
 QY 322 IleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp 341  
 Db 637 -----AAAGTCATTCCTCGGGATTAACTACTGAACAC 669  
 QY 342 LeuSerGlyLysAlaLysCysGlyAlaLeuGlnLysGluLeuGly-----Leu 358  
 Db 670 TTT-----GGTCTGTCTAGTAAAGATTGCTCGCCAAACAGTTG 708  
 QY 359 ProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGly 378  
 Db 709 GGGATTGCTTCAGATTCTCAGATAATCTTGTATGTAGGACGCTTTGACCCCGCAAGGA 768  
 QY 379 IleAspLeuIle-----GlnLeuIleIlePro 387  
 Db 769 GTTGAACCCCTGGTCAGAGCTTGGCCCAATTTGCTTCAGCATTTCACTCTATCTAGTT 828  
 QY 388 AspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGlu 407  
 Db 829 GGTGGTTGCGGTGAAGAT-----GGAGCAGACTTCAAAGAA----- 864  
 QY 408 AspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGly----- 423  
 Db 865 -----CAACACCGCATTTGAAGTTTGGTGAATGACTGGG-ATTGGAAGCGGTACAGT 917  
 QY 424 -----TrpValGlyPheSerValProValSerHisArgIle-ThrAlaGlyCysAspIle 441  
 Db 918 TTTCACTGACGCAATTTCTCAAGCACTGTTACTTACTTACTTATGCGCAGGG---GATAT 974  
 QY 441 IleLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyraAlaMetGlnTy 461  
 Db 975 CTGCGTTGTACCGAGTTACTTACGCTTTTGGTTAGTGGCGCAATGGAAGCAATGGCAGC 1034  
 QY 461 rGlyThrValProValValHisAlaThrGlyLeuArgAspThrValGluAsnPheAs 481  
 Db 1035 CAGAACACCGGTAATTTGCTAGTAAATGTGGAGGATTTGCAGCATACGTTAGTGCAT----- 1089  
 QY 481 nPropheGlyGluAsnGly 487  
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Db 1090 -----GGTCAAACTGGA 1101
RESULT 23
US-10-932-182A-191168
; Sequence 191168, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191168
; LENGTH: 1459
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-191168
Alignment Scores:
Pred. No.: 0.00905 Length: 1459
Score: 122.50 Matches: 73
Percent Similarity: 34.9% Conservative: 40
Best Local Similarity: 22.5% Mismatches: 82
Query Match: 4.2% Indels: 129
DB: 9 Gaps: 17
US-10-628-525A-21 (1-539) x US-10-932-182A-191168 (1-1459)
QY 220 IleLeuValIleHisAsn-----LeuAlaHisGlnGlyValGluPro 233
Db 374 ATCCAAATGTTCTATCTCATGTAGCGCTTCCACGCTTCACGAGGAAATCTTCAT 433
QY 234 AlaSerThrTyProAspLeuGlyLeuProGluTrpTyGlyAlaLeuGluTrpVal 253
Db 434 GCTAATACTATG-----GGATTGAGAACTGTG 460
QY 254 PheProGlu-----TrpAlaArgArgHis 261
Db 461 TTCACGGACCAATTCCTCTACCGTTTAACTTAACGTCGATTTGGGTGAATTAAG--- 517
QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAspArg 281
Db 518 -----TTGCTAACATTTACCTTGACAAACATAGATCGG 550
QY 282 IleValThrValSerLysGlyTySerTrpGluValThrAlaGluGlyGlyGlnGly 301
Db 551 GTTATATGTTTCTAAT-----ACATGCAAGAA----- 580
QY 302 LeuAsnGluLeuLeuSerSerArgLysSer-----ValLeuAsnGlyIleValAsnGly 319
Db 581 ---AATATGATTGTTAGAACAGAAATTAAGTCTCTGATATAATCTCAGTAATTTCCCAACGCA 637
QY 320 IleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTySerVal 339
Db 638 GTGCTAGCGCAAGATTTCACCAACG----- 664
QY 340 AspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuPro 359
Db 665 ---GATCCTACTGTTGGCCACCAAGAAACAAAGTAGGATAAG----- 706
QY 360 IleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyTrpGlnLysGlyIle 379
Db 707 -----ATAGTGATCGTGTCTATCGGAAGGCTCTTCCAAACAAAGGCTCC 751
QY 380 AspLeuIleGlnLeuIleProAspLeu-----MetArgGluAspValGlnPheVal 397
Db 752 GATTTACTTACTCGCATTAATTCGAAAGATTGTTCTCTCATGATGAAGATGTCGAATTTATA 811
QY 398 MetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePhe 417
Db 812 GTAGCGGCGCATGGT---CCAAAGTTCATAGATTTTCAACAATGATTGAA----- 859
QY 418 LysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAla 437
Db 860 -----AGTCATAGACTACAAAAA 877
QY 438 GlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTy 457
Db 878 CGTGTGCAACTCTTA----- 892
QY 458 AlaMetGlnTyThrValProValValHisAlaThrGlyGlyLeuArgAspThrVal 477
Db 893 -----GGCTCTGTTCCA-----CATGAGAA-----GTCAGGGATGTATTA 928
QY 478 GluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaPro 497
Db 929 -----TGTCAGGTGCATATATATTTACACGCTAGT 958
QY 498 LeuThrThrGlu-----AsnMetPheValAspIleAlaAsnCysAsnIleTyIleGln 515
Db 959 TTAACAGAACCATTTGGTACATTTAGTTGAGCGCCATCTTGTAAATTTGCTAAATTTGTA 1018
QY 516 GlyThrGlnVal 519
Db 1019 ACGACACACAGTC 1030
RESULT 24
US-10-932-182A-191168
; Sequence 191168, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191168
; LENGTH: 1459
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-191168
Alignment Scores:
Pred. No.: 0.00905 Length: 1459
Score: 122.50 Matches: 73
Percent Similarity: 34.9% Conservative: 40
Best Local Similarity: 22.5% Mismatches: 82
Query Match: 4.2% Indels: 129
DB: 9 Gaps: 17
US-10-628-525A-21 (1-539) x US-10-932-182A-191168 (1-1459)
QY 220 IleLeuValIleHisAsn-----LeuAlaHisGlnGlyValGluPro 233
Db 374 ATCCAAATGTTCTATCTCATGTAGCGCTTCCACGCTTCACGAGGAAATCTTCAT 433
QY 234 AlaSerThrTyProAspLeuGlyLeuProGluTrpTyGlyAlaLeuGluTrpVal 253
Db 434 GCTAATACTATG-----GGATTGAGAACTGTG 460
QY 254 PheProGlu-----TrpAlaArgArgHis 261
Db 461 TTCACGGACCAATTCCTCTACCGTTTAACTTAACGTCGATTTGGGTGAATTAAG--- 517
QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAspArg 281
Db 518 -----TTGCTAACATTTACCTTGACAAACATAGATCGG 550
QY 282 IleValThrValSerLysGlyTySerTrpGluValThrAlaGluGlyGlyGlnGly 301
Db 551 GTTATATGTTTCTAAT-----ACATGCAAGAA----- 580
QY 302 LeuAsnGluLeuLeuSerSerArgLysSer-----ValLeuAsnGlyIleValAsnGly 319
Db 581 ---AATATGATTGTTAGAACAGAAATTAAGTCTCTGATATAATCTCAGTAATTTCCCAACGCA 637
QY 320 IleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTySerVal 339
Db 638 GTGCTAGCGCAAGATTTCACCAACG----- 664
QY 340 AspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuPro 359
Db 665 ---GATCCTACTGTTGGCCACCAAGAAACAAAGTAGGATAAG----- 706
QY 360 IleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyTrpGlnLysGlyIle 379
Db 707 -----ATAGTGATCGTGTCTATCGGAAGGCTCTTCCAAACAAAGGCTCC 751
QY 380 AspLeuIleGlnLeuIleProAspLeu-----MetArgGluAspValGlnPheVal 397
Db 752 GATTTACTTACTCGCATTAATTCGAAAGATTGTTCTCTCATGATGAAGATGTCGAATTTATA 811
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QY 262 AlaLeuAspLysGlyGluAlaValAenPheLeuLysGlyAlaValValThralaAspArg 281
Db 518 -----TTGCTAACATTACCTTGACCAACATAGATCG 550
QY 282 IleValThrValSerLysGlyTyrSerTrpGluValThrThralaGluGlyGlnGly 301
Db 551 GTTATATGTTCTTAAT-----ACATGCAAGAA-----580
QY 302 LeuAenGluLeuSerSerArgLysSer-----ValLeuAenGlylleValAenGly 319
Db 581 ----AATATGATTGTTAGACAAAGTAAGTCCGTGATATAATCTCAGTAATCCCAACGCA 637
QY 320 IleAspIleAenAspTrpAenProAlaThrAspLysCysIleProCysHisTyrSerVal 339
Db 638 GTGGTGAGCAAGATTTCACCAAG-----664
QY 340 AspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuPro 359
Db 665 --GATCCTACTGCTGGCCACCAAGAAACAAAGTAGGATAAG-----706
QY 360 IleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIle 379
Db 707 -----ATAGTGATCGTGGTCAATCGGAAGCTCTTTCCAAACAAAGGGTCC 751
QY 380 AspLeuIleGlnLeuIleProAspLeu-----MetArgGluAspValGlnPheVal 397
Db 752 GATTACTTACTCGCATTAATTCGAAGTTGTTCTCATGAGAGATGTCGAATTATA 811
QY 398 MetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePhe 417
Db 812 GTAGCGGCGATGGT---CCAAAGTTATAGATTTTCAACAAATGATTCAA-----859
QY 418 LysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAla 437
Db 860 -----AGTCATAGACTACAAAAA 877
QY 438 GlyCysAspIleLeuMetProSerArgPheGluProCysGlyLeuAenGlnLeuTyr 457
Db 878 CGTGTGCAACTCTTA-----892
QY 458 AlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrVal 477
Db 893 -----GGCTCTGTTCCA-----CATGAGAAA-----GTCAGGAGATGATTA 928
QY 478 GluAenPheAsnProPheGlyGluAenGlyGluGlnGlyThrGlyTrpAlaPheAlaPro 497
Db 929 -----TGTCAAGGTGACATATATTTACACGCTAGT 958
QY 498 LeuThrThrGlu-----AsnMetPheValAspIleAlaAenCysAenIleTyrIleGln 515
Db 959 TTAACAGAGCATTGGTACATTCTAGTTGAGCGCATCTGTAAATTGCTAATTGTA 1018
QY 516 GlyThrGlnVal 519
Db 1019 ACGACACAGTC 1030
RESULT 25
US-10-301-480-65765/c
; Sequence 65765, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65765
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-679174
Alignment Scores:
Pred. No.: 0.0393
Score: 112.00
Percent Similarity: 44.3%
Best Local Similarity: 26.4%
Query Match: 3.9%
Length: 584
Matches: 37
Conservative: 25
Mismatch: 50
Indels: 28
Gaps: 7
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; SEQ ID NO 65765
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-65765
Alignment Scores:
Pred. No.: 0.0393
Score: 112.00
Percent Similarity: 44.3%
Best Local Similarity: 26.4%
Query Match: 3.9%
Length: 584
Matches: 37
Conservative: 25
Mismatch: 50
Indels: 28
Gaps: 7
US-10-628-525A-21 (1-539) x US-10-301-480-65765 (1-584)
QY 248 GlyAlaLeuGluTrpValPhe---ProGluTrpAla-----258
Db 477 GGTTCCTTTTCTGGTCTTCTTGGCCAGCTCGAGTTTGGGGTCAGGAGAAAAGTCTTG 418
QY 259 -----ArgArgHisAlaLeuAspLysGlyGluAlaValAenPheLeuLysGly 274
Db 417 GGCCTGCGATTACAAAGACATTTCTAGACAGGCGAGCTTGTGTACCTGAGTC-----364
QY 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThr 294
Db 363 TCTCTTGGCAGCTCTGCCACCCTTCTCTGTATCTCTTGGTATATAAAATGGGAGTCTTCA 304
QY 295 ThrAlaGluGlyGlyGlnGlyLeuAenGluLeuLeuSerArgLysSerValLeuAen 314
Db 303 ACCAGTGAGGAGGAGAGACAGCTTCTTCTTGGCAGAGCTCTCAATCTATC-----250
QY 315 GlyIleValAenGlyIleAspIleAenAspTrpAenProAlaThrAspLysCys 332
Db 249 TCACTTGCAGGTGTATCAGGCTCACCTGATGG---TGTGAGAGGAGCTTTTGTCCAATC 193
QY 333 -----IleProCysHisTyrSerValAspAspLeuSerGlyLysAla 346
Db 192 CACTGGGAAAAAGTGTCTGAGCTGTCTTCTGTAGATCAGGTATCAGAAATGCC 133
QY 347 LysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeu 366
Db 132 AGTTGTGTGGCTTTCTTCTG-----TTGGGTGAGGAGCTTCAAAACATTCTGCCACTA 79
RESULT 26
US-10-301-480-679174/c
; Sequence 679174, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 679174
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-679174
Alignment Scores:
Pred. No.: 0.0393
Score: 112.00
Percent Similarity: 44.3%
Best Local Similarity: 26.4%
Query Match: 3.9%
Length: 584
Matches: 37
Conservative: 25
Mismatch: 50
Indels: 28
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DB: 10 Gaps: 7
US-10-628-525A-21 (1-539) x US-10-301-480-679174 (1-584)
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Db 477 GGTTCCTTTTCTGGTCTTGTGCGCCAGCTTGTGGGTTCAGGAGAAAGTCTTG 418
Qy 259 -----ArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274
Db 417 GGCCTGCAGTGTACAAAGACATTTCTAGACAGGCGAGCTTGCTGTACCTGAGTC----- 364
Qy 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThr 294
Db 363 TCTCTGCCAGCTGTCGCCACCTTCTCTGTATCTCTGGTATATAAAATGGAGTCTTCA 304
Qy 295 ThrAlaGluGlyGlnGlyLeuAsnGluLeuSerArgLysSerValLeuAsn 314
Db 303 TCTCTGCCAGCTGTCGCCACCTTCTCTGTATCTCTGGTATATAAAATGGAGTCTTCA 304
Qy 295 ThrAlaGluGlyGlnGlyLeuAsnGluLeuSerArgLysSerValLeuAsn 314
Db 303 ACCAGTGAGGAGGAGGAGGAGCTTCTGTGTGTTGGCAGAGCTCTCAATCTATC----- 250
Qy 315 GlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys----- 332
Db 417 GGCCTGCAGTGTACAAAGACATTTCTAGACAGGCGAGCTTGCTGTACCTGAGTC----- 364
Qy 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThr 294
Db 363 TCTCTGCCAGCTGTCGCCACCTTCTCTGTATCTCTGGTATATAAAATGGAGTCTTCA 304
Qy 295 ThrAlaGluGlyGlnGlyLeuAsnGluLeuSerArgLysSerValLeuAsn 314
Db 303 ACCAGTGAGGAGGAGGAGGAGCTTCTGTGTGTTGGCAGAGCTCTCAATCTATC----- 250
Qy 315 GlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys----- 332
Db 417 GGCCTGCAGTGTACAAAGACATTTCTAGACAGGCGAGCTTGCTGTACCTGAGTC----- 364

RESULT 27
US-10-301-480-65766/c
; Sequence 65766, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65766
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-65766
Alignment Scores:
Pred. No.: 0.138 Length: 584
Score: 107.00 Matches: 36
Percent Similarity: 43.6% Conservative: 25
Best Local Similarity: 25.7% Mismatches: 51
Query Match: 3.7% Indels: 28
DB: 9 Gaps: 7
US-10-628-525A-21 (1-539) x US-10-301-480-65766 (1-584)
Qy 248 GlyAlaLeuGluTrpValPhe---ProGluTrpAla----- 258
Db 477 GGTTCCTTTTCTGGTCTTGTGCGCCAGCTTGTGGGTTCAGGAGAAAGTCTTG 418
Qy 259 -----ArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274
Db 417 GGCCTGCAGTGTACAAAGACATTTCTAGACAGGCGAGCTTGCTGTACCTGAGTC----- 364
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Qy 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThr 294
Db 363 TCTCTGCCAGCTGTCGCCACCTTCTCTGTATCTCTGGTATATAAAATGGAGTCTTCA 304
Qy 295 ThrAlaGluGlyGlnGlyLeuAsnGluLeuSerArgLysSerValLeuAsn 314
Db 303 ACCAGTGAGGAGGAGGAGGAGCTTCTGTGTGTTGGCAGAGCTCTCAATCTATC----- 250
Qy 315 GlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys----- 332
Db 249 TCACCTGCAGGTGGTATCAGGCTCACCTGATGG---TGTACAGGAGGAGCTTTGTGCCAATC 193
Qy 333 -----IleProCysHisTyrSerValAspAspLeuSerGlyLysAla 346
Db 192 CACTGGGAAAAAGTGTCTCCTGAGCTGTTTCTGTGCTAGATCAGGTATCAGGAAATGCC 133
Qy 347 LysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeu 366
Db 132 AGTTGTGATGGCTTCTCTCTG-----TTGGGTGAGGAGCTTCAAAACATTTCTGCCACTA 79

RESULT 28
US-10-301-480-679175/c
; Sequence 679175, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 679175
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-679175
Alignment Scores:
Pred. No.: 0.138 Length: 584
Score: 107.00 Matches: 36
Percent Similarity: 43.6% Conservative: 25
Best Local Similarity: 25.7% Mismatches: 51
Query Match: 3.7% Indels: 28
DB: 10 Gaps: 7
US-10-628-525A-21 (1-539) x US-10-301-480-679175 (1-584)
Qy 248 GlyAlaLeuGluTrpValPhe---ProGluTrpAla----- 258
Db 477 GGTTCCTTTTCTGGTCTTGTGCGCCAGCTTGTGGGTTCAGGAGAAAGTCTTG 418
Qy 259 -----ArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274
Db 417 GGCCTGCAGTGTACAAAGACATTTCTAGACAGGCGAGCTTGCTGTACCTGAGTC----- 364
Qy 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThr 294
Db 363 TCTCTGCCAGCTGTCGCCACCTTCTCTGTATCTCTGGTATATAAAATGGAGTCTTCA 304
Qy 295 ThrAlaGluGlyGlnGlyLeuAsnGluLeuSerArgLysSerValLeuAsn 314
Db 303 ACCAGTGAGGAGGAGGAGGAGCTTCTGTGTGTTGGCAGAGCTCTCAATCTATC----- 250
Qy 315 GlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys----- 332
Db 249 TCACCTGCAGGTGGTATCAGGCTCACCTGATGG---TGTACAGGAGGAGCTTTGTGCCAATC 193
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QY 333 -----IleProCysHisTyrSerValAspLeuSerGlyLysAla 346
Db 192 CACTGGGAAAAGTGTTCCTGAGCTGTTCTGTTCTAGATCAGGATCAGGAATGCC 133
QY 347 LysCysLysGlyAlaLeuGlnLysGluLeuProIleArgProAspValProLeu 366
Db 132 AGTTGTGATGGCTTCTTCTG-----TTGGGTGAGGAGCTTCMAAACATCTCTGCCACTA 79

RESULT 29
US-10-932-182A-5377
; Sequence 5377, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5377
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-5377

Alignment Scores:
Pred. No.: 0.66 Length: 1353
Score: 105.00 Matches: 63
Percent Similarity: 36.3% Conservatives: 40
Best Local Similarity: 22.2% Mismatches: 101
Query Match: 3.6% Indels: 80
DB: 9 Gaps: 12

US-10-628-525A-21 (1-539) x US-10-932-182A-5377 (1-1353)
QY 220 IleLeuValIleHisAsn-----LeuAlaHisGlnGlyValGluPro 233
Db 256 ATCCAGATGTTTCATCTCTCATGAGCTTCCACATTTGCCCATGAGGGGATCTGTCAT 315
QY 234 AlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTrpVal 253
Db 316 GCCAATACGATG-----GGATTAAGAAGACTGTC 342
QY 254 PheProGlu-----TyrAlaArgHis 261
Db 343 TTCACAGACCATTCATCTTATGTTTCATATCTAACCTCGATTTGGGTGAACAG--- 399
QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAspArg 281
Db 400 -----TTATTAACCTTTTCTTGACAAATATAGATAGG 432
QY 282 IleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGly 301
Db 433 GTATCTGTGTTTCAAT-----ACATGCAAGAAATAATATGATGTT 474
QY 302 LeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp 321
Db 475 AGAACAGAAATG-----AAACAGATATATTTCGTGATTCGGAACGACGATGGTC 525
QY 322 IleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp 341
Db 526 AGTGAAGATTTTAAGCCAGA-----GACCGCTGATAAT 558
QY 342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg 361
Db 559 AACACGAGAGAAAGACGGGTAAA----- 582
QY 362 ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381
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Db 583 ---GATAAGATAGTGTAGTTATTTGGAAGACTCTTTCCGAATAAAGGGTCTGATTG 639
QY 382 IleGlnLeuIleIleProAspLeu-----MetArgGluAspValGlnPheValMetLeu 399
Db 640 CTTACTCGTATCATTTCCAAAAGTTTGTCTCCACACATGAGAAGATAGATTTATAGTTGCT 699
QY 400 GlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAsp 419
Db 700 GGTGATGGT---CCCAAAATTCATTTTCAACAAATGATTGAAACTTATAGACTGCAG 756
QY 420 LysPheArgGlyTrpValGlyPheSerValProValSerHisArg-----Ile 435
Db 757 AAACGTGTTCAACTTTTGGGA-----TCCGTTGCTCATGAAAAGGTAAGAGATGTT 807
QY 436 ThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGln 455
Db 808 TTGTGTCAGGCGATATATATTTGATGCTAGTTTGCACAGAAGCATTTGGTACAATCTA 867
QY 456 LeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAsp 475
Db 868 GTAGAGGCTGCATCTCTGCAATTTACTGATTGTAACACCAGGTTGGGGGTATTCCAGAG 927
QY 476 ThrValGluAsn 479
Db 928 GTGCTACCCCAAT 939

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US-10-932-182A-5377
; Sequence 5377, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5377
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-5377

Alignment Scores:
Pred. No.: 0.66 Length: 1353
Score: 105.00 Matches: 63
Percent Similarity: 36.3% Conservatives: 40
Best Local Similarity: 22.2% Mismatches: 101
Query Match: 3.6% Indels: 80
DB: 9 Gaps: 12

US-10-628-525A-21 (1-539) x US-10-932-182A-5377 (1-1353)
QY 220 IleLeuValIleHisAsn-----LeuAlaHisGlnGlyValGluPro 233
Db 256 ATCCAGATGTTTCATCTCTCATGAGCTTCCACATTTGCCCATGAGGGGATCTGTCAT 315
QY 234 AlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTrpVal 253
Db 316 GCCAATACGATG-----GGATTAAGAAGACTGTC 342
QY 254 PheProGlu-----TyrAlaArgHis 261
Db 343 TTCACAGACCATTCATCTTATGTTTCAATATCTAACCTCGATTTGGGTGAACAG--- 399
QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAspArg 281
Db 400 -----TTATTAACCTTTTCTTGACAAATATAGATAGG 432
QY 282 IleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGly 301
Db 433 GTATCTGTGTTTCAAT-----ACATGCAAGAAATAATATGATGTT 474
QY 302 LeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp 321
Db 475 AGAACAGAAATG-----AAACAGATATATTTCGTGATTCGGAACGACGATGGTC 525
QY 322 IleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp 341
Db 526 AGTGAAGATTTTAAGCCAGA-----GACCGCTGATAAT 558
QY 342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg 361
Db 559 AACACGAGAGAAAGACGGGTAAA----- 582
QY 362 ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381
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Db 400 -----TTATTAACCTTTTCTTGTGACAAATATAGATAGG 432
Qy 282 IleValThrValSerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGlyGlnGly 301
Db 433 GTTATCTGTGTGTTTCCAAT-----ACATGCAAAAGAAATATGATTGTT 474
Qy 302 LeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp 321
Db 475 AGAACAGAAATG-----AAACACAGATATTATTTCCGTGATTCGGAACGCGAGTGGTC 525
Qy 322 IleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp 341
Db 526 AGTGAAGATTTTAAGCCAGA-----GACCCCTGATTAAT 558
Qy 342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg 361
Db 559 AACAGCGAGAGAGAAAGCGGTAAA----- 582
Qy 362 ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381
Db 583 ---GATAAGATAGTGTGATTGTTATTTGGAAGACTCTTCCGAATAAAGGCTCTGATTG 639
Qy 382 IleGlnLeuIleIleProAspLeu-----MetArgGluAspValGlnPheValMetLeu 399
Db 640 CTTACTCGTATCATTCGAAAGTTTGTCCACACATGAGAGTAGAATTTATAGTTGCT 699
Qy 400 GlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAsp 419
Db 700 GGTGATGGT---CCCAATTCATTGATTTTCAACAAATGATTGAAACTTATAGACTCAA 756
Qy 420 LysPheArgGlyTrpValGlyPheSerValProValSerHisArg-----Ile 435
Db 757 AAACGTGTTCACCTTTTGGGA-----TCCGTTGCTCATGAAAAGGTAAGAGATGTT 807
Qy 436 ThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGln 455
Db 808 TTGTGTCAGGCCGATATATATTGCTAGTCTGATGTTGACAGAGCATTGGTACAAATTTCTA 867
Qy 456 LeuTyrAlaMetGlnTyrGlyThrValProValHisAlaThrGlyGlyLeuArgAsp 475
Db 868 GTAGAGGCTGCATCTCGCAATTTACTGATTGTAAACAACCCAGGTTGGGGGTATTCAGAG 927
Qy 476 ThrValGluAsn 479
Db 928 GTGCTACCCCAAT 939
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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 20:18:18 ; Search time 14734.2 Seconds  
(without alignments)  
2022.653 Million cell updates/sec

Title: US-10-628-525A-21

Perfect score: 2893

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Scoring table: BLOSUM62

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Ygapop 10.0	Ygapext 0.5
Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 7914768 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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-TRANS-human40 cdi -LIST=150 -DOCLALIGN=200 -THR SCORE=spct -THR MAX=100  
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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38: /cgn2\_6/ptodata/1/pna/US099D COMB.seq:  
39: /cgn2\_6/ptodata/1/pna/US099E COMB.seq:  
40: /cgn2\_6/ptodata/1/pna/US100A COMB.seq:  
41: /cgn2\_6/ptodata/1/pna/US100B COMB.seq:  
42: /cgn2\_6/ptodata/1/pna/US101 COMB.seq:  
43: /cgn2\_6/ptodata/1/pna/US102A COMB.seq:  
44: /cgn2\_6/ptodata/1/pna/US102B COMB.seq:  
45: /cgn2\_6/ptodata/1/pna/US103A COMB.seq:  
46: /cgn2\_6/ptodata/1/pna/US103B COMB.seq:  
47: /cgn2\_6/ptodata/1/pna/US103C COMB.seq:  
48: /cgn2\_6/ptodata/1/pna/US103D COMB.seq:  
49: /cgn2\_6/ptodata/1/pna/US103E COMB.seq:  
50: /cgn2\_6/ptodata/1/pna/US103F COMB.seq:  
51: /cgn2\_6/ptodata/1/pna/US104 COMB.seq:  
52: /cgn2\_6/ptodata/1/pna/US105 COMB.seq:  
53: /cgn2\_6/ptodata/1/pna/US106A COMB.seq:  
54: /cgn2\_6/ptodata/1/pna/US106B COMB.seq:  
55: /cgn2\_6/ptodata/1/pna/US107A COMB.seq:  
56: /cgn2\_6/ptodata/1/pna/US107B COMB.seq:  
57: /cgn2\_6/ptodata/1/pna/US107C COMB.seq:  
58: /cgn2\_6/ptodata/1/pna/US107D COMB.seq:  
59: /cgn2\_6/ptodata/1/pna/US107E COMB.seq:  
60: /cgn2\_6/ptodata/1/pna/US107F COMB.seq:  
61: /cgn2\_6/ptodata/1/pna/US107G COMB.seq:  
62: /cgn2\_6/ptodata/1/pna/US108 COMB.seq:  
63: /cgn2\_6/ptodata/1/pna/US109A COMB.seq:  
64: /cgn2\_6/ptodata/1/pna/US109B COMB.seq:  
65: /cgn2\_6/ptodata/1/pna/US109C COMB.seq:  
66: /cgn2\_6/ptodata/1/pna/US110A COMB.seq:  
67: /cgn2\_6/ptodata/1/pna/US110B COMB.seq:  
68: /cgn2\_6/ptodata/1/pna/US110C COMB.seq:  
69: /cgn2\_6/ptodata/1/pna/US110D COMB.seq:  
70: /cgn2\_6/ptodata/1/pna/US111A COMB.seq:  
71: /cgn2\_6/ptodata/1/pna/US111B COMB.seq:  
72: /cgn2\_6/ptodata/1/pna/US112 COMB.seq:  
73: /cgn2\_6/ptodata/1/pna/US117 COMB.seq:  
74: /cgn2\_6/ptodata/1/pna/US600 COMB.seq:  
75: /cgn2\_6/ptodata/1/pna/US601 COMB.seq:  
76: /cgn2\_6/ptodata/1/pna/US602A COMB.seq:  
77: /cgn2\_6/ptodata/1/pna/US602B COMB.seq:  
78: /cgn2\_6/ptodata/1/pna/US603 COMB.seq:  
79: /cgn2\_6/ptodata/1/pna/US604A COMB.seq:  
80: /cgn2\_6/ptodata/1/pna/US604B COMB.seq:  
81: /cgn2\_6/ptodata/1/pna/US605 COMB.seq:  
82: /cgn2\_6/ptodata/1/pna/US606 COMB.seq:  
83: /cgn2\_6/ptodata/1/pna/US607 COMB.seq:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2893	100.0	1620	28	US-09-625-406-20
2	2893	100.0	1620	53	US-10-628-525-20
3	2893	100.0	1620	53	US-10-628-525A-20
4	2861	98.9	1749	24	US-09-402-254-52
5	2861	98.9	1749	49	US-10-336-753-52
6	2861	98.9	1752	53	US-09-625-406-12
7	2861	98.9	1752	53	US-10-628-525-12

Sequence 20, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 52, Appl  
Sequence 52, Appl  
Sequence 12, Appl  
Sequence 12, Appl



## RESULT 1

US-09-625-406-20  
 ; Sequence 20, Application US/09625406  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keeling, Peter  
 ; APPLICANT: Guan, Hanning  
 ; TITLE OF INVENTION: Starch Encapsulation  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
 ; STREET: 5370 Manhattan Circle  
 ; CITY: Boulder  
 ; STATE: CO  
 ; COUNTRY: US  
 ; ZIP: 80303  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/625,406  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/941,445  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Winner, Ellen P  
 ; REGISTRATION NUMBER: 28,547  
 ; REFERENCE/DOCKET NUMBER: 89-97  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 499-8080  
 ; TELEFAX: (303) 499-8089  
 ; INFORMATION FOR SEQ ID NO: 20:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1620 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: not relevant  
 ; MOLECULE TYPE: cDNA to mRNA  
 ; HYPOTHEICAL: NO  
 ; FEATURES:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..1620  
 ; US-09-625-406-20

Alignment Scores:  
 Pred. No.: 0 Length: 1620  
 Score: 2893.00 Matches: 539  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 28 Gaps: 0

US-10-628-525A-21 (1-539) x US-09-625-406-20 (1-1620)

QY 1 CysValAlaLeuSerArgGluAsePLeuGluProGluGlyIleAlaGluGly 20  
 DB 1 TCGCTCGCGAGCTGAGCAGGGAGGACCTCGGCTCGAACCTGAAGGATTCGTAAGGT 60  
 QY 21 SerIleAspAsnThrValValAlaLaserGluGlnAspSerGluIleValValGlyLys 40  
 DB 61 TCCATCGATAACACAGTAGTTGTGGCAAGTACGACAGATTCGAGATTGTGGTGAAG 120  
 QY 41 GluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluLaserPro 60  
 DB 121 GAGCAAGCTCGAGCTAAAGTAACACAAAGCATGTCTTGTAAACCGCGAAGCTTCTCT 180  
 QY 61 TyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAla 80  
 DB 181 TATGCANAGTCTGGGGGTCTAGAGATGTTTGTGGTTCATTGCCAGTTCTCTGTCTCT 240

QY 81 ArgGlyHisArgValMetValMetProArgTyrLeuAsnGlyThrSerAspLysAsn 100  
 DB 241 CGTGGTCACCGTGTGATGGTTGTAATGCCAGATATTTAAATGGTACCTCCGATAAGAT 300  
 QY 101 TyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHis 120  
 DB 301 TATGCAATGTCATTTTACACAGAAAAACACATTCGGATTCCATGCTTTGGCGGTGAACAT 360  
 QY 121 GluValThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisPro 140  
 DB 361 GAAGTTACCTTCTTCATGAGTATAGAGATTGAGTTGACTGGGTGTTTGTGTGATCATCCC 420  
 QY 141 SerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGln 160  
 DB 421 TCATATCACAGACCTCGAAATTTATATGCAGATAAGTTTGGTCTCTTTTGGTATATCAG 480  
 QY 161 PheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaPheLeuLeuLeuGly 180  
 DB 481 TTCAGATACACACTCCTTTGCTATGCTGATGTGAGGCTCCTTTGATCCTTGAATTGGGA 540  
 QY 181 GlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuVal 200  
 DB 541 GGATATATTATGGACAGAAATTCATGTTTGTGTCAATGATTGGCATGCTCTAGTG 600  
 QY 201 ProValLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
 DB 601 CCAGTCTCTTCTGCTGCAAAATATACACCATATGGTGTATTATAAGACATCCCGACGATT 660  
 QY 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240  
 DB 661 CTTGTAATACATAAATTTAGCACATCAGGGGTGTAGAGCTGCAAGACATATCTCGACCTT 720  
 QY 241 GlyLeuProGluTrpTyrGlyAlaLeuGluTyrValPheProGluTrpAlaAaArg 260  
 DB 721 GGGTTGCCACCTGAATGGTATGAGCTCTGGAGTGGGTATTCCCTGAATGGCGAGAGG 780  
 QY 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAsp 280  
 DB 781 CATGCCCTTTGACAAAGGTGAGGAGTTAATTTTGAAGGTGACGTGTGACAGCAGAT 840  
 QY 281 ArgIleValThrValSerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGln 300  
 DB 841 CGAATCGTACTGTCTAGTAAGGTTATTCTGCGAGGTCACTGCTCGAAGGTGACAG 900  
 QY 301 GlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320  
 DB 901 GGCCTCATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACGGAATTTGAAATGGAAT 960  
 QY 321 AspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340  
 DB 961 GACATTAATGATTGGAACCTTCGCCACAGACAAATGTATCCCTGTCTATTTCTGTGAT 1020  
 QY 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIle 360  
 DB 1021 GACCTCTCTGAAAGGCCAAATGTAAGGTGATGCAATGTCAGAGAGCTGGGTATTACCTATA 1080  
 QY 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380  
 DB 1081 AGGCCTGATGTTCTCTGATGGCTTATTTGAAAGGTGCGATTATCAGAAAGCATTTGAT 1140  
 QY 381 LeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
 DB 1141 CTCATTCACTTATCATACCAGATCTCATCGGGAGAGATGTTCAATTTGTCTGCTTGA 1200  
 QY 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys 420  
 DB 1201 TCTGTGTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATCTTCAAGGATAA 1260  
 QY 421 PheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440  
 DB 1261 TTTCTGGATGGTGGATTGATTTAGTGTTCAGTTTCCACCGAATAACTCCCGCTCGCAT 1320

QY 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460  
 Db 1321 ATATTGTTAATGCCATCCAGATTCGAACCTTGTGCTCTCAATCAGCTATATGCTATGCGAG 1380  
 QY 461 TyrGlyThrValProValValHisAlaThrGlyLeuArgAspThrValGluLeuPhe 480  
 Db 1381 TATGGCACAGTTCCTGTTGTCATGCACTGGGGGCTTTAGAGATACCGTGAGAACTTC 1440  
 QY 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTTPAlaPheAlaProLeuThrThr 500  
 Db 1441 AACCTTTTCGGTGAGATGAGAGCGAGGTACAGGTGGGCAATTGCCACCCCTAACCCACA 1500  
 QY 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520  
 Db 1501 GAAACATGTTTGTGGACATTCGAACCTGCAATATCTACATACAGGGAACCAAGTTCCTC 1560  
 QY 521 LeuGlyArgAlaAsnGluAlaArgHisVallysArgLeuHisValGlyProCysArg 539  
 Db 1561 CTGGGAAGGGCTAATGAAGCGAGCATGTCAAAAGACTTCACGTGGGACCATGCGCGC 1617

RESULT 2

US-10-628-525-20  
 ; Sequence 20, Application US/10628525  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keeling, Peter  
 ; Guan, Hanning  
 ; TITLE OF INVENTION: Starch Encapsulation  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
 ; STREET: 5370 Manhattan Circle  
 ; CITY: Boulder  
 ; STATE: CO  
 ; COUNTRY: US  
 ; ZIP: 80303  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/628,525  
 ; FILING DATE: 28-Jul-2003  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/941,445  
 ; FILING DATE: 30-SEP-1997  
 ; APPLICATION NUMBER: US 60/036,855  
 ; FILING DATE: 30-SEP-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Winner, Ellen P  
 ; REGISTRATION NUMBER: 28,547  
 ; REFERENCE/DOCKET NUMBER: 89-97  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 499-8080  
 ; TELEFAX: (303) 499-8089  
 ; INFORMATION FOR SEQ ID NO: 20:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1620 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: Not Relevant  
 ; MOLECULE TYPE: cDNA to mRNA  
 ; HYPOTHETICAL: NO  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..1620  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
 US-10-628-525-20  
 Alignment Scores:  
 Pred. No.: 0 Length: 1620  
 Score: 2893.00 Matches: 539

Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 53 Gaps: 0  
 US-10-628-525a-21 (1-539) x US-10-628-525-20 (1-1620)  
 QY 1 CysValAlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyLeuAlaGluGly 20  
 Db 1 TCGTTCGGGAGCTGAGCGAGGAGGACCTCGGTCTCGAACCTCGAAGGATTCGTGAAGT 60  
 QY 21 SerIleAspAsnThrValValValAlaSerGluGlnAspSerGluIleValValGlyLys 40  
 Db 61 TCCATCGATAACACAGTAGTTGTGCAAGTAGCAGCAAGATTCTGAGATTGTGGTGGAAAG 120  
 QY 41 GluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyLysAlaSerPro 60  
 Db 121 GAGCAAGCTCGAGCTAAAGATAACACAAAGCATTTGTTTGTAAACCGCGGAAGCTTCTCCT 180  
 QY 61 TyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAla 80  
 Db 181 TATGCAAAAGTCTGGGGGCTTAGAGATGTTTGTGGTTCAATGCCAGTTGCTTTTGTGCT 240  
 QY 81 ArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsn 100  
 Db 241 CGTGTCAACCGTGTGATGTTGTAATGCCAGATATTTAAATGGTACCTCCGATAAAGAT 300  
 QY 101 TyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHis 120  
 Db 301 TATGCAAAATGCAATTTTACACAGAAAAACACATTCGATTCATGCTTTTGGCGGTGAACAT 360  
 QY 121 GluValThrPhePheHisGluTyrArgAspSerValAspTTPValPheValAspHisPro 140  
 Db 361 GAAGTTACCTTCTCCATGAGTATAGAGATTCAGTTGACTGGGTGTTTGTGATCATCCC 420  
 QY 141 SerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGln 160  
 Db 421 TCATATACACAGACCTGGAAATTTATATGAGAGATAAGTTTGGTGTCTTTGGTGATAATCAG 480  
 QY 161 PheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGly 180  
 Db 481 TTCAGATACACACTCCTTTGCTATGCTGATGAGGCTCCTTTTGTATCCTTGAATGGGA 540  
 QY 181 GlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTTPHisAlaSerLeuVal 200  
 Db 541 GGATATATTTATGGACAGATTGCAATGTTTGTTCATGATTGGCATGCCAGTCTAGTG 600  
 QY 201 ProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
 Db 601 CCAGTCCCTTCTGCTGCAAAATATAGACCATATGCTGTTTATAAAGACTCCCGCAGCAT 660  
 QY 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240  
 Db 661 CTTGTAATACATAATTTTAGCACATCAGGGTGTAGAGCTGCAAGCACATATCCTGACCTT 720  
 QY 241 GlyLeuProProGluTTPThrGlyAlaLeuGluTTPValPheProGluTTPAlaArgArg 260  
 Db 721 GGGTTGCCACCTGAATGGTATGGAGCTCTGGAGTGGGTATTCCTGTAATGGCGGAGG 780  
 QY 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAsp 280  
 Db 781 CATGCCCTTGACAGGGTGAGGAGTAAATTTTTTGAAGAGGTGCAGTTGTGCAGCAGAT 840  
 QY 281 ArgIleValThrValSerLysGlyTyrSerTTPGluValThrThrAlaGluGlyGln 300  
 Db 841 CGAATCGTGACTGTCAAGGTTTATTCGTGGGAGGTCAACAATGCTGCAAGGTGGACAG 900  
 QY 301 GlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320  
 Db 901 GGCCTCAATGAGCTTTAAGCTCCAGAAAGAGTGTATTAAACGGAATTTGAATGGAATT 960  
 QY 321 AspIleAsnAspTTPAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340

Db 961 GACATTAATGATTGGAACCTCGCACAGACAAATGATATCCCTGTCATTAATTCGTGTGAT 1020  
 Qy 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIle 360  
 Db 1021 GACCTCTCTGGAAAGGCCAAATGTAAGGTGCATTGCGAAGGAGCTGGGTACCTATA 1080  
 Qy 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyLysAsp 380  
 Db 1081 AGGCCTGATGTCCTCTGATGGCTTTATTTGGAAGGTGGATTATTCAGAAAGGCATTGAT 1140  
 Qy 381 LeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
 Db 1141 CTCAATCAACTATATACACAGATCTCATGCGGGAAGATGTTCAATTTGTCTATGCTTGA 1200  
 Qy 401 SerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLys 420  
 Db 1201 TCTGSGTACCCAGAGCTTGAAGATTGGATGAGATCTACAGATCGATCTTCAAGGATAAA 1260  
 Qy 421 PheArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440  
 Db 1261 TTTGCTGGATGGGTGGATTAGTTTCCAGTTTCCACCGAATAACTGCGCGCTCGCAT 1320  
 Qy 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460  
 Db 1321 ATATTGTTAATGCAATCCAGATTCGAACCTTGTGGTCTCAATCAGCTATATGCTATGCG 1380  
 Qy 461 TyrGlyThrValProValValHisAlaThrGlyLeuArgAspThrValGluAsnPhe 480  
 Db 1381 TATGGCAGAGTCTCTGTGTGTCATGCACTGGGGGCTTAGAGATACCGTGGAGAACTTC 1440  
 Qy 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThr 500  
 Db 1441 AACCCCTTTCGGTGAGAAATGAGAGCAGGGTACAGGGTGGGCATTTCGCACCCCTTAACCA 1500  
 Qy 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520  
 Db 1501 GAATAATGTTTGTGACATTCGAACTGCAATCTACATACAGGAACCAAGTCCCTC 1560  
 Qy 521 LeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
 Db 1561 CTGGGAAGGGCTAATGAAGCGGCGCATGTCAAAGACTTCACCTGGGACCATGCCGC 1617

RESULT 3

US-10-628-525A-20  
 ; Sequence 20, Application US/10628525A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KEELING, PETER  
 ; APPLICANT: GAUN, HANPLING  
 ; TITLE OF INVENTION: STARCH ENCAPSULATION  
 ; FILE REFERENCE: 15056-04  
 ; CURRENT APPLICATION NUMBER: US/10/628, 525A  
 ; PRIOR FILING DATE: 2003-07-28  
 ; CURRENT FILING DATE: 2003-07-28  
 ; PRIOR FILING DATE: 2000-07-25  
 ; PRIOR FILING DATE: 2000-07-25  
 ; PRIOR FILING DATE: 1997-09-30  
 ; PRIOR FILING DATE: 1996-09-30  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: PatentIn Ver. 3.3  
 ; SEQ ID NO 20  
 ; LENGTH: 1620  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURES:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1617)  
 US-10-628-525A-20

Alignment Scores:

Pred. No.: 0 Length: 1620  
 Score: 2893.00 Matches: 539  
 Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 53 Gaps: 0  
 US-10-628-525A-21 (1-539) x US-10-628-525A-20 (1-1620)  
 Qy 1 CyValAlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGly 20  
 Db 1 TGGCTCGCGAGCTGAGCAGGAGGACCTCGTCTCGAACCTGAAGGGATTGCTGAAGGT 60  
 Qy 21 SerIleAspAsnThrValValAlaSerGluGlnAspSerGluIleValValGlyLys 40  
 Db 61 TCCATCGATAACACAGTAGTGTGGCAAGTAGCAAGATTCTGAGATTGTGGTGGAAAG 120  
 Qy 41 GluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerPro 60  
 Db 121 GAGCAGCTCGAGCTAAGTAAACAAAGCATTTGTTGTAAACCGCGGAAGCTTCTCCT 180  
 Qy 61 TyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAla 80  
 Db 181 TATGCAAAAGTCTGGGGGTCTAGGAGATGTTTGTGGTTCATTGCCAGTTGCTTGTCT 240  
 Qy 81 ArgGlyHisArgValMetValMetProArgTyrLeuAsnGlyThrSerAspLysAsn 100  
 Db 241 CGTGGTCACCGTGTGATGGTGTGTAATGCCCAGATATTTAAATGGTACCTCCGATAAG 300  
 Qy 101 TyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHis 120  
 Db 301 TATGCAAAATGCAATTTACACAGAAACACATTCGGATTCATGCTTTGGCGGTGAACAT 360  
 Qy 121 GluValThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisPro 140  
 Db 361 GAAGTTACCTTCTTCCATGATATAGATATTCAGTTGACTGGGTGTTGTTGTATCATCCC 420  
 Qy 141 SerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGln 160  
 Db 421 TCATATCAACAGACCTCGNAATTTATATGGAGATAAGTTTGGTGGTCTTTTGGTGAATCAG 480  
 Qy 161 PheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluGly 180  
 Db 481 TTCAGATACACACTCTCTTGTCTATGCTGATGTAGAGGCTCTTTTGAATTTGGGA 540  
 Qy 181 GlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrPheHisAlaSerLeuVal 200  
 Db 541 CGATATATTTATGGACAGAAATTCATGTTGTTGTCATGATTTGGCATGCCAGTCTAGTG 600  
 Qy 201 ProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
 Db 601 CCAGTCTCTTCTGCTGCAAAATATAGACCATATATGGTGTATTAAGACTCCCGCAGCAT 660  
 Qy 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240  
 Db 661 CTGTATATACATATTTAGCACATCATAGGTGTAGAGCTTGCAGAGCACATATCTCTGACT 720  
 Qy 241 GlyLeuProProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArg 260  
 Db 721 CGGTTGCCACCTGAAATGGTATGGAGCTCTGGAGTGGGTATTCCTCAATGGCGGAGAGG 780  
 Qy 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAsp 280  
 Db 781 CATGCCCTTGAACAGGGTGAAGCAGTTAAATTTTTGAAAGGTGCATTTGTGACAGAGAT 840  
 Qy 281 ArgIleValThrValSerLysGlyTyrSerTyrGluValThrThrAlaGluGlyGlyGln 300  
 Db 841 CGAATCGTACCTGTCAAGTAAAGGGTATTCGTGGAGGTCACAACTGCTGNAGGTGACAG 900  
 Qy 301 GlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320  
 Db 901 GGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACCGAATTTGTAATGCAATT 960  
 Qy 321 AspIleAsnAspTyrPheAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340  
 Db 961 GACATTAATGATTGGAAACCTCGCACAGACAAATGATATCCCTGTCATTAATTCGTGTGAT 1020

341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProfil 360  
 1021 GACCTCTCTGGAAAGGCCAAATGTAAGGTGATTCAGAGAGAGCTGGTTTACCTATA 1080  
 361 ArgProAspValProLeuLeuGlyPheLeuGlyArgLeuAspTyrGlnLysGlyLeuAsp 380  
 1081 AGGCTGTGATGTTCTCTGATTGGCTTTATTTGGAAGGTTGGATTATCAGAAAGCATTTGAT 1140  
 381 LeuLeuGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 400  
 1141 CTCATTTCACTTATCATACAGATCTCATGCGGAGAGATGTTCAATTTGTCTATGCTTGA 1200  
 401 SerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLys 420  
 1201 TCTGTGTACCCAGAGCTTGAAGATTGGATGAGATCTACAGATCGATCTTCAAGGATATA 1260  
 421 PheArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440  
 1261 TTTCTGTGGATGGTTGGATTAGTTGTTCCAGTTTCCACCGAATAACTGCGCGCTGCCAT 1320  
 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460  
 1321 ATATTGTTAATGCCATCCAGATTCGAACCTTGTGTCTCAATCAGCTATATGCTATGCAG 1380  
 461 TyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPhe 480  
 1381 TATGSCACAGTTCCTGTGTGTCATGCACTGGGGGCTTAGAGATACCGTGAGAACTTC 1440  
 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThr 500  
 1441 AACCCCTTTCCGTGAGAAAGCAGAGCAGGCTCAGAGGTGGGCATTCGACCCCTAACCCACA 1500  
 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520  
 1501 GAANAACATGTTTGTGGACATTCGAACTCGCAATATCTACATACAGGGAACACAGTCTCTC 1560  
 521 LeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
 1561 CTGGGAAGGGCTAATGAACGAGGATGTCANAGACCTTCACGTGGACCATGCCGC 1617

RESULT 4

US-09-402-254-52  
 ; Sequence 52, Application US/09402254  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Guan, Hanning  
 ; APPLICANT: Keeling, Peter L.  
 ; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN  
 ; TITLE OF INVENTION: HOSTS  
 ; FILE REFERENCE: 2461-52  
 ; CURRENT APPLICATION NUMBER: US/09/402,254  
 ; CURRENT FILING DATE: 1999-10-01  
 ; EARLIER APPLICATION NUMBER: PCT/US98/06660  
 ; EARLIER FILING DATE: 1998-04-03  
 ; EARLIER APPLICATION NUMBER: 60/042,939  
 ; EARLIER FILING DATE: 1997-04-04  
 ; NUMBER OF SEQ ID NOS: 77  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 52  
 ; LENGTH: 1749  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1749)  
 US-09-402-254-52  
 Alignment Scores:  
 Pred. No.: 0 Length: 1749  
 Score: 2861.00 Matches: 539  
 Percent Similarity: 92.5% Conservative: 0  
 Best Local Similarity: 92.5% Mismatches: 0  
 Query Match: 98.9% Indels: 44

DB: 24 Gaps: 1  
 US-10-628-525a-21 (1-539) x US-09-402-254-52 (1-1749)  
 QY 1 CysValAlaGluLeuSerArgGlu----- 8  
 DB 1 TGCCTCGCGAGCTGAGCAGGAGGCGCGCGCGCGCGCTGCGACCCCGCTGCTG 60  
 QY 8 ----- 8  
 DB 61 GCGCCCCGCTCGTCCCGGCTTCCTCGCGCGCGCGCGCGAGCCCGGTCAGCGCGCA 120  
 QY 9 -----AspLeuGlyLeuGluProGluGly 16  
 DB 121 TCGACGCGCGCGCGCTGCCCGACCGCGCGCTCGGTCGCTCGCACTCGAAGGG 180  
 QY 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36  
 DB 181 ATTGCTGAAGGTTCCATCGATAACACAGTAGTTGTGGCAAGTGAGCAAGATTCTGAGATT 240  
 QY 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
 DB 241 GTGGTTGGAAGGAGCAAGCTCGAGCTAAAGTAAACACAAAGCATTTGTCTTTGTAACCGC 300  
 QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
 DB 301 GAAGCTTCTCTTATGCAAGCTCGGGGCTTAGGAGATGTTTGTGTTTCATTGCCAGTT 360  
 QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96  
 DB 361 GCTCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
 QY 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
 DB 421 TCCGATAAGAAATATGCAATGCAATTTACACAGAAACACATTCGGGATTCATGCTTT 480  
 QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136  
 DB 481 GCGGTGACATGAAGTTACCTTCTCCATGAGTATAGAGATTTCAGTTGACTGGGTGTTT 540  
 QY 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
 DB 541 GTTGATCATCCTCATATACAGACCTGCAATTTATATGAGATAAAGTTTGGTGTCTTT 600  
 QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
 DB 601 GGTGATAATCATGTCAGTACAGATACACACTCTCTTCTATGCTGCAATGAGGCTCTTGTATC 660  
 QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196  
 DB 661 CTGTGAATTTGGAGGATATATTTATGACAGAAATTCATGTTGTTGTTGTTGTTGTTGTTGTT 720  
 QY 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
 DB 721 GCCAGTCTAGTCCAGTCTCTCTGCTGCAAAATATAGACCATATGTTGTTTATATAAGAC 780  
 QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
 DB 781 TCCCGCAGCATTTCTTGTATATACATAATTTAGCACATCAGGGGTGAGAGCTCGAAGCACA 840  
 QY 237 TyrProAspLeuGlyLeuProGluTyrPyrGlyAlaLeuGluTyrPyrValPheProGlu 256  
 DB 841 TATCTGACCTTGGGTTGCCACTGCAATGGTATGAGGCTCTGAGTGGGTATTTCCCTGAA 900  
 QY 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
 DB 901 TGGGCGAGGAGCATGCCCTTGAAGGCTGAGGAGTTAAATTTTGAAGGTTGAGATT 960  
 QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrThrAla 296  
 DB 961 GTGACAGACAGATCGAATCTGTGCTGATAGGGGTTATTCGTGGAGGTGCAACTGCT 1020  
 QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle 316





















437 AlaclyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456  
 833 GCCGGCTCGGATATATTTAATGCCATCCAGATTCGAACCTTGTGGTCTCAATCAGCTA 774  
 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
 773 TATGCTATGAGTATGAGCAGATTCCTTGTGTCATGCAACTGGGGCCCTTAGAGATACC 714  
 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAla 496  
 713 GTGGAGAACTTCAACCCCTTTCGGTGAGATGGAGAGCAGGTA CAGGGTGGCAATTCGCA 654  
 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
 653 CCCCTAACCCACAGAAACATGTTTGTGGACATTCGCAACTGCAATATCTACATACAGGA 594  
 517 ThrGlnValLeuLeuGlyAtrGAlaAsnGluAlaArgHisValIysArgLeuHisValGly 536  
 593 ACACAGTCTCTCTGGAGGGCTTAATGAAGCGAGGCAATGTCAAAAGACTTTCAGTGGGA 534  
 537 ProCysArg 539  
 533 CCATGCCGC 525

RESULT 12  
 US-60-094-436-12  
 ; Sequence 12, Application US/60094436  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lightner, Jonathan E.  
 ; APPLICANT: Broglie, Karen E.  
 ; APPLICANT: E. I. du Pont de Nemours and Company  
 ; TITLE OF INVENTION: Modification of Starch Biosynthetic Enzyme Gene  
 ; TITLE OF INVENTION: Expression to Produce Starches in Grain Crops  
 ; FILE REFERENCE: BB-1147-P1  
 ; CURRENT APPLICATION NUMBER: US/60/094,436  
 ; CURRENT FILING DATE: 1998-07-28  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: Microsoft Word version 7.0A  
 ; SEQ ID NO 12  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 US-60-094-436-12

Alignment Scores:  
 Pred. No.: 0 Length: 2008  
 Score: 2832.00 Matches: 538  
 Percent Similarity: 92.3% Conservative: 0  
 Best Local Similarity: 92.3% Mismatches: 1  
 Query Match: 97.9% Indels: 45  
 DB: 74 Gaps: 1

US-10-628-525A-21 (1-539) x US-60-094-436-12 (1-2008)

Qy 1 CysValAlaGluLeuSerArgGlu----- 8  
 Db 119 TGGTGGCGGAGCTGAGCAGGAGGGGCGCGCGCGCGCTGCCACCGCGCTGCTG 178  
 Qy 8 ----- 8  
 Db 179 GCGCCCGCGCTGTCGCGCGCTTCCTCGCGCGCGCGCGCGCGCGCGCGCGCA 238  
 Qy 9 -----AspLeuGlyLeuGluProGluGly 16  
 Db 239 TCGACGCGCGCGCGCTGCGCGCGCGCGCGCGCTCGGCTCGGACCTCGGACCTGAGGG 298  
 Qy 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36  
 Db 299 ATTGCTGAAGGTTCCATCGATAACACAGTAGTGTGGCAAGTTCGAGATTCTGAGATT 358  
 Qy 37 ValValGlyLysGluGlnAlaArgAlaIysValThrGlnSerIleValPheValThrGly 56  
 Db 359 GTGGTTGGAAAGAGGAGCTCGAGCTAAAGTAAACAAAGCAATGTCTTTTGAACCGGC 418

Qy 57 GluAlaSerProTyrAlaIysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
 Db 419 GAAGCTTCTCTTATGCANAGTCTGGGGTCTAGGAGATGTTGTGGTTCATTGCCAGTT 478  
 Qy 77 AlaLeuAlaalaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96  
 Db 479 GCTCTGCTGCTGCTGCTACCGTGTGATGTTAATGCGCCAGATATTTAAATGGTACC 538  
 Qy 97 SerAspIysAsnTyrAlaAsnAlaPheTyrThrGluIysHisIleArgIleProCysPhe 116  
 Db 539 TCCGATGAAGATTTATGCANATGATTTTACAGAAAAACACATTCGGATTCATGCTTT 598  
 Qy 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPhe 136  
 Db 599 GCGGTGAAACATGAAGTTACTTCTTCCATGAGTATAGAGATTCAGTTGACTGGGTGTT 658  
 Qy 137 ValAspIleProSerTyrHisArgProGlyAsnLeuTyrGlyAspIysPheGlyAlaPhe 156  
 Db 659 GTTGATCATCTCTCATATCAAGACCTGGAAATTTATATGAGATTAAGTTTGGTGTCTTT 718  
 Qy 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
 Db 719 GGTGATATTCAGTTTCAGATACACCTCTTGTCTGCTGCTGAGGTCTCTTTGATC 778  
 Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis 196  
 Db 779 CTTGAATTCGGAGATATATTTATGACAGAAATTCATGTTGTTCATGATTCGAT 838  
 Qy 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
 Db 839 GCCAGTCTAGTGCAGTCTCTTGTCTGCAAAATATAGACCATATGTTGTATTAAGAC 898  
 Qy 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
 Db 899 TCCCGCAGCATTCCTGTATATACATAATTTAGACATCAGGGGTAGAGCTCGAAGCACA 958  
 Qy 237 TyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256  
 Db 959 TATCTCTGACCTTGGTGGTCCACCTGAATGGTATGGAGCTCTGGAGTGGTATTCCTGAA 1018  
 Qy 257 TrpAlaArgHisAlaLeuAspIysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
 Db 1019 TGGCGAGGAGGATGCTCCCTTGAAGGGGTAGGCGAGTTAAATTTTGAAGGGTGCAGTT 1078  
 Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
 Db 1079 GTGACAGCAGATCGAATCGTGTGCTGCTGAGTAAAGGGTATTCGTGGGAGGTCAACATGCT 1138  
 Qy 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316  
 Db 1139 GAAGGTGGACAGGGCTCTAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACGGAAAT 1198  
 Qy 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
 Db 1199 GTAAATGGAATTCACATTAATGATTCGAACCTCGCCACAGACAAATGTATATCCCTGTCAT 1258  
 Qy 337 TyrSerValAspAspLeuSerGlyIysAlaIysCysLysGlyAlaLeuGlnLysGluLeu 356  
 Db 1259 TATTCCTGTGATGACCTCTCGAAAGGGCAATGTAAAGGTGCTATTCGAGAGAGGAGCTG 1318  
 Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
 Db 1319 GGTTCATCTAAGGCTGATGTTCTCTGATGGCTTTATTTGGAAGGTGGATATATCAG 1378  
 Qy 377 LysGlyIleAspLeuGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396  
 Db 1379 AAAGCATTCATCTCACTTATCATACCATCTCATGCGGGAAGATGTTCAATTT 1438  
 Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIle 416  
 Db 1439 GTCATGCTGGATCTGGTACCAGAGCTTGAAGATTTGATGATGATCTACAGAGTCGATC 1498

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QY 417 PheLysAspLysPheArgGlyTTPValGlyPheSerValProValSerHisArgIleThr 436
Db 1499 TTCAAGGATAAAATTTCTGGATGGGTGGATTTAGTTTCCAGTTTCCACCGAATAACT 1558
QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456
Db 1559 GCGGGCTGGCATATATTTGTAATGCCATCCAGATTCGAACCTTTGGTCTCAATCAGCTA 1618
QY 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476
Db 1619 TATGCTATGCAATNGCAGATTCCTGTTCCATGCAACTGGGGGCTTTAGAGATACC 1678
QY 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTTPAlaPheAla 496
Db 1679 GTGGAGAACTTCAACCTTTTCGGTGAGATGGAGACAGGGTACAGGGTGGGCAATTCGCA 1738
QY 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516
Db 1739 CCCCTAACACACAGAAACATGTTT-GTGGACATTTGCCAATTCGCAATATCTACATACAGGGA 1797
QY 517 ThrGlnValLeuLeuGlyValArgAlaAsnGluAlaAtqHisValLysArgLeuHisValGly 536
Db 1798 ACACAAGTCTCTCTGGGAAGGGCTAATGAAGCGAGGATGTCAAAAGACTTCACGTRGGGA 1857
QY 537 ProCysArg 539
Db 1858 CCATGCCGC 1866

RESULT 13
US-60-094-436-9
; Sequence 9, Application US/60094436
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Modification of Starch Biosynthetic Enzyme Gene
; FILE REFERENCE: BB-1147-P1
; CURRENT APPLICATION NUMBER: US/60/094,436
; CURRENT FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 9
; LENGTH: 2491
; TYPE: DNA
; ORGANISM: Zea mays
US-60-094-436-9

Alignment Scores:
Pred. No.: 0 Length: 2491
Score: 2832.00 Matches: 538
Percent Similarity: 92.3% Conservative: 0
Best Local Similarity: 92.3% Mismatches: 1
Query Match: 97.9% Indels: 45
DB: 74 Gaps: 1

US-10-628-525A-21 (1-539) x US-60-094-436-9 (1-2491)
QY 1 CysValAlaGluLeuSerArgGlu----- 8
Db 262 TCGTCGCGAGCTGAGCAGGGAGGGCCCGCGCGCGCGCTGCCACCCCGCTGCTG 321
QY 8 ----- 8
Db 322 GCGCCCCCTCGTGCCTCGGCTTCTCTGCGCGCGCGCGCGAGCCCAAGCGGCGGCA 381
QY 9 -----AspLeuGlyLeuGluProGluGly 16
Db 382 TCGACGCCGCCCGCTGCGCCGACCGCGCGCTGGGGACCTCGGTCTCGAACCCTGAAGG 441
QY 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36
Db 442 ATTGCTGAAGGTTCCATCGATAACACAGTAGTTGTGGCAAGTGAGCAAGATTCTGAGATT 501
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QY 37 ValValGlyGlyGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56
Db 502 GTGGTTGGAAAGAGAGAGCTGAGCTAAAGTAACACAAAGCATTTCTTTGTAAACCGGC 561
QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76
Db 562 GAAGCTTCTCCTTATGCAAAAGTCTGGGGCTCTAGGAGATGTTTGTGGTTCAATGCCAGTT 621
QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrIleAsnGlyThr 96
Db 622 GCTCTTGTGCTCGTGGTCAACGCTGATGGTGTAAATGCCAGATATTTAAATGGTACC 681
QY 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116
Db 682 TCCGATAGAAATATGCAANTGCATTTTACACAGAAAAACACATTCGGATTCCTGCTTT 741
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTTPValPhe 136
Db 742 GCGGTGAACATGAAGTTACCTTCTTCCATGATATAGAGATTCAGTTGACCTGGGTGTT 801
QY 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156
Db 802 GTTGATCATCCCTCATATCACAGACCTCGAAATTTATATGAGATAAAGTTTGGTGTCTTT 861
QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176
Db 862 GGTGATAATCAGTTTCAAGATACACATCTCTTCTGTCATGTCATGTAGAGCTCTCTTGATC 921
QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTTPHis 196
Db 922 CTTGAATTTGGGAGGATATATTTATGACAGAAATTCATGTTTGTCTCAATGATGGCAT 981
QY 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216
Db 982 GCCAGTCTAGTCCAGTCTCTTCTGCTGCAAAATATAGACCATATGCTGTTTATAAAGAC 1041
QY 217 SerArgSerIleLeuValIleHisLeuAlaHisGlnGlyValGluProAlaSerThr 236
Db 1042 TCCCGCAGCATTTCTTGTAAATACATAATTTAGCACATCAGGGGTAGAGCTCGAAGCACA 1101
QY 237 TyrProAspLeuGlyLeuProGluTTPTyrGlyAlaLeuGluTTPValPheProGlu 256
Db 1102 TATCTGACCTTGGGTGGCCACTGATGGTATGAGGCTCTGAGTGGGTATTCCTCGAA 1161
QY 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276
Db 1162 TGGGCGAGGAGCATGCCCTTGACAAGGGTGAGGCGAGTTAAATTTTGAAGGTGCAGTT 1221
QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTTPGluValThrAla 296
Db 1222 GTGACAGCAGATCGAATCTGTCTGTAGTAGGGTTATTCGTGGAGGTCAACACTGCT 1281
QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316
Db 1282 GAAGGTGGACAGGGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACCGGAAT 1341
QY 317 ValAsnGlyIleAspIleAsnAspTTPAsnProAlaThrAspLysCysIleProCysHis 336
Db 1342 GTAAATGGAATTTGACATTAATGATTTGGAACCTCGCCACAGACAAAATGTATCCCTGTCAT 1401
QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysValLysGlyAlaLeuGlnLysGluLeu 356
Db 1402 TATCTGTGTGATGACCTCTCTGGAAGGCCAANTGTAAAGGTGCATTCGAAAGGAGCTG 1461
QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
Db 1462 GGTTTTACCTATAAGSCCTGATGTTCTCTGATTGGCTTTTATTGGAAGGTGGATTATATCAG 1521
QY 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396
Db 1522 AAAGCATTTGATCTCATTTCACTTATATACAGATCTCATCGGGAAGATGTTCAATTT 1581
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Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416
Db 1582 GTCATGCTGGATCTGGTACCCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATC 1641
Qy 417 PheLeuAspLeuGlyPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr 436
Db 1642 TTCAGGATAAATTCGTGGATGGTTGGATTAGTTGTTCCAGTTTCCACCGAATAACT 1701
Qy 437 AlaGlyCysAspLeuLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456
Db 1702 GCCGGCTGCGCATATATTTAAATGCCATCCAGATTCGAACCTCTGTGGTCTCAATCAGCTA 1761
Qy 457 TyrAlaMetGlnTyrGlyThrValProValHisAlaThrGlyGlyLeuArgAspThr 476
Db 1762 TATGCTATGAGATGATGCAAGTTCCTGTGTTCATGCAACTGGGGGCTTAGAGATACC 1821
Qy 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAla 496
Db 1822 GTGGAGAACTTCAACCTTTCGGTGAGATGGAGAGAGGGTACAGGGTGGGCATTCGCA 1881
Qy 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516
Db 1882 CCCCTAACCCACAGAAACATGTTTGTGGACATTGGCAACTGCAATATCTACATACAGGA 1940
Qy 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisVallysArgLeuHisValGly 536
Db 1941 ACACAGTCTCTCTGGAGGGCTTAATGAAGCGAGGATGTCAAAGACTTCAAGTGGGA 2000
Qy 537 ProCysArg 539
Db 2001 CCATGCGC 2009
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RESULT 14

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US-09-077-564-1
; Sequence 1, Application US/09077564
; GENERAL INFORMATION:
; APPLICANT: Knight, Mary E.
; APPLICANT: Keeling, Peter L.
; TITLE OF INVENTION: Modification of Starch Synthesis in
; TITLE OF INVENTION: Plants
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA Ag Products
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,564
; FILING DATE: 14-DEC-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/02990
; FILING DATE: 04-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9524938.9
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: SEE 45052/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2992 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:
; CLONE: NUMBER 1
US-09-077-564-1
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Alignment Scores:

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Pred. No.: 0 Length: 2992
Score: 2757.00 Matches: 523
Percent Similarity: 90.9% Conservative: 8
Best Local Similarity: 89.6% Mismatches: 8
Query Match: 95.3% Indels: 45
DB: 20 Gaps: 1
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US-10-628-525A-21 (1-539) x US-09-077-564-1 (1-2992)

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Qy 1 CysValAlaGluLeuSerArgGlu-----8
Db 719 TGCCTGCGGAGCTGAGCAGGAGGGGCCGCCGCCGCTGCCACCCGCGCTGCTG 778
Qy 8 -----8
Db 779 GCGCCCGCGCTGCTGCCGCGCTTCCTGCGCGCGCGCGCGCGCGCGCGCGCA 838
Qy 9 -----AspLeuGlyLeuGluProGluGly 16
Db 839 TCGACGCCGCCGCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGG 898
Qy 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36
Db 899 ATTGCTGAAGGTTCCATCGCATACACAGTAGTTGTGCAAGTTCAGAGATT 958
Qy 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56
Db 959 GTGGTTGGAAGAGCAGCTCGAGCTAAAGTAAACAAGCAAGCATTTGTTTGAACCGGC 1018
Qy 57 GluAlaSerPro-TyrAlaLysSerGlyLeuGlyAspValCysGlySerLeuProVa 76
Db 1019 GAAGCTTCTCTTAATCGAAAGTCTCGGGGCTCTAGGAGATGTTTGTGTTCAATGCCAGT 1078
Qy 76 lAlaLeuAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyIth 96
Db 1079 TGTCTTGTGCTCGCGGTCACCGTGTGATGTTGTAATGCCCGCAGACATTTAAATGTGAC 1138
Qy 96 rSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPh 116
Db 1139 CTCGGATAAGAATTATGCAAAATGCAATTTTACTCAGAAAAACACATTCGGGATTCATTCTT 1198
Qy 116 eGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPh 136
Db 1199 TGGCGGTGAACATGAAGTTACCTTCTCCATGAGTATAGAGATTCAATTGACCTGGGTGTT 1358
Qy 136 eValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPh 156
Db 1259 TGTGTATCATCCCTCATATACAGACCTGGAATTTATATAGGAGATAAGTTTGGTCTTT 1318
Qy 156 eGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuI 176
Db 1319 TGTGTATAATCAGTTCAGATACACACTCTCTTGTATGCTGCGATGAGGCTCCTTTGGT 1378
Qy 176 eLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHi 196
Db 1379 CCTTGAATGGGAGGATATATTATGACAGAAATTCGATGTTGGTTGTCATGATTGGCA 1438
Qy 196 sAlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrIysAs 216
Db 1439 TGCAGTCTAGAGCCAGTCTCTTCTGTCAAAAATATAGACCATATAGTGTGTTTATATAAGA 1498
Qy 216 pSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerTh 236
Db 1499 CTCCCGCAGCATTTCTTGTAAATACATAAATTTAGCACATCAGGGGTGTAGAGCCTCAAGCAC 1558
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QY 236 rTyrProaspLeuGlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProG 256
Db 1559 ATATCTGACCTTGGGTGGCTGAAATGGATGGAGCTCTGGATGGGTATTCCTCA 1618
QY 256 uTrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVa 276
Db 1619 ATGGCGAGAGGCGATGCCCTTGACAAAGGCTGAGGCAATTAATTTTGAAGGTGCA 1678
QY 276 lValThrAlaAspArgLysValThrValSerLysGlyTyrSerTrpGluValThrAl 296
Db 1679 TGTGACAGAGATCGAATCGTACTCTCAGTAAAGGTTATTCATGGGAGGTCAACATCG 1738
QY 296 aGluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyI 316
Db 1739 TGAAGGTGACAGGCGCTCAATGAGCTCTTAAGCTCCAGAAAGATGTTAATACGGAAT 1798
QY 316 eValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHi 336
Db 1799 TGTAAATGGAATTGACATTAATGATTTGGAACCTCGCCACAGACAAATGATCCCTGTCA 1858
QY 336 sTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLe 356
Db 1859 TTATTCGTGTGATGACCTCTCTGAAAGGCTAAATGTAAGGTGCAATTCGAAAGGAGCT 1918
QY 356 uGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGl 376
Db 1919 GGGTTTACCTATAAGCCCTGATGTTCTCTGATTTGCTTTATTTGGNAGATTGGATTATCA 1978
QY 376 nLysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPh 396
Db 1979 GAAAGCAATGATCTCATTAATCATATCATACAGATCTCATCGGAGAAATGTTCAAT 2038
QY 396 eValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIl 416
Db 2039 TGTCAAGTATGATCTGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2098
QY 416 ePheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleTh 436
Db 2099 CTTCAAGGATAAATTTCTGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2158
QY 436 rAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLe 456
Db 2159 TGGCGTGGCGATATATTTGTAATGCATCCAGATTCGAACTTGGTGGTCTCAATCAGCT 2218
QY 456 uTyrAlaMetGlnTyrGlyThrValProValHisAlaThrGlyGlyLeuArgAspTh 476
Db 2219 ATATGCTATGAGTATGGCACAGTTCCTTTGTCCATGCAACTGGGGGCTTAGAGATAC 2278
QY 476 rValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAl 496
Db 2279 CGTGGAGAACTTCAACCTTTTGGTGGATGGAGAGCAGGTACAGGGTGGGCATTTCG 2338
QY 496 aProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGl 516
Db 2339 ACCCTTAACACAGAAACATGTTTGTGGACATTTGCAATTCGAACTGCAATATCTACATACAGG 2398
QY 516 yThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGl 536
Db 2399 AACACAAATTAATTTGGGAAGGCTTAATGAAGCCAGGCTATGCAAAAGAGATTTCATGGTGG 2458
QY 536 yProCysArg 539
Db 2459 ACCATGCCGC 2468

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RESULT 15

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US-10-767-701-13043
; Sequence 13043, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihui
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

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; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 13043
; LENGTH: 2670
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS52_1
US-10-767-701-13043

Alignment Scores:
Pred. No.: 0 Length: 2670
Score: 2753.00 Matches: 522
Percent Similarity: 90.3% Conservative: 6
Best Local Similarity: 89.2% Mismatches: 11
Query Match: 95.2% Indels: 47
DB: 61 Gaps: 1

US-10-628-525A-21 (1-539) x US-10-767-701-13043 (1-2670)
QY 1 CysValAlaGluLeuSerArgGlu----- 8
Db 270 TCGCTCGCGAGCTGAGCAGGAGGCTCCGCGCGAGCGCGCGCGCTGCCACCGCG 329
QY 8 ----- 8
Db 330 CTGCTGGCGCCCCGCTCGTGCCTCTCTCGCGCGCGCGCTCCGAGCCCGAGGGGTGAG 389
QY 9 -----AspLeuGlyLeuGluPro 14
Db 390 CCGGCGTCGACACCGCGCGCGCTGCGCGCGCGCTCTCGGCGACCTCGGTCTCCAACT 449
QY 15 GluGlyIleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSer 34
Db 450 GAAGGATTTGCTGAGGGTTCATCGATGAGCAGTAGTTGTGGCAAGTCAGCAAGATTCT 509
QY 35 GluIleValValGlyGlyGlnAlaArgAlaLysValThrGlnSerIleValPheVal 54
Db 510 GAGATCGTGGTGGAAAGGAGCAAGCTCGAGTAAAGTAAACACAAAGCATTTGTCTTTGA 569
QY 55 ThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeu 74
Db 570 ACTGGCGAAGCTTCTCTTATGCAAGCTCGGGGTCTAGGAGATGTTTGTGTTCAATTG 629
QY 75 ProValAlaLeuAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsn 94
Db 630 CCAGTTGCTCTTGTCTGCTCGTGTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 689
QY 95 GlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIlePro 114
Db 690 GGTACTCTGTATGAAGATTTACGCAATGCAATTTTACACAGAAAGCACATTCGGATTCCA 749
QY 115 CysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrp 134
Db 750 TGTCTTGGCGGTGAACATGAGTTACCTTTTCCATGAGTACAGAGATTTCAGTTGACTGG 809
QY 135 ValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGly 154
Db 810 GTGTTTGTGATCATCCCTCATATCACAGACCTGGAATTTTATATGAGAGATTAAGTTTGT 869
QY 155 AlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaPro 174
Db 870 GCTTTTGGTGAATTAATCAGTTACAGATCACAGCTCTCTTGTCTATGCTGATGAGGCTCT 929
QY 175 LeuIleLeuGluLeuGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAsp 194
Db 930 TTGGTCTTGAATTCGGAGGATATATTTATGACAGAAATTCATGTTTGTGTTGATGAT 989
QY 195 TrpHisAlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyr 214
Db 990 TGGCATGCGAGTCTAGTGCAGTCTCTTCTGTCGCAAAATATAGACCATATGTTGTTTAT 1049

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Qy 215 LysAppSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAla 234  
Db 1050 AAAGACTCCGCGCAGCATCTTGTAAATACATAAATTAGCACATCAGGCGTAGACCTGCA 1109  
Qy 235 SerThrTyProAspLeuGlyLeuProGluTyrGlyAlaLeuGluTyrValPhe 254  
Db 1110 AGCACAATCTCGACCTGGGTGCGCACCTGAATGGTATGGAGCTCTGGAGTGGTATTC 1169  
Qy 255 ProGluTyrAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274  
Db 1170 CCTGAATGGCGCAGGAGCATGCCCTTGACAGGGGTGAGCGAGTAAATTTTGAAGGT 1229  
Qy 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrGluValThr 294  
Db 1230 GCAGTTGTGACAGCAGATCGAATTTGTGACTCTCAGTAAGGTTATTCTATCGGAGTCA 1289  
Qy 295 ThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsn 314  
Db 1290 ACTGCTGAAGGTGACAGGGTCTCAATGAGCTCTTAAGCTCCCGAAGAGTGTATTAAAC 1349  
Qy 315 GlyIleValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCysIlePro 334  
Db 1350 GGAATTTGAATGGAATTTGACATTAATGATTTGACCTCTGCGACGGACAAATGATCCCT 1409  
Qy 335 CysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLys 354  
Db 1410 TGTCAATATTCTGTGATGACCTCTCTGGAAGAACCAATGTAAGTGCATTGCGAAG 1469  
Qy 355 GluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAsp 374  
Db 1470 GAGCTGGGTTTACCTAAGGCTGAGAGTCTCTGATGTTGTTTATTGGAAGATTGGAT 1529  
Qy 375 TyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspVal 394  
Db 1530 TATCAGAAAGGCAATGATCTCACTCACTTATCACTATCACTATCCAGTTCAGTCCGCGACGCT 1589  
Qy 395 GlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGlu 414  
Db 1590 CAATTTGTCTGCTGATGCTGCTGACCCAGAGCTCGAAGACTGGATGAGATCTACAGAG 1649  
Qy 415 SerIlePheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArg 434  
Db 1650 TCGGACTTCAAGGATAAATTTCTGGATGGGTGGATTTTATGTTTCCAGTTTCCACCGA 1709  
Qy 435 IleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsn 454  
Db 1710 ATAACTGCGGCTGCGATATTTGTTAATGCCATCCAGATCCAGACTTGTGTCTCAAT 1769  
Qy 455 GlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArg 474  
Db 1770 CAGCTATATGCTATGAGTATGACACAGTTCTGTTGTCCTCACTGCGGCGCTTAGA 1829  
Qy 475 AspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAla 494  
Db 1830 GATACTGTGGAGAACTTCAACCTTTTGGTGGATGGGTGGATTTTATGTTTCCAGTTTCCACCGA 1889  
Qy 495 PheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIle 514  
Db 1890 TTGCGACCCCTAACCGAAGAACATGTTTGTGGTGGATGGAGAACAGAGGTACAGGCTGGCA 1948  
Qy 515 GlnGlyThrGlnValLeuLeuGlyArgAlaAsnGlyAlaArgHisValLysArgLeuHis 534  
Db 1949 CAAGGAGCACAATCTCTCTGCGAGGCTCATGAAGAGGGCTCATGAAGAGGGCTATGCAAGAGCTTCA 2008  
Qy 535 ValGlyProCysArg 539  
Db 2009 GTGGGACCATGCGCG 2023

## RESULT 16

US-09-654-617-451753

; Sequence 451753, Application US/09654617

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jingdong  
; TITLE OF INVENTION: Annotated Plant Genes  
; FILE REFERENCE: 38-21(15097)D  
; CURRENT APPLICATION NUMBER: US/09/654,617  
; CURRENT FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 463173  
; SEQ ID NO 451753  
; LENGTH: 2216  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
US-09-654-617-451753

Alignment Scores:  
Pred. No.: 0 Length: 2216  
Score: 2735.00 Matches: 508  
Percent Similarity: 98.1% Conservative: 5  
Best Local Similarity: 97.1% Mismatches: 10  
Query Match: 94.5% Indels: 0  
DB: 29 Gaps: 0

US-10-628-525A-21 (1-539) x US-09-654-617-451753 (1-2216)

Qy 17 IleAlaGluGlySerIleAspAenThrValValAlaSerGluGlnAspSerGluIle 36  
Db 1 ATTGCTGAAGGTTCCATCGATGAGACAGTAGTTGTGCAAGTGAGCAAGATTCTGAGATC 60  
Qy 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
Db 61 GTGGTTGGAAGGAGCAGCTCGAGCTAAAGTAACCAAGCAAGCATTTGTTTGAACGGC 120  
Qy 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
Db 121 GAAGCTTCTCTATGCAAGTCTGGGGTCTAGGAGATGTTTGTGGTTCATTGGCCAGTT 180  
Qy 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96  
Db 181 GCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
Qy 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
Db 241 TCTGATAAGAAATTTACGCAATGCAATTTTACAGAAAGACACATTCGATTCATGCTTT 300  
Qy 117 GlyGlyGluHisGluValThrPhePheHisGlyTyrArgAspSerValAspTyrValPhe 136  
Db 301 GCGGTTGAACATGACGTTACCTTTTCCATGACTACAGAGATTTCAGTTGACTGGGTGTT 360  
Qy 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
Db 361 GTTGATCATCCCTCATATCATCAGACCTGGAAATTTATATGGAGATAAGTTTGGTGTCTTT 420  
Qy 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
Db 421 GGTGATAATCAGTTTCAAGTACACGCTCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis 196  
Db 481 CTTGAAATGGAGGATATATTTATGACAGAAATTTGCAATGTTTGTGTAATGATTGGCAT 540  
Qy 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 541 GCCAGTCTAGTGCAGCTCTCTTCTGCTGCAAAATATAGACCATATGCTGTTTATAAAGAC 600  
Qy 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
Db 601 TCCCGCAGCATTTCTGTAATACATAAATTTAGCACATCAGGGGTGAGCCCTGCAAGCACA 660  
Qy 237 TyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256  
Db 661 TATCTCTGACCTTGGGTTGCCACTGTAATGGTATGGAGCTCTGGAGTGGGTATTTCCCTGAA 720  
Qy 257 TrrAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
|||||

Db 721 TGGGCAAGGAGGCGATGCCCTTGACAAGGGGTAGGCGAGTTAAATTTTGTGAAGGTGCAGTT 780  
Qy 277 ValThrAlaAspArgIleValThrValSerIleGlyTyrSerTrpGluValThrAla 296  
Db 781 GTACAGCAGATCGAATGTGACTGTGCTAGTAAGGGTTATTTCATGGGAGGTCAACATGCT 840  
Qy 297 GluGlyGlyGlnGlyLeuAenGluLeuLeuSerArgIleSerValLeuAenGlyIle 316  
Db 841 GAAGGTGGACAGGCTCTCAATGAGCTCTTAAGCTCCGGAAGAGTGTATTAAACGGAAT 900  
Qy 317 ValAenGlyIleAspIleAenAspTrpAenProAlaThrAspIleCysIleProCysHis 336  
Db 901 GTAAATGGAATTCACATTAATGATTGGAACCTCGCAGCGACAAATGTATCCCTTGTCAAT 960  
Qy 337 TyrSerValAspAspLeuSerGlyIleAlaIleCysIleGlyAlaLeuGlnIleGluLeu 356  
Db 961 TATCTCTGTGATGACCTCTCTGGAAGGCCAAATGTAAAGTGCAATGGCAGAGGAGCTG 1020  
Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTrpGln 376  
Db 1021 GGTTTACCTATAAGGCTGAGTCTCTGATTTGCTTTTATTGGAAGATTGGATTATCAG 1080  
Qy 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396  
Db 1081 AAAGGCATGATCTCATTTCACTTATCATACACATCTCATGCGGACGACGTTCAATTT 1140  
Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416  
Db 1141 GTCATGCTTGGATCTGGTGACCCAGAGCTCGAAGACTGGATGAGATCTTACAGAGTCGGAC 1200  
Qy 417 PheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr 436  
Db 1201 TTCAGGATTAATTTCTGTGATGGGTGGATTAGTTAGTTGTTCCAGTTTCCACCGAATACT 1260  
Qy 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAenGlnLeu 456  
Db 1261 GCGGCTGCGCATATATTTTAATGCCATCCAGATTCCAACTTGTGGTCTCAATCAGCTA 1320  
Qy 457 TyrAlaMetGlyTyrGlyThrValProValValHisAlaThrGlyLeuArgAspThr 476  
Db 1321 TATGCTATGAGTATGGCAGATCTCTGTGTCATGGCAACTGGGGGCTTATAGAGATCT 1380  
Qy 477 ValGluAenPheAenProPheGlyGluAenGlyGlnGlyThrGlyTrpAlaPheAla 496  
Db 1381 GTGGAGAACTTCAACCTTTGGTGAGATGGAGAACAGGTACAGGTGGGCTTCGCA 1440  
Qy 497 ProLeuThrThrGluAenMetPheValAspIleAlaAenCysAenIleTyrIleGlnGly 516  
Db 1441 CCCCTAACCCAGGAAACATGTTGTGGACATTTGCGAACTGCAATTTCCGACATACAAGGA 1500  
Qy 517 ThrGlnValLeuLeuGlyArgAlaAenGluAlaArgHisValIleArgLeuHisValGly 536  
Db 1501 GCACAATCTTCTGGGAAGGGCTCATGAAGGGGCGCATGTCAAAAGACTTTCACGTGGGA 1560  
Qy 537 ProCysArg 539  
Db 1561 CCATGCCGC 1569

RESULT 17  
US-09-684-016-451753  
; Sequence 451753, Application US/09684016  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong Annotated Plant Genes  
; TITLE OF INVENTION: 38-21(15097)D  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/684,016  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 09/654,617  
; PRIOR FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 463173  
; SEQ ID NO 451753  
; LENGTH: 2216

; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
US-09-684-016-451753  
Alignment Scores: 0 Length: 2216  
Pred. No.: 0 Matches: 508  
Score: 2735.00  
Percent Similarity: 98.1% Conservative: 5  
Best Local Similarity: 97.1% Mismatches: 10  
Query Match: 94.5% Indels: 0  
DB: 29 Gaps: 0  
US-10-628-525A-21 (1-539) x US-09-684-016-451753 (1-2216)  
Qy 17 IleAlaGluGlySerIleAspAenThrValValAlaSerGluGlnAspSerGluIle 36  
Db 1 ATTGCTGAAGGTTCATCGATCAGACAGTAGTGTGGCAAGTGAGCAAGATTCTTGAGATC 60  
Qy 37 ValValGlyLysGluGlnAlaArgAlaIleValThrGlnSerIleValPheValThrGly 56  
Db 61 GTGGTTGGAAGAGGACAGCTCGAGTAAAGTAAACAAAGCATTTCTTTGTAAGTGGC 120  
Qy 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
Db 121 GAAGCTTCTCCTTATGCAAGTCTGGGGCTTAGGAGATGTTTGTGGTTCATTGCCAGTT 180  
Qy 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrIleAenGlyThr 96  
Db 181 GCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
Qy 97 SerAspLysAenTyrAlaAenAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
Db 241 TCTGATTAAGATTAAGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 300  
Qy 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136  
Db 301 GCGGCTGAACATGAAGTTACCTTTTCCATGAGTACAGAGATTCAGTTGACCTGGGTGTTT 360  
Qy 137 ValAspHisProSerTyrHisArgProGlyAenLeuTyrGlyAspLysPheGlyAlaPhe 156  
Db 361 GTTGATCATCTCCCTCATATCACAGACTGGAAATTTATATGGAGATAAGTTTGGTGTCTTT 420  
Qy 157 GlyAspAenGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
Db 421 GGTGATATCATGTTCAAGTACAGCTCTCTTCTGCTATGCTGCTGCTGCTGCTGCTGCTGCT 480  
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAenCysMetPheValValAenAspTrpHis 196  
Db 481 CTTGAATGGGAGGATATATTTATGACACAGAAATTCATGTCATGCTGCTGCTGCTGCTGCTGCT 540  
Qy 197 AlaSerLeuValProValLeuLeuAlaIleTyrTyrArgProTyrGlyValTyrLysAsp 216  
Db 541 GCGAGTCTAGTGCCAGTCTCTTCTGCTGCAAAATATAGACCATATGCTGCTGCTGCTGCTGCTGCT 600  
Qy 217 SerArgSerIleLeuValIleHisAenLeuAlaHisGlnGlyValGluProAlaSerThr 236  
Db 601 TCCCGCAGCATTTCTTGTAAATACATAATTTAGCACATCAGGGGTAGAGGCTCGAAGCACA 660  
Qy 237 TyrProAspLeuGlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGlu 256  
Db 661 TATCTGACCTTGGGTTGCGACCTGAAATGCTATGAGCTCTCGAGTGGGTATTTCCCTGAA 720  
Qy 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAenPheLeuLysGlyAlaVal 276  
Db 721 TGGCAAGGAGGATGCGCTTGCAGAGGGTAGGCGAGTTAAATTTTGAAGAGGTGCGATT 780  
Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrThrAla 296  
Db 781 GTGACAGCAGATCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
Qy 297 GluGlyGlnGlyLeuAenGluLeuSerSerArgLysSerValLeuAenGlyIle 316  
Db 841 GAAGGTGGACAGGCTCTCAATGAGCTCTTAAAGCTCCCGAAAGAGTGTATTAAACGGAAT 900

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QY 317 ValHengGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336
Db 901 GTAATGGAATGCAATTAATGATGGAAACCTCGACGGCAAAATGATATCCCTTGTCAT 960
QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356
Db 961 TATTCGTGTGATGACCTCTGGAAAGCCAAATGTAAAGTCATTCGACGAGAGCTG 1020
QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
Db 1021 GGTTTACTATAAGCCCTCAAGTTCCTCTGATTTGTTTATTTGGAAGATTGGATTATCAG 1080
QY 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396
Db 1081 AAAGGCATGATCATCTCAACTTATCATACCATCTCTATCGCGGACGAGCTTCAATTT 1140
QY 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416
Db 1141 GTCATGCTTGGATCTGGTACCCAGAGCTCGAGACTGGATGAGATCTACAGAGTCGGAC 1200
QY 417 PheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr 436
Db 1201 TTCAAGCATAAATTTTCGTGATGGTTGGATTTAGTGTTCAGTTTCCACCGGATTAAT 1260
QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456
Db 1261 GCCGGCTCGCATATATTGTTAAATGCCATCCAGATTCGAACCTTGTGGTCTCAATCAGTA 1320
QY 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476
Db 1321 TATGCTATGAGTATGACAGATTCCTCTGTTGTCATGCAACTGGGGCCCTTAGAGATACT 1380
QY 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrPalapheAla 496
Db 1381 GTGAGAACTTCAACCTTTTCGGTGAATGGAGAACAGGGTACAGGGTGGGCATTCGCA 1440
QY 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516
Db 1441 CCCTTACCAACGGAACATATTTGTGGACATTCGGAATTCGCAATTTTCGACATACAGGA 1500
QY 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536
Db 1501 GCACAAATCTTCTGGGAAGGGCTCATGAAGAGGGGCATGTCAAAAGACTTCAAGTGGGA 1560
QY 537 ProCysArg 539
Db 1561 CCATGCGC 1569
```

## RESULT 18

```
US-10-425-115-184334
; Sequence 184334, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 184334
; LENGTH: 1988
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_996C.1
; US-10-425-115-184334
```

Alignment Scores:

Pred. No.: 0 Length: 1988

```
Score: 2681.00 Matches: 499
Percent Similarity: 99.8% Conservativity: 3
Best Local Similarity: 99.2% Mismatches: 1
Query Match: 92.7% Indels: 1
DB: 51 Gaps: 0
```

US-10-628-525A-21 (1-539) x US-10-425-115-184334 (1-1988)

```
QY 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56
Db 2 ATGGTTGGAAAGGAGCAGCTCGAGCTAAAGTAACACAAACATGTCTTTGTAACTGGC 61
QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76
Db 62 GAAGCTTCTCTTATGCAAAAGTCTGGGGTCTAGGAGATGTTGTGGTTCATTGCCAGTT 121
QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96
Db 122 GCTCTTGCTGCTCGTGGTCACTCCGTCGTGTGTTGTAATGCCAGATATTTAAATGGTACC 181
QY 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116
Db 182 TCCGTAAGAAATTAATGCAATGCAATTTACACAGAAACACATTCGATTCGATGCTTT 241
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136
Db 242 GCGGTGAAACATCAAGTTACCTTCTTCCATGAGTATAGAGATTCAGTTGACTGGTGT 301
QY 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156
Db 302 GTTGATCATCCCTCATATCACAGCTCGAAATTTATATGAGATTAAGTTGGTGTCTTT 361
QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176
Db 362 GGTGTAATACAGTTTCAGATACACATCTCTTGTGTATGCTGATGTAGGGTCTCTTGGTC 421
QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196
Db 422 CTGTAATGGGAGGATATATTTATGGACAGAAATTCATGTTGTGTGTTGTTGTTGTTG 481
QY 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216
Db 482 GCAGTCTAGTGCAGCTCTCTTGTGCAAAATATAGACCATATGTTGTTTATAAAGAC 541
QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236
Db 542 TCCCGCAGCATCTCTGTATATACATAATTTAGCAACATCAGGGTGTAGAGCTCGAAGACA 601
QY 237 TyrProAspLeuGlyLeuProProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256
Db 602 TATCTTGACCTTGGTGGTTCACCTGAATGGTATGGAGCTCTGGAGTGGGTATTCCCTGAA 661
QY 257 TrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276
Db 662 TGGCGAGGAGGAGCATGCCCTTGAAGGGGTGAGGCGAGTTAAATTTTGAAGGTGCAAGTT 721
QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296
Db 722 GTGACAGCAGATGCAATCTGACTGTGCTAGTAAAGGTTATTCATGGGAGGTACACACTGCT 781
QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316
Db 782 GAAGGTGGACAGGGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACGGAAAT 841
QY 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336
Db 842 GTAAATGGAAATTCATTAATGATGGAACCTCCGACACACAAATGTATATCCCTGTCAT 901
QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356
Db 902 TATTCGTGTAGTACCTCTCTGGAAAGGCCAAATGTAAAGGTGCATTCGAAAGAGGAGCTG 961
QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
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Db      387 TGGGTTGGATTAGTTCAGTTTCCACCGAATAAATGCCGCTCGATATATTGTTA 328
Qy      444 MetProSerArgPheGluProCysGlyLeuAasnGlnLeuTyrAlaMetGlnTyrGlyThr 463
Db      327 ATGCCATCCAGATTCCGAACCTTGTGGTCTCAATCAGCTATATGCTATGCGAGTATGGCACA 268
Qy      464 ValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAasnPheAasnProPhe 483
Db      267 GTTCCTCTGTGTCATGCAACTGGGGGCTTAGAGATACCGTGGAGAACTTCAACCCCTTTC 208
Qy      484 GlyGluAasnGlyGluGlnGlyThrGlyTTPAlaPheAlaProLeuThrThrGluAasnMet 503
Db      207 GGTGAGAAATGGAGCGAGGTACAGGTGGCATTCGACCCCTAACACAGAAAAATG 148
Qy      504 PheValAspIleAlaAasnCysAasnIleTyrIleGlnGlyThrGlnValLeuLeuGlyValArg 523
Db      147 TT-GTGGACATTGGCACTGCAATATCTACATACAGGGACACAAAGTCTCTCTGGGAAGG 89
Qy      524 AlaAasnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
Db      88 GCTAATGAAGCGAGGCATGTCAAAAGACTTTCAGGTGGGACCATGCCGC 41

RESULT 20
US-10-219-999-13937
; Sequence 13937, Application US/10219999
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)C
; CURRENT APPLICATION NUMBER: US/10/219,999
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/324,109
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/312,544
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 63520
; SEQ ID NO 13937
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1308)
; OTHER INFORMATION:
US-10-219-999-13937

Alignment Scores:
Pred. No.: 0 Length: 1855
Score: 2538.00 Matches: 471
Percent Similarity: 99.8% Conservative: 0
Best Local Similarity: 99.8% Mismatches: 1
Query Match: 87.7% Indels: 1
DB: 43 Gaps: 0

US-10-628-525A-21 (1-539) x US-10-219-999-13937 (1-1855)

Qy      68 GlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetVal 87
Db      1 GGAGATGTTTGTGTTTCATTGCCAGTTGCTCTTGCTGCTCGTGTGTCCCGTGTGATGGTT 60
Qy      88 ValMetProArgTyrLeuAasnGlyThrSerAspLysAasnTyrAlaAasnAlaPheTyrThr 107
Db      61 GTAATGCCAGATATTAAATGGTACCTCCGATAGAAATATTATGCAATATGCAATTTTACACA 120
Qy      108 GluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPheHisGlu 127
Db      121 GAAAAACACATTCGGATTCCATCTTTGGCGGTGAACATGAAGTTTACCTTCTTCCATGAG 180
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Qy      128 TyrArgAspSerValAspTTPValPheValAspHisProSerTyrHisArgProGlyAasn 147
Db      181 TATAGAGATTTCAGTTGACTGGGTGTTTGTGATCATCCCTCATATCACAGACCTTGGAAAT 240
Qy      148 LeuTyrGlyAspLysPheGlyAlaPheGlyAspAasnGlnPheArgTyrThrLeuLeuCys 167
Db      241 TTTATGGAGATAAGTTTGGTGTCTTTTGGTATAAATCAGTTTCAGATACACACTCTCTTGC 300
Qy      168 TyrAlaAlaCysGluAlaProLeuLeuLeuGluLeuGlyGlyTyrIleTyrGlyGlyAasn 187
Db      301 TATGCTGCATGAGGCTCTCTTTGATCCTTGAATTTGGAGGATATATTATGGACAGAA 360
Qy      188 CysMetPheValValAasnAspTTPHisAlaSerLeuValProValLeuLeuAlaAlaLys 207
Db      361 TGCATGTTTGTCTCAATGATTGGCATGCCAGTCTAGTGCAGTCTCTTCTGTGCAAAA 420
Qy      208 TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAasnLeuAla 227
Db      421 TATAGACCATATGTTGTTTATAAAGACTCCCGCAGCATTTCTTGTATAATACATAATTTAGCA 480
Qy      228 HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProProGluTTPThr 247
Db      481 CATCAGGTGTAGAGCTGCAACACATATCTCTGACCTTGGGTGGCCACTGAAATGTAT 540
Qy      248 GlyAlaLeuGluTTPValPheProGluTTPAlaArgArgHisAlaLeuAaspLysGlyGlu 267
Db      541 GGAGCTCTGGAGTGGGTATTCCCTGAATGGCGAGGAGCATGCTCCCTTGACAAAGGTGAG 600
Qy      268 AlaValAasnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLys 287
Db      601 GCAGTTAAATTTTGTAAAGGTGCAGTTGTACACAGCAGATCGAATCGTACTGTCTAGTAAG 660
Qy      288 GlyTyrSerTTPGluValThrThrAlaGluGlyGlyGlnGlyLeuAasnGluLeuLeuSer 307
Db      661 GGTATTCTGTGGAGGTCAAACTGCTGAAGGTGGACAGGCTCTCAATGAGCTCTTAAGC 720
Qy      308 SerArgLysSerValLeuAasnGlyIleValAasnGlyIleAspIleAasnAspTTPAasnPro 327
Db      721 TCCAGAAAGAGTGTATTAACCGAATGTTAAATGGAAATGACATTAAATGATGGACCT 780
Qy      328 AlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLys 347
Db      781 GCCACAGACAAATGTATCCCTGTCTATTATTTCTGTTGATGACCTCTCTGGAAGGCGCAAA 840
Qy      348 CysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuLe 367
Db      841 TGTAAAGGTGCATTGCAAGAGGAGCTGGGTTTTACCTATAGGCTCTGATGTTCTCTGANT 900
Qy      368 GlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleIlePro 387
Db      901 GGCTTTATTGGAAGGTTCGATTATCAGAAAGGCATTGATCTCATCTCACTTATCATACCA 960
Qy      388 AspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGlu 407
Db      961 GATCTCATCGGGAGAGATGTTCAATTTGTCTGATCTGGTCTGATCCAGACCTGAA 1020
Qy      408 AspTTPMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTTPValGlyPhe 427
Db      1021 GATTGATCAGATCTACAGAGTCGATCTTCAAGGATAAATTTCTGTTGAGTGGGTGATTT 1080
Qy      428 SerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArg 447
Db      1081 AGTGTTCAGTTTCCACCGAATAACTGCGGCTGCGATATATTGTTAATGCCATCCAGA 1140
Qy      448 PheGluProCysGlyLeuAasnGlnLeuTyrAlaMetGlnTyrGlyThrValProValVal 467
Db      1141 TTCGAACCTTGTGTTCTCAATCAGCTATATGCTATGCTATGCTATGCTATGCTATGCTATGCT 1200
Qy      468 HisAlaThrGlyGlyLeuArgAspThrValGluAasnPheAasnProPheGlyGluAasnGly 487
Db      1201 CATGCAACTGGGGGCTTAGAGATACCGTGGAGAACTTCAACCCCTTTCGTGTGAATGGA 1260
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QY 488 GluGlnGlyThrGlyTirpAlaPheAlaProLeuThrThrGluAenMetPheValAspIle 507  
Db 1261 GAGCAGGTACAGGGTGGGCAATTCGACCCCTAACACACAGAAACATGTT-GTGGACATT 1319  
QY 508 AlaAsnCyAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAenGluAla 527  
Db 1320 GCGAACTGCAATATCTACATACAGGGAACACAAAGTCCTCTCGGAAGGCTAATGAAGC 1379  
QY 528 ArgHisValIleArgLeuHisValGlyProCysArg 539  
Db 1380 AGGCATGTCAAAGACTTCACGTGGGACCATGCGC 1415  
RESULT 22  
US-10-425-114-19497  
; Sequence 19497, Application US/10425114  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 19497  
; LENGTH: 1855  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3150-035-F10\_PLI  
US-10-425-114-19497

Alignment Scores:  
Pred. No.: 0 Length: 1855  
Score: 2538.00 Matches: 471  
Percent Similarity: 99.8% Conservative: 0  
Best Local Similarity: 99.8% Mismatches: 1  
Query Match: 87.7% Indels: 1  
DB: 51 Gaps: 0

US-10-628-525A-21 (1-539) x US-10-425-114-19497 (1-1855)

QY 68 GlyAspValCysGlySerLeuProValAlaLeuAlaAArgGlyHisArgValMetVal 87  
Db 1 CGAGATGTTTGTGGTTTCATTGCGAGTTGCTCTTGCTGCTCGTGGTCACCGTGTGATGTT 60  
QY 88 ValMetProArgTyrIleuAenGlyThrSerAspLysAenTyrAlaAsnAlaPheTyrThr 107  
Db 61 GTAATGCCAGATATTTAAATGGTACCTCCGATAGAATTATGCAAAATGCATTTTACACA 120  
QY 108 GluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlu 127  
Db 121 GAAAAACACATTCGGATTCATGCTTTGGGGTGAACATGAAGTTACCTTCTTCATGAG 180  
QY 128 TyrArgAspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAen 147  
Db 181 TATAGAGATTCAGTTGACTGGGTGTTTGTGATCATCCCTCATATCACAGACTCGNAAT 240  
QY 148 LeuTyrGlyAspLysPheGlyAlaPheGlyAspAenGlnPheArgTyrThrIleuLysCys 167  
Db 241 TTATATGGAGATAAGTTTGGTGTCTTTGGTGATAATCAGTTTCCAGATACACATCTCTTGC 300  
QY 168 TyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAen 187  
Db 301 TATGCTGCATGTGAGGCTCTTTGATCTTGAATGGGAGGATATATTTATGGACAGAT 360  
QY 188 CysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaLys 207  
Db 361 TGCATGTTTGTGTTCAATGATTTGGCATGCCAGTCTAGTGCCAGTCTCTTCTTCTGCAAA 420

QY 208 TyrArgProTyrGlyValTyrIysAspSerArgSerIleLeuValIleHisAenLeuAla 227  
Db 421 TATAGACCATATGGTGTATTAAGACTCCCGACGATTTCTTGTAATACATAATTTAGCA 480  
QY 228 HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyr 247  
Db 481 CATCAGGGTGTAGAGCTCGAAGCACATATCTGACCTTGGGTGGCACCTGANTGGTAT 540  
QY 248 GlyAlaLeuGluTyrPheProGluTyrPheProGluTyrPheProGluTyrPheProGlu 267  
Db 541 GGAGCTCTGGAGTGGGTATTCCTGAATGGGCGAGGCGCATGCCCTTGACAGGGGTGAG 600  
QY 268 AlaValAenPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerIys 287  
Db 601 GCAGTTAAATTTTGAAGGTGCAGTTGTGACAGCAGATCGAATCTGTACTGTGCTAAG 660  
QY 288 GlyTyrSerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAenGluLeuLeuSer 307  
Db 661 GGTATTCCTGGAGGTCACTGCTGAAGGTGGACAGGGCTCAATGAGCTCTTAAGC 720  
QY 308 SerArgLysSerValLeuAenGlyIleValAenGlyIleAspIleAenAspTrpAenPro 327  
Db 721 TCCAGAAAGAGTGTATTAACCGAATTTGTAATGGAATGACATTAATGATTGGAACCT 780  
QY 328 AlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLys 347  
Db 781 GCCACAGACAAATGATCCCTGTCTATTATCTGTTGATGACCTCTCTCGAAGGCCAA 840  
QY 348 CysLysGlyValaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIle 367  
Db 841 TGTAAGGTGCATTCGACAGAGGAGCTGGGTTTACCTATAGGCGCTGATGTTCTCTGAT 900  
QY 368 GlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIlePro 387  
Db 901 GGCTTTATTTGGAAGGTGGATTTATCAGAAAGCAATGATCTCATTCACCTTATCATCCA 960  
QY 388 AspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGlu 407  
Db 961 GATCTCATCGGGAGAGATGTTCAATTTGTCATGCTTGGATCTGGTGACCCAGAGCTTGA 1020  
QY 408 AspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPhe 427  
Db 1021 GATTGGATGAGATCTACAGAGTCGATCTTCAAGGATAAATTTCTGGATGGGTGGATTT 1080  
QY 428 SerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArg 447  
Db 1081 AGTGTTCAGATTTCCACCGAATAACTGCCGCTCGATATATTTGTTAATGCCATCCAGA 1140  
QY 448 PheGluProCysGlyLeuAenGlnLeuTyrAlaMetGlnTyrGlyThrValProValVal 467  
Db 1141 TTCGAACCTTGGGTCTCAATCAGCTATATGCTATGCTAGTATGGCACAGTCTCTGTGTG 1200  
QY 468 HisAlaThrGlyGlyLeuArgAspThrValGluAenPheAsnProPheGlyGluAenGly 487  
Db 1201 CATGCACTGGGGCTTTAGAGATACCGTGGAGAACTTCAACCTTTCGTGGAGATGGA 1260  
QY 488 GluGlnGlyThrGlyTyrPheAlaPheAlaProLeuThrThrGluAenMetPheValAspIle 507  
Db 1261 GAGCAGGGTACAGGGTGGGCATTCGCACCCCTTAACACAGAAAAACATGTT-GTGGACAT 1319  
QY 508 AlaAenCysAenIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAenGluAla 527  
Db 1320 GCGAACTGCAATATCTACATACAGGGAACACAAAGTCTCTCTGGGAAGGCTAATGAAGC 1379  
QY 528 ArgHisValLysArgLeuHisValGlyProCysArg 539  
Db 1380 AGGCATGTCAAAGACTTCACGTGGGACCATGCGC 1415

RESULT 22

US-10-425-114A-19497  
; Sequence 19497, Application US/10425114A  
; GENERAL INFORMATION:





```
; NAME/KEY: CDS
; LOCATION: (3)...(1307)
; OTHER INFORMATION: Clone ID: LIB3150-035-F10_FLI
US-60-312-544-3744

Alignment Scores:
Pred. No.: 0 Length: 1854
Score: 2532.00 Matches: 470
Percent Similarity: 99.8% Conservative: 0
Best Local Similarity: 99.8% Mismatches: 1
Query Match: 87.5% Indels: 1
DB: 78 Gaps: 0

US-10-628-525A-21 (1-539) x US-60-312-544-3744 (1-1854)

QY 69 AspValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValVal 88
DB 3 GATGTTGGTTCATTTGCCAGTTGCTCTTGCTGCTGGTGCACCGTGTGATGGTTGTA 62
QY 89 MetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGlu 108
DB 63 ATGCCAGATATTTAAATGGTACCTCCGATAGAATTATGCAATGCAATTTACACAGAA 122
QY 109 LysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyr 128
DB 123 AAACACATTCGGATTCATGCTTTGGCGGTGAACATGAAGTTTACCTTCTTCATGAGTAT 182
QY 129 ArgAspSerValAspTyrValPheValAspHisProSerTyrHisArgProGlyAsnLeu 148
DB 183 AGAGATTCATGTTGACTGGGTGTTGTTGATCATCTCCCTCATATACACAGACCTGGAAATTTA 242
QY 149 TyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyr 168
DB 243 TATGGAGATAAATTTGGTCTTTTGGTGATATCAGTTCAGATACACATCTCTTTGCTAT 302
QY 169 AlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCys 188
DB 303 GCTGCATGTGAGGCTCTTTGATCTCTTGAATGGGAGGATATATTATGGACAGAAATTCG 362
QY 189 MetPheValValAsnAspTyrHisAlaSerLeuValProValLeuLeuAlaIalysTyr 208
DB 363 ATGTTTGTTCATGATGGATCCAGTCTAGTGCACGATCTCTTCTGCTGCAAAATAT 422
QY 209 ArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHis 228
DB 423 AGACCATATGGTGTATTAAGACTCCCGACATCTCTTGTATATCATATTTAGACAT 482
QY 229 GlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProProGluTyrTyrGly 248
DB 483 CAGGGGTAGAGCCTGCAAGCACATATCTGACCTTGGGTGGCCACCTGAATGGTATGGA 542
QY 249 AlaLeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeuAspLysGlyGluAla 268
DB 543 GCTCTGGAGTGGGTATTCCTGAATGGGCGAGGAGGCGATGCCCTTGACAAAGGTCAGGCA 602
QY 269 ValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGly 288
DB 603 GTTATATTTTGAAGGTGCATTTGTGACAGCAGATCGATCTGACTGTCTAGTAAAGGT 662
QY 289 TyrSerTyrGluValThrThrAlaGluGlyGlnGlyLeuAsnGlnLeuLeuSerSer 308
DB 663 TATTCGTGGAGGTCAACAATCTGCTGAAGGTGCACAGGCGCTCAATGAGCTCTTAAGCTCC 722
QY 309 ArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTyrAsnProAla 328
DB 723 AGAAAGAGTGTATTAACCGAATTTGAATGAATTTGACATTAATGAATGGAAACCTGCC 782
QY 329 ThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCys 348
DB 783 ACAGACAAATGTATCCCTGTCATTTATCTGTGATGACCTCTCTGGAAAGGCCAAATGT 842
QY 349 LysGlyAlaLeuGlnLysGlnLeuGlyLeuProIleArgProAspValProLeuIleGly 368
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DB 843 AAAGGTGCATTGCAGAAAGGAGCTGGGTTTACCTATATAAGGCGCTGATGTTCTCTGATTGGC 902
QY 369 PheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIlelleProAsp 388
DB 903 TTTATTTGGAAGGTTCGATTTATCAGAAAGCATTTGATCTCATTTCACTTATCATACCAGAT 962
QY 389 LeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAsp 408
DB 963 CTCATCGGGAGAGATGTTCAATTTGTCATGCTTGGATCTGGTGACCCAGAGCTTTGAAGAT 1022
QY 409 TrpMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPheSer 428
DB 1023 TCGATGAGATCTACAGAGTCGATCTTCAAGGATAAAATTTTCGTGGATGGGTTCGATTTAGT 1082
QY 429 ValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPhe 448
DB 1083 GTTCCAGTTTCCACCGCAATAACTCCGCGCTCGCATATATTGTTAATGCCATCCAGATTC 1142
QY 449 GluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHis 468
DB 1143 GAACTTGTGGTCTCAATCAGCTATATGCTATGCAATGCGACAGATTCCTGTTGTCCAT 1202
QY 469 AlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGlu 488
DB 1203 GCAACTGGGGGCTTAGAGATACCGTGGAGAACTTCAACCTTTCGGTCAGAAATGGAGAG 1262
QY 489 GlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAla 508
DB 1263 CAGGCTACAGGCTGGGCAATTCGACCCCTTAACACAGAAACATGTT-GTGGACATTTGCG 1321
QY 509 AsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArg 528
DB 1322 AACTGCATATCTCATACAGGGAACACAGTCTCTCTGGGAAGGCTTAATGAAGCGAGG 1381
QY 529 HisValLysArgLeuHisValGlyProCysArg 539
DB 1382 CATGTCAAAGACTTCACGTGGGACCATGCCGC 1414

RESULT 24
PCT-US03-41098-141
; Sequence 141, Application PC/TUS0341098
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations, AG
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: STRESS-RELATED POLYPEPTIDES AND USES THEREFOR
; FILE REFERENCE: 1392-10-20 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/41098
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US 60/436,564
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patencin version 3.2
; SEQ ID NO 141
; LENGTH: 1881
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1881)
PCT-US03-41098-141

Alignment Scores:
Pred. No.: 0 Length: 1881
Score: 2525.50 Matches: 475
Percent Similarity: 95.8% Conservative: 31
Best Local Similarity: 80.5% Mismatches: 33
Query Match: 87.3% Indels: 51
DB: 2 Gaps: 3

US-10-628-525A-21 (1-539) x PCT-US03-41098-141 (1-1881)

QY 1 CysValAlaGluLeuSerArgGlu-----:::
|||||
```

Db 100 TCGTGGCGGAGCTGACGAGGACGGTGGTGGCGGACGCCCGCTGGCACCGCGCCG 159  
Qy 8 ----- 8  
Db 160 CTGGTGAAGCAGCGCGTCTCGCGACCTTCTCGTGGCGAGCTGCAGCCACCGCGGCC 219  
Qy 9 -----AspLeuGly----- 11  
Db 220 ACGCAGTGGCGGCGCGCGCGCGACCCCGCGCGCTGGCGGACTCCGCGCTGGGGAG 279  
Qy 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAenThrValValAla 29  
Db 280 ATCAGCGCCGATCTAGAGGTCTCACAGAGATTCATCCACAAACAATTTTGGCT 339  
Qy 30 SerGluClnAspSerGluIleValValGlyGluGlnAlaAlaArgAlaValThrGln 49  
Db 340 AGTGAGCAGGAGCTGAGATCATGGATGTGAGGAGCAAGCTCAAGCTAAAGTAACACGC 399  
Qy 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69  
Db 400 AGCGTGTCTTGTAAACCGGTGAAGCTTCTCTTATGCAAAAGTCAGGTGAGCTAGGAGAT 459  
Qy 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValMet 89  
Db 460 GTTGTGGTTCATGCCAATGTCTTGTCTTCTGTGGTTCATCGTGTGATGGTTGTAAG 519  
Qy 90 ProArgTyrLeuAenGlyThrSerAspLysAsnTyrAlaAenAlaPheTyrThrGluLys 109  
Db 520 CCAGATACATGAACCGGGCTTGAACAAAATTTTGCAAACGCAATTTTACACGTAGNAG 579  
Qy 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129  
Db 580 CACATTAAGATTCATGCTTGTGGCGAGAACATGAAGTTACTTTTTCACGAGTAGG 639  
Qy 130 AspSerValAspTyrValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyr 149  
Db 640 GATTCCTGTGATGGGTGTGTGTGATCATCCCTCATCATAGACTGGAATTTGTAT 699  
Qy 150 GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla 169  
Db 700 GGAGATAAATTTGGTGTCTTGGCGATATATCATCTCAGATACACATCTCTGTGCTATGCG 759  
Qy 170 AlaCysGluAlaProLeuIleLeuGluGlyTyrIleTyrGlyGlnAenCysMet 189  
Db 760 GCGTGTGAAGCCCATTAATCTTGAACCTGGGAGSATATATCTATGACAGAAATGCATG 819  
Qy 190 PheValValAsnAspTyrHisAlaSerLeuValProValLeuLeuAlaLysTyrArg 209  
Db 820 TTTGTTGTGAATGGCATGCCAGTCTGTGCCAGTCTTCTGCTGCAAAATATAGA 879  
Qy 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGln 229  
Db 880 CCATATGGTGTTTACAGGAGATGCCGAGTGTCTTGTGTATCATATCTAGCACATCAG 939  
Qy 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProProGluTyrTyrGlyAla 249  
Db 940 GGTGTGGAGCCCTGCCAGTACATATCTGACCTGGGATGCCACTGAATGGTATGGAGCA 999  
Qy 250 LeuGluTyrValPheProGluTyrAlaArgAtcHisAlaLeuAspLysGlyGluAlaVal 269  
Db 1000 TTAGATGGGTGTTCAGAGTGGCGAGCGGCGCATGCCCTTGACAAAGGGTGGAGGATC 1059  
Qy 270 AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr 289  
Db 1060 AATTTTTTAAAGGCGCAGTTGTGACAGCAGATCGAATTTGTGACTGTGACCGAGGGTAT 1119  
Qy 290 SerTyrGluValThrAlaGluGlyGlyGlnGlyLeuAenGlnLeuLeuSerArg 309  
Db 1120 TCATGGAGGTCAAACTGCTGAAGGTGGCGAGGCTCAATGAGCTCTTAAGCTCCCG 1179  
Qy 310 LysSerValLeuAenGlyIleValAenGlyIleAspIleAsnAspTrpAsnProAlaThr 329  
Db 1180 AAGAGTGTATTGATGGAATTTGAAATGAATGAATTAATGAATTTGGAACCATCCACA 1239

Qy 330 AspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLys 349  
Db 1240 GACAAGTTTCTCCCTTATCATTTCTGTGTGACCTGTCCGGAAGGCCAAGTGTAAA 1299  
Qy 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe 369  
Db 1300 GCTGAATTTGCAGAGGAGCTGGGTTTACCTATTAAGGCCCGATGTCCCTCTGATGGCTTT 1359  
Qy 370 IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeu 389  
Db 1360 ATTGGAGATTGGACTATCAAAAGGCAATGATCTAATTAACTTGGCATTCAGATCTC 1419  
Qy 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyr 409  
Db 1420 ATGCGGGCAATAATTCAATTCGTCTGCTTGGATCTGTCACCCAGGTTTTTGAAGGATGG 1479  
Qy 410 MetArgSerThrClnSerIlePheLysAspLysPheArgGlyTyrValGlyPheSerVal 429  
Db 1480 ATGAGATCCACAGAATCAGGATACAGGATAAATTTTCGTGGATGGGTTGGATTTAGTGT 1539  
Qy 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449  
Db 1540 CCAGTTTCCACCAATAATCTGAGGTTCGATATATTGTGATGCCATCCAGATTCGAA 1599  
Qy 450 ProCysGlyLeuAenGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469  
Db 1600 CCTTGTGGCTCAATCAGCTATATGCTATGCAATATGTTACAGTCTGTTGTTTCATGGA 1659  
Qy 470 ThrGlyGlyLeuArgAspThrValGluAenPheAsnProPheGlyGluAenGlyGluGln 489  
Db 1660 ACTGGAGGCTCAGAGATACAGTGGAGAAATTTTAACCCGTTTCTCGAAGAAAGGAGAGCAG 1719  
Qy 490 GlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsn 509  
Db 1720 GTTACAGGTGGGCTCTCGCCACTAACCATTTGAAATAAATGCTGTGGGCTATGGCGAT 1779  
Qy 510 CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAenGluAlaArgHis 529  
Db 1780 GGCAATTTTCGACATACAGGGAACACAAAGTCTCTTGGGAGGCTCTAATGAAGCGAGCAT 1839  
Qy 530 ValLysArgLeuHisValGlyProCysArg 539  
Db 1840 GTCAAGCGACTTTACATGGGACCATGCCGC 1869  
RESULT 25  
PCT-US03-41200-307  
; Sequence 307, Application PC/TUS0341200  
; GENERAL INFORMATION:  
; APPLICANT: Cooper, Bret  
; TITLE OF INVENTION: CELL PROLIFERATION-RELATED POLYPEPTIDES AND USES THEREFOR  
; FILE REFERENCE: 1392-10-19-2  
; CURRENT APPLICATION NUMBER: PCT/US03/41200  
; CURRENT FILING DATE: 2003-12-23  
; PRIOR APPLICATION NUMBER: US 60/436,565  
; PRIOR FILING DATE: 2002-12-26  
; NUMBER OF SEQ ID NOS: 349  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 307  
; LENGTH: 1881  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1881)  
PCT-US03-41200-307  
Alignment Scores:  
Pred. No.: 0 Length: 1881  
Score: 2525.50 Matches: 475  
Percent Similarity: 85.8% Conservative: 31  
Best Local Similarity: 80.5% Mismatches: 33  
Query Match: 87.3% Indels: 51



## Alignment Scores:

Pred. No.: 0  
 Score: 2525.50  
 Percent Similarity: 85.8%  
 Best Local Similarity: 80.5%  
 Query Match: 87.3%  
 DB: 52  
 Gaps: 3

Length: 1881  
 Matches: 475  
 Conservative: 31  
 Mismatches: 33  
 Indels: 51  
 Gaps: 3

US-10-628-525A-21 (1-539) x US-10-533-176-141 (1-1881)

QY 1 CysValAlaGluLeuSerArgGlu-----8  
 DB 100 TCGTGGCGGAGCTGAGCAGGAGCGGTGGGTGGCGGCGGCGCGCTGGCACCAGCGCGCG 159  
 QY 8 -----8  
 DB 160 CTGCTGAAGCAGCGGCTCTCGCGACCTCTCTCGTGGCGAGCTGCGACCGCCGCGCC 219  
 QY 9 -----AspLeuGly-----11  
 DB 220 ACCGAGTCGCGCGCGCGCGCGCGCGCGCGCGCGCTGGCGGAGCTCGCGGCGGAG 279  
 QY 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAenThrValValAla 29  
 DB 280 ATCAGCCCGATCTAGAGGCTCTCAGAGAAGATTCATCCAGCAAAACAATTTTGTGGCT 339  
 QY 30 SerGluGlnAspSerGluIleValValGlyGlyGluGlnAlaArgAlaLysValThrGln 49  
 DB 340 AGTGAGCAGGAGCTGAGATCATGATGTGAGGAGCAAGCTCAAGCTAAGTAACACGC 399  
 QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69  
 DB 400 AGCGTGTCTTGTAAACCGGTGAAGCTTCTCTATGCAAAAGTCAGGTGAGTACAGAT 459  
 QY 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValMet 89  
 DB 460 GTTGTGTTGCTGCTGCAATGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519  
 QY 90 ProArgTyrLeuAenGlyThrSerAspLysAenTyrAlaAenAlaPheTyrThrGluLys 109  
 DB 520 CCGAGATACATGAACGGGCTTGAACAAAATTTTGAACCGATTTTACATGAGAG 579  
 QY 110 HisIleArgIleProCysPheGlyGlyGluGluGluValThrPhePheHisGluTyrArg 129  
 DB 580 CACATTAAGATTCATGCTTGGCGGAGAACATGAGTACTTTTTCACGAGTATAG 639  
 QY 130 AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAenLeuTyr 149  
 DB 640 GATTCGTGATGTTGGGTGTTGTGATCATCCCTCATATCATAGACCTGGAATTTGTAT 699  
 QY 150 GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla 169  
 DB 700 GGAGATAATTTTGGTCTTGGGATATCAGTTGAGATACACATCTCTGCTGCTATGCG 759  
 QY 170 AlaCysGluAlaProIleLeuLeuGluGlyGlyTyrIleTyrGlyGlnAenCysMet 189  
 DB 760 GCGTGTGAAGCCCAATTAATCTTGAACCTGGGAGATATATCTATGACAGAAATGCATG 819  
 QY 190 PheValValAspAspTrpHisAlaSerLeuValProValLeuLeuAlaLysTyrArg 209  
 DB 820 TTTGTTGTGAATGATTTGGCATGCGAGTCTTGTGCCAGCTCTTGTCTGCAAAATATAGA 879  
 QY 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAenLeuAlaHisGln 229  
 DB 880 CCATATGTTGTTACAGGATGCGCGAGTCTTGTCTATACATATCTAGCACATCAG 939  
 QY 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAla 249  
 DB 940 GGTGTGGAGCTGCCAGTACATATCTGACCTGGGATGGCACCTGAATGTTATGAGCA 999  
 QY 250 LeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeuAspLysGlyGluAlaVal 269

DB 1000 TTAGAATGGGTGTTTCCAGAGTGGGCAAGCGGCATCCCTTGCAGAGGGTGAAGCAGTC 1059  
 QY 270 AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr 289  
 DB 1060 AATTTTTTAAAGCGCGATGTTGACAGCAGATCGAATTTGACTGTCCAGCCAGGGTAT 1119  
 QY 290 SerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAenGluLeuLeuSerSerArg 309  
 DB 1120 TCATGGGAGGTCAACTGCTGAAGGTGGCAAGGCTCAATGAGCTCTTAAGCTCCCGG 1179  
 QY 310 LysSerValLeuAenGlyIleValAenGlyIleAspIleAenAspTrpAenProAlaThr 329  
 DB 1180 AAGAGTGTATTTGAATGGAATTTGAATGGAATTTGACATTAATGATGGAACCCCATCCACA 1239  
 QY 330 AspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLys 349  
 DB 1240 GACAGTTCCTCTTATCATTAATTTCTGTTGATGACCTGTCGGNAAGGCCAAGTGA 1299  
 QY 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe 369  
 DB 1300 GCTGAATTTGCAAGGAGCTGGGTTTACCTATAAGGCCGATGTGCTCTGATTGGCTTT 1359  
 QY 370 IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeu 389  
 DB 1360 ATTGGAAGATTGGACTATCAAAAGGCAATGATCTAATTAACCTTGCATTTCCAGATCTC 1419  
 QY 390 MetArgCysLeuAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyr 409  
 DB 1420 ATCGGGGACAAATTCATTCGTCTGTTGGATCTGGTGACCCAGGTTTGAAGGATGG 1479  
 QY 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerVal 429  
 DB 1480 ATGAGATCCACAGATCAGGGTACAGGATAAATTTCTGTGATGGTGGATTTAGTGT 1539  
 QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449  
 DB 1540 CCAGTTTCCACCGCAATACTGAGGTGGCATATATTTGTATGCCATCCAGATTCGAA 1599  
 QY 450 ProCysGlyLeuAenGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469  
 DB 1600 CTTTGGGCTCATCAGCTATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 1659  
 QY 470 ThrGlyGlyLeuArgAspThrValGluAenPheAsnProPheGlyGluAenGlyGluGln 489  
 DB 1660 ACTGGAGGCTCAGAGATACAGTGGAGAAATTTTAAACCGTTTCTGAGAAAGGAGAGCAG 1719  
 QY 490 GlyThrGlyTrpAlaPheAlaProLeuThrThrGluAenMetPheValAspIleAlaAen 509  
 DB 1720 GGTACAGGGTGGGCTTCTGCCCACTAACCAATTTGAAAAAATGCTGTGGGCAATTCGGGAT 1779  
 QY 510 CysAenIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAenGluAlaArgHis 529  
 DB 1780 GGCAATTTCCAGATACAGGAGACAGGATCTCTTGGGAGGTCTTAATGAAAGCGAGCAT 1839  
 QY 530 ValLysArgLeuHisValGlyProCysArg 539  
 DB 1840 GTCAAGCGCTTTATCATGGGACCATGCCGC 1869

## RESULT 27

US-09-654-617-385863  
 ; Sequence 385863, Application US/09654617  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kovalic, David K.  
 ; TITLE OF INVENTION: Annotated Plant Genes  
 ; FILE REFERENCE: 38-21(15097)D  
 ; CURRENT APPLICATION NUMBER: US/09/654,617  
 ; CURRENT FILING DATE: 2000-09-05  
 ; NUMBER OF SEQ ID NOS: 463173  
 ; SEQ ID NO 385863  
 ; LENGTH: 2606  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa

US-09-654-617-385863

Alignment Scores:

Pred. No.: 0 Length: 2606  
 Score: 2525.50 Matches: 475  
 Percent Similarity: 85.8% Conservative: 31  
 Best Local Similarity: 80.5% Mismatches: 33  
 Query Match: 87.3% Indels: 51  
 DB: 29 Gaps: 3

US-10-628-525A-21 (1-539) x US-09-654-617-385863 (1-2606)

QY 1 CysValAlaGluLeuSerArgGlu-----8  
 DB 238 TCGTGGCGGAGCTGAGCAGGACGGTGGTGGCGCCAGCGCCGCTGGCAGCGGCGCG 297  
 QY 8 -----8  
 DB 298 CTGGTGAAGCAGCGGCTCTCGCGACCTTCTCGTCCGACGCTCGACGCCACCGCGGCC 357  
 QY 9 -----AspLeuGly-----11  
 DB 358 AGCGAGTCCCG 417  
 QY 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAsnThrValValAla 29  
 DB 418 ATCGACCCGATCTAGAGGCTCTCAGAGGATTCATCGACAAACAATTTTGTGGCT 477  
 QY 30 SerGluGlnAspSerGluIleValValGlyGlyGlnAlaArgAlaLysValThrGln 49  
 DB 478 AGTGACGAGAGTCTGAGATCATGGATGTGAAGGAGCAAGCTCAAGCTAAAGTAACAGC 537  
 QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69  
 DB 538 ACGGTGCTTTGTAAACCGGTGAAGCTTCTCTATGCAAGTCAGGTGGACTAGAGAT 597  
 QY 70 ValCysGlySerLeuProValAlaLeuAlaArgGlyHisArgValMetValMet 89  
 DB 598 GTTGTGGTTCACTGCCAATGCTCTGTCTTCTGGTGCATCGTGTGATGTTAATG 657  
 QY 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109  
 DB 658 CCGAGATACATGAACGGGGCTTGAACAAAAATTTTGCACAGCAATTTTACACTGAGAG 717  
 QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129  
 DB 718 CACATTGAATTCATGCTTGGCGGAGAACATGAAGTTACTTTTTTCCAGGATATAG 777  
 QY 130 AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyr 149  
 DB 778 GATTCTGTTGATGGTGTGTTGTGATCATCCCTCATATCATAGACCTGGAAATTTGTAT 837  
 QY 150 GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla 169  
 DB 838 GGAGATAATTTTGGTGTCTTTGGCGATATATCAGTTGAGATACACATCTCTGTGCTATGG 897  
 QY 170 AlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMet 189  
 DB 898 GCGTGTGAAGCCCCATTAATCTTGAACCTGGGAGATATATCTATGGACAGAAATGTCATG 957  
 QY 190 PheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaLysTyrArg 209  
 DB 958 TTTGTTGTGAATGATGGCATGCCAGTCTTGTGGCCAGTCTTCTTGTGCAAAATATAGA 1017  
 QY 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGln 229  
 DB 1018 CCATATGGTGTATTACAGGATGCCGAGTGTCTTGTGTCATCATATAATCTAGCATCATAG 1077  
 QY 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTrpTyrGlyAla 249  
 DB 1078 GGTGTGGAGCTCCAGATCATATCTGACCTGGGATGCGACCTGAATGGTATGAGCA 1137  
 QY 250 LeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGlyGluAlaVal 269

DB 1138 TTAGAATGGTCTTCCAGAGTGGCAAGCGGCATGCCCTTGACAAAGGTGAGGCAGTC 1197  
 QY 270 AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr 289  
 DB 1198 AATTTTTTAAAGGCGCAGTTGTGACAGCAGATCGAATTTGTGACTGTACCGACGGGTAT 1257  
 QY 290 SerTrpGluValThrThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArg 309  
 DB 1258 TCATGGAGGTCAACATGCTGAAGTGGCAAGGCTCAATGAGCTCTTAAGTCCCGG 1317  
 QY 310 LysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThr 329  
 DB 1318 AAGAGTGTATTGAATGGAATTCGAATGAATTAATTAATGATGGAAACCATCCACA 1377  
 QY 330 AspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLys 349  
 DB 1378 GACAAAGTTTCCCTTATCATTTATCTGTGTGATGACCTGCGGAAAGCCCAAGTGA 1437  
 QY 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe 369  
 DB 1438 GCTGAATTCAGAGAGCTGGGTTTACCTAAGGCCCGGATGGCTCTGATTTGCTTT 1497  
 QY 370 IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeu 389  
 DB 1498 ATTGGAAGATTGGACTATCAAAAGGCATTGATCTAATTAATTTGCCATTCAGATCTC 1557  
 QY 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrp 409  
 DB 1558 ATGCGGGCAATTAATCAATTCGTCTGCTGATGCTGTGATCTGTGTGATGCTGTG 1617  
 QY 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPheSerVal 429  
 DB 1618 ATGAGATCCACAGAAATCAGGGTACAGGGGATAAATTTCTGTGGATGGTGTGATTT 1677  
 QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449  
 DB 1678 CCAGTTTCCACCGAATACTGCAGGTTGCGATATATTTGTTGATGCCATCCAGATTCGA 1737  
 QY 450 ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469  
 DB 1738 CTTGTGGCTCAATCAGCTATATGCTATGCAATATGTTACAGTGCCTGTTGTTTATGGA 1797  
 QY 470 ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln 489  
 DB 1798 ACTGAGGCTCAGAGATACAGTGGAGAAATTTTAAACCGCTTGTGAGAAAGAGAGCAG 1857  
 QY 490 GlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsn 509  
 DB 1858 GGTACAGGTTGGGCTTCTCGCCACTAACCAATTGAAAAAATGCTGTGGGCTTGGGAT 1917  
 QY 510 CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529  
 DB 1918 GGCAATTTTCGACATACAGGAAACACAGTCTCTTTGGGAGGCTCTAATGAAGCGGCAT 1977  
 QY 530 ValLysArgLeuHisValGlyProCysArg 539  
 DB 1978 GTCAAGCGACTTTACATGGACCATGCGCG 2007

RESULT 28

US-09-684-016-385863  
 ; Sequence 385863, Application US/09684016  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Liu, Jingdong  
 ; TITLE OF INVENTION: Annotated Plant Genes  
 ; FILE REFERENCE: 38-21(15097)D  
 ; CURRENT APPLICATION NUMBER: US/09/684,016  
 ; CURRENT FILING DATE: 2000-10-10 US 09/654,617  
 ; PRIOR APPLICATION NUMBER: 2000-09-05  
 ; PRIOR FILING DATE: 2000-09-05 463173  
 ; NUMBER OF SEQ ID NOS: 463173  
 ; SEQ ID NO 385863



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; LENGTH: 2606
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-684-016-385863

Alignment Scores:
Pred. No.: 0 Length: 2606
Score: 2525.50 Matches: 475
Percent Similarity: 85.8% Conservative: 31
Best Local Similarity: 80.5% Mismatches: 33
Query Match: 87.3% Indels: 51
DB: 29 Gaps: 3

US-10-628-525A-21 (1-539) x US-09-684-016-385863 (1-2606)

Qy 1 CysValAlaGluLeuSerArgGlu-----8
Db 238 TGGTGGCGGAGCTGACGAGCGGTGGGTGGCGCGCGCGCTGGCACCGCGCGG 297
Qy 8 -----8
Db 298 CTGGTGAAGCAGCGCGTCTCTCGCGACCTTCTCTGGTGGCGAGCTGCGACCGCACCGCGCGCC 357
Qy 9 -----AspLeuGly-----11
Db 358 ACGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGGCGGAGCTGGCGGCGGAG 417
Qy 12 LeuGluPro-----GluGlyLeAlaGluGlySerIleAspAenThrValValAla 29
Db 418 ATCGAGCGCGATCTAGAGGTCTCAGAGAGTCTCAGAGAGTCCATCGCAACAACTTTTGGCT 477
Qy 30 SerGluGlnAspSerGluIleValValGlyLeGluGlnAlaArgAlaValThrGln 49
Db 478 AGTGAGCAGGAGCTCAGATCATGGATGTCAGAGCAAGCTCAAGCTAAAGTAAACACGC 537
Qy 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69
Db 538 AGCGTGTCTTGTAAACCGGTGAAGCTTCTCTTATGCAAGTCAAGTGGAGTGGAGAT 597
Qy 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValMet 89
Db 598 GTTGTGTGTTCACTGCCAATGTCTTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 657
Qy 90 ProArgTyrLeuAenGlyThrSerAspLysAsnTyrAlaAenAlaPheTyrThrGluLys 109
Db 658 CCAGATACATGACGCGGCTTGAACAAATAATTTTGAACCGCATTTTACACTGAGAG 717
Qy 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129
Db 718 CACATTAAGATTCATGCTTTGGCGGAGAACATGAAGTTACTTTTTCACGAGTATAGG 777
Qy 130 AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAenLeuTyr 149
Db 778 GATTCCTGTGATGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 837
Qy 150 GlyAspLysPheGlyAlaPheGlyAspAenGlnPheArgTyrThrLeuLeuCysTyrAla 169
Db 838 GGAGATAAATTTGGTGTCTTTGGCGGATATACAGTTCAGATACACACTCTCTGTCTATGG 897
Qy 170 AlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAenCysMet 189
Db 898 GCGTGTGAAGCCCCCATTAATCTTGAACCTGGGAGGATATATCTATGACAGAAATGATG 957
Qy 190 PheValValAenAspTrpHisAlaSerLeuValProValLeuLeuAlaIalysTyrArg 209
Db 958 TTGTGTGTGATGATGGCATGGCATGCTTGTGCCAGTCTTCTGTGCAAAATATAGA 1017
Qy 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAenLeuAlaHisGln 229
Db 1018 CCATATGGTGTATACAGGATGCCCGCAGTGTCTTGTCTATACATATCTAGCACATCAG 1077
Qy 230 GlyValGluProIleAspThrTyrProAspLeuGlyLeuProGluTyrGlyValAla 249

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Db 1078 GGTGTGGAGCCTGCCAGTACATATCTCTGACCTGGGATTTGCCACCTGAATGGTATGGAGCA 1137
Qy 250 LeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGlyGluAlaVal 269
Db 1138 TTAGATGGGTGTTCAGAGTGGGCAAGCGGCGATGCCCTTTGCAAGGGTGAAGCGAGTC 1197
Qy 270 AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr 289
Db 1198 AATTTTTTAAAGCGCGAGTTGTGACAGCAGATCGAATTTGTACTGTCTGACCGCGGTAT 1257
Qy 290 SerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAenGluLeuLeuSerSerArg 309
Db 1258 TCATGGAGGTCAACTGCTGAAGGTGGCAAGGCGCTCAATGAGCTCTTAAGCTCCCGG 1317
Qy 310 LysSerValLeuAenGlyIleValAenGlyIleAspIleAenAspTyrAenProAlaThr 329
Db 1318 AAGATGTATTAATGGAATTTGAATGGAATTTGACATTAATGATGGAACCCCATCCACA 1377
Qy 330 AspLysCysIleProCysHisTyrSerValAspLeuSerGlyLysAlaLysCysLys 349
Db 1378 GACAAGTTCTCCCTTATCATTTCTGTGTGATGACCTGCTCCGAAAGGCCAAGTGTAAA 1437
Qy 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe 369
Db 1438 GCTGAATTCAGAAAGGAGCTGGGTTTACCTATAAGGCCCGATGTCCTCTGATTTGGCTTT 1497
Qy 370 IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeu 389
Db 1498 ATTGGAAGATTGAGCTATCAAAAGGCATTTGATTAATTAACCTTGCCATTCAGATCTC 1557
Qy 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyr 409
Db 1558 ATCGCGGACAAATATTCAATTCGTGTCATGCTTGGATCTGGTGACCCAGGTTTTGAAGGATGG 1617
Qy 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPheSerVal 429
Db 1618 ATGAGATCCACAGAAATCAGGGTACAGGGATAAAATTTCTGTGATGGGTGGATTTAGTGT 1677
Qy 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449
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Qy 490 GlyThrGlyTrpAlaPheAlaProLeuThrThrGluAenMetPheValAspIleAlaAen 509
Db 1858 GGTACAGGGTGGGCATCTCGCCATTAACCAATGGAATAAATGCTGTGGGCATTTGGGAT 1917
Qy 510 CysAenIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAenGluAlaArgHis 529
Db 1918 GGCAATTTGCGACATACAGGGACACAAAGTCTCTCTTGGGAGGGTCTTAATGAAGCGAGCAT 1977
Qy 530 ValLysArgLeuHisValGlyProCysArg 539
Db 1978 GTCAAGCGACTTTACATGGGACCATTCGCCG 2007

RESULT 29
US-09-887-272A-3846
; Sequence 3846, Application US/09887272A
; GENERAL INFORMATION:
; APPLICANT: Hou, Yu-Ming
; APPLICANT: Quan, Sheng
; APPLICANT: Chang, Hur-Song
; APPLICANT: Zhu, Tong
; APPLICANT: Whitham, Steve
; APPLICANT: Goff, Steve
; APPLICANT: Glazebrook, Jane

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; APPLICANT: Chen, Wenquiong  
 ; APPLICANT: Katagiri, Fumiaki  
 ; APPLICANT: Xie, Zhiyi  
 ; APPLICANT: Tao, Yi  
 ; APPLICANT: Zou, Guangzhou  
 ; APPLICANT: Cooper, Bret  
 ; TITLE OF INVENTION: PLANT GENES INVOLVED IN DEFENSE AGAINST  
 ; FILE REFERENCE: 1360.003US2  
 ; CURRENT APPLICATION NUMBER: US/09/887,272A  
 ; PRIOR FILING DATE: 2001-06-23  
 ; PRIOR APPLICATION NUMBER: 60/213,634  
 ; PRIOR FILING DATE: 2000-06-23  
 ; PRIOR APPLICATION NUMBER: 60/214,926  
 ; PRIOR FILING DATE: 2000-06-23  
 ; PRIOR APPLICATION NUMBER: 60/261,320  
 ; PRIOR FILING DATE: 2001-01-12  
 ; PRIOR APPLICATION NUMBER: 60/264,353  
 ; PRIOR FILING DATE: 2001-01-26  
 ; PRIOR APPLICATION NUMBER: 60/273,879  
 ; PRIOR FILING DATE: 2001-03-07  
 ; PRIOR APPLICATION NUMBER: 09/887,271  
 ; PRIOR FILING DATE: 2001-06-22  
 ; NUMBER OF SEQ ID NOS: 6813  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3846  
 ; LENGTH: 1926  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa  
 ; US-09-887-272A-3846

Alignment Scores:  
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 Score: 2511.50 Matches: 476  
 Percent Similarity: 85.9% Conservative: 31  
 Best Local Similarity: 80.7% Mismatches: 32  
 Query Match: 86.8% Indels: 52  
 DB: 34 Gaps: 3

US-10-628-525A-21 (1-539) x US-09-887-272A-3846 (1-1926)

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 Db 100 TCGTGGCGGAGCTGAGCAGGACGGTGGTGGCGCGCGCGCGTGGCACCAGCGCGC 159  
 Qy 8 -----8  
 Db 160 CTGGTGAAGCAGCGGCTCTGCGGACCTTCTCTGTCGCGACGTCGACGCCGCCGCC 219  
 Qy 9 -----AspLeuGly-----11  
 Db 220 AGCAGTCCCGGAG 279  
 Qy 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAsnThrValValAla 29  
 Db 280 ATCGAGCCCGATCTAGAAAGGCTCTCAGAGAGATTCATCGACAAAACAATTTTGTGGCT 339  
 Qy 30 SerGluGlnAspSerGluIleValValGlyLysGluGlnAlaArgAlaLysValThrGln 49  
 Db 340 AGTGAGCAGGAGTCTGAGATCATGGATGTGAAGGAGCAAGCTCAAGCTAAAGTAACAGC 399  
 Qy 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69  
 Db 400 ACGGTGTCTTTGAACCGGTGAGCTTCTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCG 459  
 Qy 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValMet 89  
 Db 460 GTTTGGTTCACCTGCAATGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 519  
 Qy 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109  
 Db 520 CCGAGATACATGACCGCGCGCTTGAACAAAAATTTTGCAACAGCACTTTTACACTGAGAG 579

Qy 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129  
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 Db 640 GATTCTGTGATTGGGTGTTTGTGATCATCTCCATCATATCATAGACCTCGAAATTTGTAT 699  
 Qy 150 GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla 169  
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 Qy 170 AlaCysGluAlaProLeuIleLeuGluGlyGlyTyrIleTyrGlyGlnAsnCysMet 189  
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 Qy 190 PheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaLysTyrArg 209  
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 Qy 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGln 229  
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 Qy 270 AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr 289  
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 Qy 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPheSerVal 429  
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 Qy 450 ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469  
 Db 1600 CCTTGTGCGCTCAATCAGCTATATGCAATATGTTGATGAGTCTGCTTTGTTATGGA 1659  
 Qy 470 ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln 489



Db 1672 ATGAGATCCACAGATCAGGGTACAGGGATAAATTTCTGGATGGGTTGGATTAGTGT 1731  
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Db 1792 CCTTGTGGCTCAATCAGCTATATGCTATGCAATATGGTACAGTGCCTGTGTTCATGGA 1851  
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Qy 510 CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529  
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Qy 530 ValLysArgLeuHisValGlyProCysArg 539  
Db 2031 GTCAAGCGACTTTACATGGGACCATGCCGC 2060

Search completed: April 2, 2006, 03:27:19  
Job time : 14820.2 secs

GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 21:21:57 ; Search time 1008.01 Seconds  
(without alignments)  
1603.719 Million cell updates/sec

Title: US-10-628-525A-21

Perfect score: 2893

Sequence: 1 CVAELSRDGLPEGLAEG.....LLGRNFAHVKRLHVGPCR 539

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Pgapop 6.0 , Pgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6698573 seqs, 1499593917 residues

Total number of hits satisfying chosen parameters: 13397146

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-Q=/abs/ABSSWEB spool/US10628525/runat\_31032006\_095132\_17106/app\_query.fasta\_1  
-DB=Pending Patents NA New -QFMT=fastap -SUPPIX=p2n.xnpn -MINMATCH=0.1  
-LOOPCI=0 -LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62  
-TRANS=human40.cdi -LIST=150 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abes06h  
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Database :

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2: /SID55/ptodata/2/pna/US06 NEW COMB.seq:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2861	98.9	1749	US-11-330-822-56	Sequence 56, Appl
2	2525.5	87.3	1881	US-10-542-516-9	Sequence 9, Appl
3	2525.5	87.3	1881	US-10-533-232A-307	Sequence 307, App
4	1130.5	39.1	2423	US-11-330-822-52	Sequence 52, Appl
5	1050.5	36.3	3006	US-60-757-216-1	Sequence 1, Appl

6	1050.5	36.3	3006	12	US-60-757-810-1	Sequence 1, Appl
7	1012	35.0	558	10	US-11-227-183A-16489	Sequence 16489, A
8	993	34.3	555	10	US-11-227-183A-16488	Sequence 16488, A
9	978.5	33.8	2007	8	US-11-330-822-54	Sequence 54, Appl
10	838	29.0	1915	8	US-11-330-822-50	Sequence 50, Appl
11	802.5	27.7	598	10	US-11-292-078-969	Sequence 969, App
12	789	27.3	1882	1	PCT-US05-47111-476	Sequence 476, App
13	789	27.3	1882	12	US-60-752-355-476	Sequence 476, App
14	739.5	25.6	2160266	7	US-10-513-024-1373	Sequence 1373, Ap
15	732	25.3	1431	11	US-11-348-024-13913	Sequence 6913, Ap
16	704	24.3	411	8	US-11-353-150-38224	Sequence 38224, A
17	673	23.3	407	8	US-11-329-388-3028	Sequence 3028, Ap
18	633	21.9	1434	8	US-11-275-569-11	Sequence 11, Appl
19	634.5	21.6	1409	8	US-11-298-234A-9	Sequence 9, Appl
20	597	20.6	374	10	US-11-227-183A-29117	Sequence 29117, A
21	590.5	20.4	635	8	US-11-330-364-17004	Sequence 17004, A
22	587	20.3	1488	8	US-11-330-822-36	Sequence 36, Appl
23	567	19.6	334	8	US-11-353-150-66579	Sequence 66579, A
24	537.5	18.6	1434	7	US-10-953-349-11887	Sequence 11887, A
25	516	17.8	3693	7	US-10-542-516-5	Sequence 5, Appl
26	503	17.4	3444	7	US-10-542-516-15	Sequence 15, Appl
27	498.5	17.2	436	8	US-11-239-591A-7048	Sequence 7048, Ap
28	492.5	17.0	3078	7	US-10-542-516-7	Sequence 7, Appl
29	476	16.5	289	8	US-11-329-388-1791	Sequence 1791, Ap
30	456.5	15.8	5025	7	US-10-542-516-17	Sequence 17, Appl
31	455.5	15.7	4836	7	US-10-542-516-13	Sequence 13, Appl
32	453.5	15.7	4887	7	US-10-542-516-11	Sequence 11, Appl
33	419	14.5	521	10	US-11-314-834-4110	Sequence 4110, Ap
34	416	14.4	406	8	US-11-329-388-1872	Sequence 1872, Ap
35	409	14.1	270	10	US-11-227-183A-8615	Sequence 8615, Ap
36	397.5	13.7	512	8	US-11-330-082-6506	Sequence 6506, Ap
37	382	13.2	658	8	US-11-331-019-741	Sequence 741, App
38	380.5	13.2	402	8	US-11-331-019-35897	Sequence 35897, A
39	380	13.1	11870	8	US-11-298-234A-18	Sequence 18, Appl
40	379.5	13.1	1230025	8	US-11-366-942-1	Sequence 1, Appl
41	374	12.9	11997	8	US-11-398-034A-29	Sequence 29, Appl
42	358.5	12.4	578	8	US-11-330-082-10140	Sequence 10140, A
43	358	12.4	599	10	US-11-292-078-14976	Sequence 14976, A
44	357	12.3	581	8	US-11-329-388-8116	Sequence 8116, Ap
45	346	12.0	626	8	US-11-329-388-6669	Sequence 6669, Ap
46	343	11.9	567	10	US-11-227-183A-20736	Sequence 20736, A
47	342.5	11.8	594	8	US-11-329-388-10800	Sequence 10800, A
48	334	11.5	278	10	US-11-227-183A-21291	Sequence 21291, A
49	334	11.5	638	7	US-10-953-349-37494	Sequence 37494, A
50	329.5	11.4	449	10	US-11-314-834-2066	Sequence 2066, Ap
51	329	11.4	560	8	US-11-329-388-9900	Sequence 9900, Ap
52	328.5	11.4	580	8	US-11-329-388-5264	Sequence 5264, Ap
53	326	11.3	578	10	US-11-292-078-9340	Sequence 9340, Ap
54	321	11.1	512	8	US-11-330-082-11484	Sequence 11484, A
55	316.5	10.9	378	8	US-11-331-019-3373	Sequence 3373, Ap
56	315	10.9	484	8	US-11-329-388-13004	Sequence 13004, A
57	312	10.8	798	1	PCT-US06-07642-15009	Sequence 15009, A
58	312	10.8	798	12	US-60-658-984A-15009	Sequence 15009, A
59	310	10.7	433	8	US-11-329-388-2698	Sequence 2698, Ap
60	309.5	10.7	431	8	US-11-331-019-39751	Sequence 39751, A
61	303.5	10.5	597	8	US-11-330-364-12149	Sequence 12149, A
62	303	10.5	434	8	US-11-353-150-38227	Sequence 38227, A
63	300	10.4	573	10	US-11-292-078-14889	Sequence 14889, A
64	298	10.3	523	8	US-11-329-388-7552	Sequence 7552, Ap
65	296	10.2	549	8	US-11-329-388-9889	Sequence 9889, Ap
66	294.5	10.2	570	8	US-11-329-388-10813	Sequence 10813, A
67	291.5	10.1	423	10	US-11-301-327-4392	Sequence 4392, Ap
68	290.5	10.0	403	10	US-11-301-327-274	Sequence 274, App
69	290.5	10.0	580	10	US-11-292-078-13329	Sequence 13329, A
70	286.5	9.9	565	8	US-11-329-388-13022	Sequence 13022, A
71	284	9.8	625	8	US-11-329-388-8047	Sequence 8047, A
72	282	9.7	649	8	US-11-329-388-8036	Sequence 8036, Ap
73	278	9.6	552	10	US-11-227-183A-20735	Sequence 20735, A
74	272.5	9.4	440	8	US-11-239-610A-23905	Sequence 23905, A
75	271	9.4	536	8	US-11-329-388-6734	Sequence 6734, Ap
76	270.5	9.4	265	10	US-11-227-183A-13663	Sequence 13663, A
77	268.5	9.3	405	8	US-11-331-019-35306	Sequence 35306, A
78	268.5	9.3	452	8	US-11-353-150-71513	Sequence 71513, A





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Qy 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 155  
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Qy 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCyStyAlaAlaCyGluAlaProLeuIle 176  
Db 601 GGTGATTAATCAGTTTCAGATACACACTCTTTGCTATGCTGCATGTGAGGCTCTTTGATC 660  
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlnAsnCySmetPheValValAsnAspTyrHis 196  
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Qy 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
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Qy 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
Db 781 TCCCGCAGCATCTTGTAAATACATAATTAGCACATCAGGGTGTAGAGCCTGCAGACCA 840  
Qy 237 TyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256  
Db 841 TATCTGACCTTGGTTGCCACCTGAATGTTAGGACTCTGGAGTGGGTATTCCTCGAA 900  
Qy 257 TrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
Db 901 TGGCGCAGGAGGATGCCCTTGACAGGGTGAGCAGTTAAATTTTTGAAAGGTGCAGTT 960  
Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
Db 961 GTGACACAGATCGAATCGTGACTGTCTAGTAAGGGTTATTTCGTGGGAGGTCCACACTGCT 1020  
Qy 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316  
Db 1021 GAAGGTGACAGGGCCTCATAGCTCTTAAGCTCCGAAAGAGTGTATTAAACGGAT 1080  
Qy 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
Db 1081 GTAAATGGAATTGACATTAATGATTGGAACCTGCCACAGCAAAATGTATCCCTGTGAT 1140  
Qy 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
Db 1141 TATTCTGTGATACCTCTCTGAAAGGCCAAATGTAAGGTGCATTCGCAAGAGGAGCTG 1200  
Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
Db 1201 GGTTHACCTATAAGGCTGATGTTCTCTGATTTGGCTTTTATGGAAGGTTGGATTATCAG 1260  
Qy 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396  
Db 1261 AAAGGCATTGATCTCAATCACTTATCATACAGATCTCATCGGGAAGATGTTCAATTT 1320  
Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416  
Db 1321 GTCATCTTGGATCTGGTGACCCAGAGCTTGAAGATTGGATGGATGAGATCTACAGATCGATC 1380  
Qy 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436  
Db 1381 TTCAGAGTAATTTGTTGATGGGTGTGATTTAGTTGTTCCAGTTTCCACCCGGAATTAAT 1440  
Qy 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456  
Db 1441 GCCGGCTCGCATATATTGTTAATGCCATCCAGATTCGAACCTTGTGCTCTCAATCAGCTA 1500  
Qy 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
Db 1501 TATGCTATGCAATATGGCAGTTCCTGTTGTCATGCAACTGGGGGCTCTAGAGATACC 1560  
Qy 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAla 496  
Db 1561 GTGGAGAACTTCAACCTTTTCGTGAGAAATGGAGACAGGGTACAGGGTGGGCATTCGCA 1620

Qy 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
Db 1621 CCCCTAACCAACAGAAACATGTTTGGACATTTGGGAATTCGGAATCTCATATACAGGA 1680  
Qy 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536  
Db 1681 ACACAAGTCTCTCTGGGAAGGCTAATGAAGCAGGAGCATGTCAAAAGACTTTCAGTGGGA 1740  
Qy 537 ProCysArg 539  
Db 1741 CCATGCCG 1749  
RESULT 2  
US-10-542-516-9  
; Sequence 9, Application US/10542516  
; GENERAL INFORMATION:  
; APPLICANT: Helm, Ute  
; APPLICANT: Herbers, Karin  
; APPLICANT: Sonnwald, Uwe  
; APPLICANT: Gluckmann, Eric  
; TITLE OF INVENTION: Expression cassette with promoters of starch synthesis 3 for the  
; TITLE OF INVENTION: expression of nucleic acids in plant tissue containing starch  
; FILE REFERENCE: 13173-00015-US  
; CURRENT APPLICATION NUMBER: US/10/542,516  
; PRIOR FILING DATE: 2005-07-18  
; PRIOR APPLICATION NUMBER: PCT/EP2004/000241  
; PRIOR FILING DATE: 2004-01-15  
; PRIOR APPLICATION NUMBER: DE 103 02 324.0  
; PRIOR FILING DATE: 2003-01-20  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 9  
; LENGTH: 1881  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1878)  
; OTHER INFORMATION: coding for SSS3  
US-10-542-516-9

Alignment Scores:  
Pred. No.: 4,56e-252 Length: 1881  
Score: 2525.50 Matches: 475  
Percent Similarity: 85.8% Conservative: 31  
Best Local Similarity: 80.5% Mismatches: 33  
Query Match: 87.3% Indels: 51  
DB: Gaps: 3

US-10-628-525A-21 (1-539) x US-10-542-516-9 (1-1881)

Qy 1 CysValAlaGluLeuSerArgGlu----- 8  
Db 100 TCGTGGCGGAGCTGAGCAGGACGGTGGTGGCGCACGGCCGCTGGCACCGCGCGC 159  
Qy 8 ----- 8  
Db 160 CTGGTGAACAGCCGGTCTCGCGACCTTCCTGTCGCCGACGTCGAGCCGCCGCCGCC 219  
Qy 9 -----AspLeuGly----- 11  
Db 220 ACCGAGTCGCCGGCGCGCGCGCGCGCCCGCGCGCGCTTCGCCGACTCCCGCGTGGGGAG 279  
Qy 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAsnThrValValAla 29  
Db 280 ATCGAGCCCGATCTAGAAGGTCTCAGAAAGATTCATCGACAAACAAATTTTGTGGCT 339  
Qy 30 SerGluGlnAspSerGluIleValValGlyLysGluGlnAlaArgAlaLysValThrGln 49  
Db 340 AGTGAGCAGGATCTGAGATCATGGATGTGAAGAGCAAGCTCAAGCTAAGTAACACGC 399  
Qy 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAsp 69



QY 30 SerGluGlnAspSerGluIleValValGlyLeuGlnAlaArgAlaValThrGln 49  
DB 340 AGTGAGCAGGAGTCTGAGATCATGATGTGAAGGAGCAAGCTCAAGCTAAAGTAACACGC 399  
QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAsp 69  
DB 400 AGCGTGTCTTGTAAACCGGTGAAGCTTCTCTATGCAAGGTGAGGTGAGGAGAT 459  
QY 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValMet 89  
DB 460 GTTGTGTCTCACTGCCAATTGCTCTTGTCTCTTGTGTGTGTGTGTGTGTGTGTGT 519  
QY 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAlaAlaPheTyrThrGluLys 109  
DB 520 CCAGAGATACATGAACGGGGCTTGAACAAATAATTTTGAACACGATTTTACACTGAGAAG 579  
QY 110 HisIleArgIleProCysPheGlyGlyGluHisLeuValThrPhePheHisGluTyrArg 129  
DB 580 CACATTAAGATTTCATGCTTTGGCGGAGAACATGAAGTTACTTTTTTTCACGAGTATAGG 639  
QY 130 AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyr 149  
DB 640 GATTCTGTGATTGGGT 699  
QY 150 GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla 169  
DB 700 GGAGATAAATTTGGTGTCTTTGGCGGATAATCAGTTTCTGATACACATCTCTGTCTATGCG 759  
QY 170 AlaCysGluAlaProLeuIleLeuGlyGlyGlyTyrIleTyrGlyGlnAsnCysMet 189  
DB 760 GCGTGTGAAGCCCAATTAATCTTGAACGTGGAGGATATATCTATGACAGAAATGCATG 819  
QY 190 PheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyrArg 209  
DB 820 TTTGTGTGAATGTTGGCATGCCATGCCATGTCCTTGTCTGTCTGTCTGTCTGTCTGTCT 879  
QY 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGln 229  
DB 880 CCATATGGTGTTTACAGGATGCCCGCAGGTCTTGTGTCTATACATTAATCTAGCACATCAG 939  
QY 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAla 249  
DB 940 GGTGTGGAGCTGCCAGTACATATCTGACCTGGGATGTCCTGAATGGTATGAGCA 999  
QY 250 LeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGlyGluAlaVal 269  
DB 1000 TTAGATGGTGTTCAGAGTGGGCGAGCGGCGCATGCCCTTGACAGGGGTGAGGAGTC 1059  
QY 270 AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr 289  
DB 1060 AATTTTAAAAAGCGCAGTTGTGACAGCAGATCGAATTGTGACTGTACGCCAGGGGTAT 1119  
QY 290 SerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGlnLeuLeuSerSerArg 309  
DB 1120 TCATGGAGGTTCACATCTGCTGAAGTGGGCGAGGCTCAATGAGCTCTTAAGCTCCCG 1179  
QY 310 LysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThr 329  
DB 1180 AGAGTGTATTGTGATGGATTGTAAATGGATTGACATTAATGATTGGAAACCCATCCCA 1239  
QY 330 AspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLys 349  
DB 1240 GACAGTGTCTCTCTTATCATTAATCTGTGTGATGACCTGTCCGGAAGGCCAAGTGATAA 1299  
QY 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe 369  
DB 1300 GCTGAATTTGACAGAGAGCTGGGTGTACCTATTAAGCCCGGATGTGCTCTGTATGGCTTT 1359  
QY 370 IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeu 389  
DB 1360 ATTGGAGATTGGACTATCAAAAGGCATGTATCTAATTAACCTTCCCATTCAGATCTC 1419

QY 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrp 409  
DB 1420 ATGCGGGACAATTAATCAATTCGTGATGCTGGTGAACCCAGCTTTTGAAGGATGG 1479  
QY 410 MetArgSerThrGluSerIlePheLeuAspLysPheArgGlyTrpValGlyPheSerVal 429  
DB 1480 ATGAGATCCACAGAATCAGGGTACAGGATAAATTTCTGTGATGGGTGGATTAGTGT 1539  
QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449  
DB 1540 CCAGTTTCCACCGATACATCTGAGGTTCGATATATTTGTGATGCATCCAGATTCGAA 1599  
QY 450 ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469  
DB 1600 CTTGTGGGCTCAATCAGCTATATGCTATGCAATATGTTACAGTGCCTGTGTTCATGGA 1659  
QY 470 ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln 489  
DB 1660 ACTGGAGGCTCAGAGATCAGTGGAGAAATTTAACCCGTTTGTCTGAGAAAGGAGAGCAG 1719  
QY 490 GlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsn 509  
DB 1720 GGTACAGGTGGGCATCTCGCACCTAACCATTTGAAAAAATCTGTGGCATTTGGGAT 1779  
QY 510 CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529  
DB 1780 GGCATATTCGACATACAGGGAAACACAAGTCTCTTTGGGAGGTCTTAATGAAGCGAGGAT 1839  
QY 530 ValLysArgLeuHisValGlyProCysArg 539  
DB 1840 GTCAGCGCATTTACATGGGACCATGCGCG 1869

## RESULT 4

US-11-330-822-52  
; Sequence 52, Application US/11330822  
; GENERAL INFORMATION:  
; APPLICANT: GUAN, HANPING  
; APPLICANT: KEELING, PETER L.  
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN  
; TITLE OF INVENTION: HOSTS  
; FILE REFERENCE: 15053-04  
; CURRENT APPLICATION NUMBER: US/11/330,822  
; CURRENT FILING DATE: 2006-01-11  
; PRIOR APPLICATION NUMBER: PCT/US98/06660  
; PRIOR FILING DATE: 1998-04-03  
; PRIOR APPLICATION NUMBER: 60/042,939  
; PRIOR FILING DATE: 1997-04-04  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: Patent in Ver. 3.3  
; SEQ ID NO 52  
; LENGTH: 2423  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1) .. (2094)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2107) .. (2304)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2308) .. (2421)  
US-11-330-822-52  
Alignment Scores:  
Pred. No.: 1,13e-106 Length: 2423  
Score: 1130.50 Matches: 254  
Percent Similarity: 57.2% Conservative: 64  
Best Local Similarity: 45.7% Mismatches: 159  
Query Match: 39.1% Indels: 80  
DB: 8 Gaps: 11  
US-10-628-525A-21 (1-539) x US-11-330-822-52 (1-2423)

QY 3 AlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyLeuAlaGluGlySerile 22  
DB 565 GTCCTTATGACAGGAGAT-----AATGAACCTGGCCCTTGGCTGGGCTAATG 618  
QY 23 AspAsnThrValValAlaSerGluGlnAspSerGluLeuValValGlyLeuGluGln 42  
DB 619 ATGAACGTCGTCGTGGCTTCT----- 642  
QY 43 AlaArgAlaLysValThrGlnSerileValPheValThrGlyGluAlaSerProTyrAla 62  
DB 643 -----GAATGTCTCTCTTCTGC 660  
QY 63 LysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGly 82  
DB 661 AAGACAGTGGCTTGGAGATGCTGGGGTGTTCCTAAGCTCTGGCAGGAGAGA 720  
QY 83 HisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAla 102  
DB 721 CACCGTGTATGGTCGTGATACCAAGATAT-----GGAGAGTATGCC 762  
QY 103 AsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluVal 122  
DB 763 GAAGCCCGGATTTAGGTGTAAGGAGACGTTCAAGGTAGCTGGACAGGATTCAGAAGTT 822  
QY 123 ThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSerTyr 142  
DB 823 ACTATTTTCATCTTACATGATGAGTGTATTTGATTTGATGAGACCCCTCCCTTC 882  
QY 143 ---HisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161  
DB 883 CGGCACCGGCACAAATAATTTATGG-----GGAGAAAGATTGATATTTGAAG 933  
QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuLeuLeuGlyGly 181  
DB 934 CGCATGATTTGTTCTGCAAGCCGCTGTGAGTTTCCATGTTATGTTCCATGTGGCGGT 993  
QY 182 TyrIleTyrGlyGln---AsnCysMetPheValValAsnAspTyrHisAlaSerLeuVal 200  
DB 994 ACTGTCATGTTGATGGCACTTAGTTTTCATGTTCTAATGTTGGATACCGACTTCTG 1053  
QY 201 ProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerile 220  
DB 1054 CTTGTCATCTAAAGCCCTATTACCGGACAATGGTTTGCATGATGCTCGCTCTG 1113  
QY 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240  
DB 1114 CTTGTGATACAAACATTCCTCATCAGGCTCGTGGCCCTGTAGACGACTTCGTCATTTT 1173  
QY 241 GlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArg 260  
DB 1174 GACTTGCCT-----GAA 1185  
QY 261 HisAlaLeuAspLys-----GlyGluAlaValAsnPheLeu 272  
DB 1186 CACTACATCGACCTTCAAACTGATGACAACTTGGTGGGATCACAGCAACGTTTTT 1245  
QY 273 LysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGlu 292  
DB 1246 GCTGGCGGCTGAAGACCGCAGACCGGCTGTGACCGTTAGCAATGGCTTACATGTGGGAG 1305  
QY 293 ValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerVal 312  
DB 1306 CTGAAGACTTCGGAGCGGGTGGGGCTTCACGACATCATTAACAGAACACTGGAG 1365  
QY 313 LeuAsnGlyIleValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCys 332  
DB 1366 CTGCAAGGCATCGTGAACGGCATCGACATGAGCGAGTGAACCCGCTGTGGAC----- 1419  
QY 333 IleProCysHisTyrSerValAspAspLeu-----Ser 343  
DB 1420 -----GTGCACCTCCACTCCGACGACTACCAACTACACGTCGTGAGACGCTGACACC 1473

QY 344 GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363  
DB 1474 GGCAGCGCAGTGCAGGCCCTTGACGGCGAGCTGGGCTGCAGGTCCTCGCAGCAG 1533  
QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 383  
DB 1534 GTGCCACTGATCGGCTTTCATCGGGCGGTGGACCAACAGAGGGCGTGACATCATCGCC 1593  
QY 384 LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403  
DB 1594 GACGCGATCCACTGATCGCGGGCAGACGTCGAGCTCGTATGCTGGGCACCGGCGG 1653  
QY 404 ProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423  
DB 1654 GCCGACCTGGAGGACATGCTGGCGGCTTCGAGTCGGAGCACAGGACAGGTGGCGGG 1713  
QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443  
DB 1714 TGGGTGGGCTTCTCGTGCCTCGCGCACCGCATCGCGCGGGCGGACATCTCTGTG 1773  
QY 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463  
DB 1774 ATGCCGTGCGGCTTCGAGCCGTCGGGCTGAACAGCTCTACGCCATGGCGTACGGGAC 1833  
QY 464 ValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPhe 483  
DB 1834 GTGCCCGTGTGCACGCGCTGGGGGGCTCCGGGACACGCTGGCGCGCTTCACCGCTTC 1893  
QY 484 GlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMet 503  
DB 1894 AACGACACC-----GGGCTCGGTGGACGTTTCGACCGCGGAGCGGAACCGGATG 1944  
QY 504 PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523  
DB 1945 ATCGACGCGCTCTCGCACTGCTC-CACCACTGACCGGAACCTACAGGAGAGCTGGCGCG 2003  
QY 524 AlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
DB 2004 CTGCAGGGCGCGGCATGTCGCGAGGACTCAGCTGGGACCAACCGCGC 2051  
RESULT 5  
US-60-757-216-1  
; Sequence 1, Application US/60757216  
; GENERAL INFORMATION:  
; APPLICANT: Claus Frobberg,  
; APPLICANT: Ralf-Christian Schmidt  
; TITLE OF INVENTION: Rice starches with improved quality  
; FILE REFERENCE: BCS 05-5011-US Provisional  
; CURRENT APPLICATION NUMBER: US/60/757,216  
; CURRENT FILING DATE: 2006-01-06  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 3006  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (227)..(2623)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: Region1  
; LOCATION: (1190)..(1279)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: Region2  
; LOCATION: (1493)..(1612)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: Region3  
; LOCATION: (2147)..(2350)  
; OTHER INFORMATION:  
; PUBLICATION INFORMATION:



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; LOCATION: (1493)..(1612)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: Region3
; LOCATION: (2147)..(2350)
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; TITLE: Nucleic acid molecules encoding enzymes from wheat which are
; TITLE: Involved in starch synthesis
; DATABASE ACCESSION NUMBER: D9745545
; DATABASE ENTRY DATE: 1998-05-21
; PATENT DOCUMENT NUMBER: WO 97 45545
; PATENT FILING DATE: 1997-05-28
; PUBLICATION DATE: 1997-12-04
; RELEVANT RESIDUES: (1)..(2825)
US-60-757-810-1

Alignment Scores:
Pred. No.: 3,33e-98 Length: 3006
Score: 1050.50 Matches: 230
Percent Similarity: 60.4% Conservative: 70
Best Local Similarity: 46.3% Mismatches: 170
Query Match: 36.3% Indels: 28
DB: 12 Gaps: 8

US-10-628-525A-21 (1-539) x US-60-757-810-1 (1-3006)
QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAsp 69
DB 1151 AACGGTTCGTCGGCTGCTGAGTGTCTCCCTGCAAAACAGGTGGTCTGGAGAT 1210
QY 70 ValCysGlySerLeuProValAlaLeuAlaAtrGlyHisArgValMetValMet 89
DB 1211 GTTGGGGTCTGCTCCCAAGCTTTGGCAAGAGGACATCGTTATGTTGTGTA 1270
QY 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109
DB 1271 CCAAGGTAT-----GGGACTATGAAGAGCCTACGATGTCGGAGTC 1312
QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129
DB 1313 CGAAATACTACAGGCTCTGGACAGGATATGGAAGTGAATTTATTCATCTTATATC 1372
QY 130 AspSerValAspTyrValPheValAspHisProSerTyr---HisArgProGlyAsnLeu 148
DB 1373 GATGGAGTTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1432
QY 149 TyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyr 168
DB 1433 TATGGG-----GGCAGCAGACAGAGAAATATATGAAGCGCATGATTTTGTCTGCAAG 1483
QY 169 AlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGln---Asn 187
DB 1484 GCGCTGTTGAGGTTCCATGCGCAGCTTCATCGCGGGTCCCTTATGGGATGGAAT 1543
QY 188 CysMetPheValValAsnAspTyrHisAlaSerLeuValProValLeuLeuAlaLys 207
DB 1544 CTGGTGTATTGCAATGATTGGACACGGCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1603
QY 208 TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla 227
DB 1604 TACAGGACCATGTTGATGTCAGTACATCTCGTCCATGATGATGATGATGATGATGATGAT 1663
QY 228 HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyr 247
DB 1664 CACCAAGGCGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1723
QY 248 GlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeuAspLysGlyGlu 267
DB 1724 -----GCACACTTCAGACTGTACGACCCCGTGGTGGTGGTGGTGGTGGTGGTGGT 1759
QY 268 AlaValAsnPheLeuLysGlyAlaValThrAlaAspArgIleValThrValSerLys 287
DB 1724 -----GCACACTTCAGACTGTACGACCCCGTGGTGGTGGTGGTGGTGGTGGTGGT

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DB 1760 CACGCCAACTACTTCGCGCGCGCTGAAGATGGCGGACAGGTTTGTGTGTAGSCCC 1819
QY 288 GlyTyrSerTyrGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSer 307
DB 1820 GGTACCTGTGGAGCTGAAGACGGTGGAGGCGCTGGGGCTTCACGACATCATACGG 1879
QY 308 SerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTyrAsnPro 327
DB 1880 CAGAACGACTGGAAGACCGCGGCTCTCAACGGCATCTCAACGGCATCTCAACGGATGGAAACCC 1939
QY 328 AlaThrAspLysCysIlePro-----CysHisTyrSerValAspAspLeu--- 342
DB 1940 GAGGTGGAGCGCCACCTCAAGTCGGACGCTACACCACTTCTCTCTGAGGACGCTGGAC 1999
QY 343 SerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgPro 362
DB 2000 TCCGCAAGCGGACGCTCAAGAGGCGCTGCGAGCGGAGCTGGGCTGCGAGTCTCGCGCC 2059
QY 363 AspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIle 382
DB 2060 GACGTGCGGCTGCTGCTGCTTCTATCGCGCTGCGAGCGGCGAGAGGGCTGGAGATCATC 2119
QY 383 GlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGly 402
DB 2120 GCGGACGCGCATGCCCTGATCGTGAAGCGGACGCTGAGTGTGATGCTGGCGACCGGG 2179
QY 403 AspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheIysAspLysPheArg 422
DB 2180 CGCCACGACCTGGAGAGCATGCTGCAGCATCTTCGAGCGGAGCACACGACAGGTGGCG 2239
QY 423 GlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeu 442
DB 2240 GGTGGGTGGGTGTTCTCGTGGCTGGCGGACCGGATCATCGCGGGCGGCGGCGGCTC 2299
QY 443 LeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGly 462
DB 2300 CTCATGCCCTCCGCTTCGAGCGGCTGCGGCTGGAACAGCTCTACGCCATGCGCTACGGC 2359
QY 463 ThrValProValValHisAlaThrGlyLeuArgAspThrValGluAsnPheAsnPro 482
DB 2360 ACCGTCGCGCTGTCACGCGCTGCGGCGCTTCAGGACACCGCTCGCGCGCTTCGACCCC 2419
QY 483 PheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsn 502
DB 2420 TTCACCACTCC-----GGGCTCGGTGGAGCTTCGACCGCGCGGCGGCGCACAG 2470
QY 503 MetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGly 522
DB 2471 CTGATCGAGGCGCTCGGCGCATGCTCCT-CCGCACTTACCGAGACTTCAAGGAGAGCTGGAG 2529
QY 523 ArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
DB 2530 GGCCCTCCAGGAGCGCGCATGCTCGAGGACTTTCAGGAGTGGGAGACGCGCGC 2580

RESULT 7
US-11-227-183A-16489
; Sequence 16489, Application US/11227183A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE OF INVENTION: Plants
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US
; CURRENT APPLICATION NUMBER: US/11/227,183A
; CURRENT FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: US 09/619,643
; FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 16489
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:

```



OTHER INFORMATION: Clone ID: LIB3150-035-Q1-N1-F10.F2  
US-11-227-183A-16489

Alignment Scores:		
Pred. No.:	2,686-95	558
Score:	1012.00	182
Percent Similarity:	100.0%	0
Best Local Similarity:	100.0%	0
Query Match:	35.0%	0
DB:	10	0
Length:		
Matches:		
Conservative:		
Mismatches:		
Indels:		
Gaps:		

US-10-628-525A-21 (1-539) x US-11-227-183A-16489 (1-558)

Qy	87	GlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetVal	87
Db	12	GGAGATGTTTGTGGTTCATTGCAGTTCCTCTGCTCGTGGTCAACCGTGTGATGGTT	71
Qy	88	ValMetProAspTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThr	107
Db	72	GTAATGCCAGATATTAAATGGTACCTCCCATAGAAATATATGCAATGCAATTTACACA	131
Qy	108	GluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlu	127
Db	132	GAANAACACATTCGGAATTCATGCTTTGGCGGTGAAACATGAAGTTACCTCTTCCATGAG	191
Qy	128	TyrArgAspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsn	147
Db	192	TATAGAGATTTCAGTTGACTGGGTGTTTGTTCATCATCCCTCATATCACAGACCTGGAAAT	251
Qy	148	LeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCys	167
Db	252	TTATATAGAGATAAGTTTGGTGCCTTTTGGTGATTAATCAGTTTCAGATACACACTCCTTTGC	311
Qy	168	TyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsn	187
Db	312	TATGCTGCATGTAGGCTCCTTTGATCCTTGAAATGGAGGATATATTATGACAGAAAT	371
Qy	198	CysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaLys	207
Db	372	TGCATGTTTGTTCATATGATTGGCATGCCAGTCTAGTGCAGTCTCTTCCTGTCGAAA	431
Qy	208	TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla	227
Db	432	TATAGACCATATGGTGTATTAAAGACTCCCGCAGCACTCTTGTGTAATACATAATTTAGCA	491
Qy	228	HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTrpTyr	247
Db	492	CATCAGGGGTATGAGCCCTGCAGACACATATCCTGACCTTGGGTGCCACCTGTAATGGTAT	551
Qy	248	GlyAla	249
Db	552	GGAGCT	557

## RESULT 8

```

US-11-227-183A-16488
; Sequence 16488, Application US/11227183A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalquidi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US
; CURRENT APPLICATION NUMBER: US/11/227,183A
; CURRENT FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: US 09/619,643
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 16488
; LENGTH: 555
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: unsure at all n locations

```

```

; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3150-035-Q1-N1-P10.F1
US-11-227-183A-16488

```

Alignment Scores:		
Pred. No.:	2,53e-93	555
Score:	993.00	180
Percent Similarity:	97.3%	Conservative: 0
Best Local Similarity:	97.3%	Mismatches: 5
Query Match:	34.3%	Indels: 0
DB:	10	Gaps: 0

US-10-628-525A-21 (1-539) x US-11-227-183A-16488 (1-555)

Qy	66	GlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAaArgGlyHisArgVal	85
Db	1	GGTACTANGTNNNTNTGTGGTTCATTGCCAGTTGCTCTTGCTGCTGGTGTCACCGTGTA	60
Qy	86	MetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPhe	105
Db	61	TAGGTGTGAATGCCCAGATATTTAAATGGTACCTCCGATAAGAAATATGCAAAATGCAATTT	120
Qy	106	TyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePhe	125
Db	121	TACACAGAAAACACATTCCGATTCCTCTTGGCGGTGAACATGAAGTTTACCTTCTTCTC	180
Qy	126	HisGluTyrArgAspSerValAspTrpValPheValAspHisProSerTyrHisArgPro	145
Db	181	CATGAGTATAGAGATTCAAGTTGACTGGGTGTTTGTGTGATCATCCCTCATATCACAGACCT	240
Qy	146	GlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeu	165
Db	241	GGAAATTTATATATGGAGATAAGTTTGGTGTCTTTTGGTGATATATCATAGTTTCAGATACACACTC	300
Qy	166	LeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGly	185
Db	301	CTTTGCTATGCTGCATGTGAGGCTCCTTTGATCCTTGAAATGGAGAGATATATTATATGGA	360
Qy	186	GlnAsnCysMetPheValValaAsnAspTrpHisAlaSerLeuValProValLeuLeuAla	205
Db	361	CAGAAATTCGATGTTTGTGTCAATGATGGCATGGCATGCCAGTCTAGTGCCAGTCTCTTCTGCT	420
Qy	206	AlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsn	225
Db	421	GCAAAATATAGACCATATGGTGTTTATAAAGACTCCCGCAGCATTTCTTGTAAATACATAAT	480
Qy	226	LeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProProGlu	245
Db	481	TTAGCACATCAGGGTGTAGAGCTTGCAGACACATATCTTGACCTTGGGTGGCCACCTGAA	540
Qy	246	TrpTyrGlyAlaLeu	250
Db	541	TGGTATGGAGCTCTG	555

## RESULT 9

```

US-11-330-822-54
; Sequence 54, Application US/11330822
; GENERAL INFORMATION:
; APPLICANT: GUAN, HANPING
; APPLICANT: KEELING, PETER L.
; TITLE OF INVENTION: PLANTS LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; TITLE OF INVENTION: HOSTS
; TYPE OF INVENTION: PLANTS
; FILE REFERENCE: 15053-04
; CURRENT APPLICATION NUMBER: US/11/330,822
; CURRENT FILING DATE: 2006-01-11
; PRIOR APPLICATION NUMBER: PC1/US98/06560
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/042,939
; PRIOR FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 54
; LENGTH: 2007

```

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/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(2007)
/ US-11-330-822-54

Alignment Scores:
Pred. No.: 5 67e-91 Length: 2007
Score: 978.50 Matches: 217
Percent Similarity: 59.2% Conservative: 76
Best Local Similarity: 43.8% Mismatches: 174
Query Match: 33.8% Indels: 29
DB: 8 Gaps: 9

US-10-628-525A-21 (1-539) x US-11-330-822-54 (1-2007)

QY 50 SerileValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAsp 69
Db 544 AACGTGATCGTGGTGGCTGCTGAATGTTCTCCATGCTGCAAAACAGGTGTTCTGGAGAT 603
QY 70 ValCysGlySerLeuProValAlaLeuAlaAArgGlyHisArgValMetValValmet 89
Db 604 GTTGTGGAGCTTTACCCAGGCTTTAGCGAGAAGAGGACATCGTGTATTATGTTGTGTA 663
QY 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109
Db 664 CNAAGTAT-----GGGGACTATGCGAAGCCCTTTGATATGGGAATC 705
QY 110 HisileArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129
Db 706 CGGAATACTACAAAGCTCGAGGACAGGACCTAGAAGTGAATTAATTCATGCAATTATT 765
QY 130 AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyr 149
Db 766 GATGAGTGCAGCTTGTGTTCATTGATGCTCTTTCCGGCACCGCTCAAGATGACATATAT 825
QY 150 GlyAspLysPheGlyValaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla 169
Db 826 GGG-----GGAAAGTAGGAGGAATCATGAAGCGCATGATTTTGTTCAGGTT 876
QY 170 AlaCysGluAlaProLeuLeuLeuGluLeuGlyTyrIleTyrGlyGln---AsnCys 188
Db 877 GCTGTGAGTTCTTGGCACGCTCCATCGCGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 936
QY 189 MetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyr 208
Db 937 GTGTTTCATTCGCAATGAAATGGCACACCTGCACCTCTGCTGCTGCTGCTGCTGCTGCTG 996
QY 209 ArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHis 228
Db 997 AGAGACCATGGTGAATGAGTACACTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 1056
QY 229 GlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTrpTyrGly 248
Db 1057 CAGGCGCGGTGCTGTACATGAATTCGCGTACATGAGCTTGTGTGAACACTAACCTTCAA 1116
QY 249 AlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGlyGluAla 268
Db 1117 CATTTTCGAGCTGTACGATCCCGTC-----GGTGGCGAGCAC 1152
QY 269 ValAsnPheLeuLysGlyAlaValVal---ThrAlaAspArgIleValThrValSerLys 287
Db 1153 GCCAATCTTTGCCCGGTGTGTTCTGAAGATGGAGACCGGGTGTGTGTGTGTGTGTGTGTGT 1212
QY 288 GlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSer 307
Db 1213 GGTACCTGTGGAGCTGAAGACAGTGAAGCGGCTGGGGCTCCACGACATCATCGCT 1272
QY 308 SerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnPro 327
Db 1273 TCTAACGACTGAAGATCAATGGCATTCGTGAACCGCATCGACCAACGAGGAGTGAACCC 1332
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QY 328 AlaThrAspLysCysIlePro-----CysHisTyrSerValAspAspLeu--- 342
Db 1333 AAGTGGACGTGCACCTCGGTGGACGGCTACCAACTACTCTCTCGACACATCGAC 1392
QY 343 SerGlyLysAlaLysCysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgPro 362
Db 1393 GCTGGAAGCGGCAGTCAAGCGGCCCTGCGAGCGGACGCTGGGCTGGAAGTGGCGAC 1452
QY 363 AspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 382
Db 1453 GACGTGCCCTGCTCGGTTCATCGGGCTCTGGATGGACAGAGGGCGGTGACATCATC 1512
QY 383 GlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGly 402
Db 1513 GGGGACGGGATGCCGTGATCGCGGGGAGGACGTGCGAGCTGTGTGTGTGTGTGTGTGT 1572
QY 403 AspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArg 422
Db 1573 CCACCTGACCTGGAACGAATGCTGCAGCACCTTGGAGCGGAGCATCCCAACAAGGTGCGC 1632
QY 423 GlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeu 442
Db 1633 GGGTGGGTGGGTTCCTGCTCCTAATGTGTGCATCGCATCACCGCGGCGGCCACCGTGTG 1692
QY 443 LeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGly 462
Db 1693 GTGATGCCCTCCGCTTCCCGGC---GGGTGAACCAAGCTCTACGCGATGCATACGCG 1749
QY 463 ThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnPro 482
Db 1750 ACCGTCCCTGTGTGCACCGCGTGGCGGGCTCAGGGACACCGTGGCGCGCTTCGACCCG 1809
QY 483 PheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsn 502
Db 1810 TTC-----GGCGACGCGCGGCTCGGGTGGAGCTTTTGACCGCGCGGAGCCCAACAG 1860
QY 503 MetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuGly 522
Db 1861 CTGATCGAGGTGCTCAGCCACTGCTT---CGACACGTACCGAAACTACGAGGAGGTGGNA 1919
QY 523 ArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyPro 537
Db 1920 GAGTCTCCAGGCGCGCGCATGTGCGAGAACCTCAGCTGGGACCA 1964

RESULT 10
US-11-330-822-50
; Sequence 50, Application US/11330822
; GENERAL INFORMATION:
; APPLICANT: GUAN, HANPING
; APPLICANT: KEELING, PETER L.
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; TITLE OF INVENTION: HOSTS
; FILE REFERENCE: 15053-04
; CURRENT APPLICATION NUMBER: US/11/330,822
; CURRENT FILING DATE: 2006-01-11
; PRIOR APPLICATION NUMBER: PCT/US98/06660
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/042,939
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 50
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1815)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1819)..(1914)
US-11-330-822-50
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**Alignment Scores:**

Pred. No.:	2,248-76	Length:	1915
Score:	838.00	Matches:	200
Percent Similarity:	54.3%	Conservative:	86
Best Local Similarity:	38.0%	Mismatches:	174
Query Match:	29.0%	Indels:	68
DB:	8	Gaps:	15

US-10-628-525A-21 (1-539) x US-11-330-822-50 (1-1915)

Qy		40	LysGluGlnAlaArg-----	169	CAGCAGCAGGGCGCGCGGGGGGCAGGTTCCTCGTCTCGTCTCGTGCGGCCACAGCCGCGC	228	-----AlaLysValThr 48
Dd							
Qy		49	GlnSerIleValPheValThrGlyLeuAlaSerProTyrAlaLysSerGlyLeuGly 68	229	ATGAACGTCGCTTCGTGGCGCCGAGATGGCGCGTGGAGCAACACCGCGGCTCGGC	288	
Dd							
Qy		69	AspValCysGlySerLeuProValAlaLeuAlaAalArgGlyHisArgValMetValVal 88	289	GACGTCTCGCGGGCTGCGCGGCCATGGCGCGAACGGCACCGTGTCATGTGTCGTC	348	
Dd							
Qy		89	MetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGlu 108	349	TCTCCCCTACTAC-----GACCAGTACAAGGACGCTGGGACACCAAGC	390	
Dd							
Qy		109	LysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyr 128	391	GTCGTGCCGAGATCAAGATGGGAGACGGGTACGAGCGGTCAAGTTCTTCCAATGCTAC	450	
Dd							
Qy		129	ArgAspSerValAspTrpValPheValAspHisProSerTyr----- 142	451	AAGCGCGGAGTGACCGCGTGTTCGTGACCAACCACCTGTTCTCTGGAGAGGTTTGGGGA	510	
Dd							
Qy		143	HisArgProGlyAsnLeuTyrGlyAspLysPheGlyAla---PheGlyAspAsnGlnPhe 161	511	AAGACCGAGGAGAAGATCTACGGGCTGTCGCTGGAAACGGACTACAGGACCAACAGCTG	570	
Dd							
Qy		162	ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGly 181	571	CGGTTACGCTGCTATGCCAGCAGCACTTCAAGCTCCAGGATCCTGAGGCTCAACAC	630	
Dd							
Qy		182	-----TyrIle-----TyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196	631	AACCCATACTCTCCGGNCCATACGGGGGAGACGTCGTGTTCTGTCACACACTGGCAC	690	
Dd							
Qy		197	AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216	691	ACCGGCGCTCTCTGCTACTCTCAAGAGCAACTACCACTGCCACGGCATCTACAGGAC	750	
Dd							
Qy		217	SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236	751	GCAAGACCGGTTCTGCATCCACAACATCTCTACCAAGGCGCGGTTGCGCTTCTCCGAC	810	
Dd							
Qy		237	TyrProAspLeuGlyLeuProGluTyrTrpTyrGlyAlaLeuGluGluTrpValPheProGlu 256	811	TACCGGAGCTGAACCTCCCGGAGAGATTCAAGTCGTCCTTCGATTTCATC-----	861	
Dd							
Qy		257	TrpAlaArgArgHisAlaLeuAspLys-----GlyGluAlaValAsnPheLeuLys 273	862	-----GACGGCTACGAGAGCCCGCTGCNAGCGCCGGAAGATCAACTGATGAAG	909	
Dd							
Qy		274	GlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGlu--- 292	910	GCGGGATCTCTGAGGCCGACAGGTCCTCACCGTCAGCCCTACTACGCGGAGGCTC	969	
Dd							
Qy		293	ValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerVal 312	970	ATCTCCGGCATCGCCAGGGCTGCGAGCTCGACACAACATCATG-----CGCTCACCGGC	1023	
Dd							
Qy		313	LeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys 332	1024	ATCACCGCATCGTCAACGCATGAGCGTCAAGCGAGTGGGACCCACAGCAGGACCACTAC	1083	
Dd							

Qy	333	IleProCysHisTyrSerValAlaAsp	---LeuSerGlyLeuAlaLysCysValGlyAla	351
Db	1084	ATCCCGCTGAAGTACGACGTGTCCAGCGCGGTGGAGGCCAAGCGCGTGAACAAGGAGGCG		1143
Qy	352	LeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGly		371
Db	1144	CTGCAGCGGAGGTGCGGCTCCCGGTGGACCGGAACATCCCGTGGTGGCGTTTCATCGGC		1203
Qy	372	ArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArg		391
Db	1204	AGGCTGGAAGACAGAAAGGCCCCGACGTCAATGGCGCGCCCATCCCGCAGCTCATGGAG		1263
Qy	392	-----GluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrp		409
Db	1264	ATGTGTGAGGACGTGCAGATCGTTCTGTCTGGGCACGCGCAAGAAGAAGTTCGAGCGCATG		1323
Qy	410	MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerVal		429
Db	1324	CTCATGAGCCCGAGGAGAAAGTTCACGACAGGTGCGCGCTGGTCAAGTTCAACGCG		1383
Qy	430	ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu		449
Db	1384	CGCGTGGCGCACCATCATGTCGCGCGCGCGACGTGCTCGCGTCACACGCGCTTCGAG		1443
Qy	450	ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla		469
Db	1444	CCCTGCGGCGCTCATCAGCTGCAGGGGATGCGATACGGAACCCCTGCGCCTGCGCGTCC		1503
Qy	470	ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln		489
Db	1504	ACCGTGGACTCGTCGACACCATC		1536
Qy	490	GlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsn		509
Db	1537	AAGACCGGGTTCACATGTCGCGCGCTCAGCGTCGAC		1572
Qy	510	CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis		529
Db	1573	TGTAACGTCGTGGA-GCCGGC		1616
Qy	530	ValLysArgLeuHisValGly	536	
Db	1617	ATTGCAGCGCGCCATCAAGGT	1637	
RESULT 11				
US-11-292-078-969				
; Sequence 969, Application US/11292078				
; GENERAL INFORMATION:				
; APPLICANT: Deikman, Jill				
; APPLICANT: Feng, Paul C.C.				
; APPLICANT: Fincher, Karen L.				
; APPLICANT: Ziegler, Todd E.				
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With				
; TITLE OF INVENTION: Plants				
; FILE REFERENCE: 16517.346 - 38-21(52274)C				
; CURRENT APPLICATION NUMBER: US/11/292,078				
; CURRENT FILING DATE: 2005-12-02				
; PRIOR APPLICATION NUMBER: US 10/021,323				
; PRIOR FILING DATE: 2001-12-12				
; PRIOR APPLICATION NUMBER: US 60/255,619				
; PRIOR FILING DATE: 2000-12-14				
; NUMBER OF SEQ ID NOS: 17880				
; SEQ ID NO 969				
; LENGTH: 598				
; TYPE: DNA				
; ORGANISM: Gossypium hirsutum				
; FEATURES:				
; OTHER INFORMATION: Clone ID: LIB3825-016-Q1-K6-D4				
US-11-292-078-969				
Alignment Scores:				
Pred. No.:		1.92e-73	Length:	598

**Alignment Scores:**

Pred. No.:

1.92e-73

Length: 598

Score: 802.50 Matches: 148  
 Percent Similarity: 86.6% Conservative: 20  
 Best Local Similarity: 76.3% Mismatches: 25  
 Query Match: 27.7% Indels: 1  
 DB: 10 Gaps: 1

US-10-628-525A-21 (1-539) x US-11-292-078-969 (1-598)

QY 301 GlyLeuAsnGlnLeuLeuSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320  
 DB 14 GGTAAATCAGCTATTAAAGCAGTCGGAGAGTGTCTGACTGGAATTAACAACGGCATT 73  
 QY 321 AspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340  
 DB 74 CATATTGCTGAATGGATCACTTCAGATGAGCATATTGCTTTCATTATTCTGCTGCT 133  
 QY 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGlnLeuGlyLeuProIle 360  
 DB 134 TCTCTATCTGGAAGGTTCAATGCAAGACTGCTCTCAACAGGAACTTGGTTTCCAAAT 193  
 QY 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380  
 DB 194 AAGCCTGATGTGCTTGAATGATTATCGGAGACTGGACTTACCAGAAAGGCATTGAC 253  
 QY 381 LeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
 DB 254 CTGATCCACTGGGCAATTCAGAACTTATGAGATGATCTACATTTGTAATGCTTGGC 313  
 QY 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys 420  
 DB 314 TCTGGGAGCCACTTTACGAAGACTGGATGAGATCAGCAGAGAATACTTACAGAGACAA 373  
 QY 421 PheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440  
 DB 374 TTTGCGGTGGTGGTGGATTTAGTTGTTCCAATCTCTCATAGGATCACTCGAGGCTGTGAC 433  
 QY 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460  
 DB 434 ATACTATTGATGCCTTCAGATTCGAGCCCTGTGGACTTAATCAGTTATATGCGATGAGA 493  
 QY 461 TyrGlyThrValProValValHisAlaThrGlyLeuArgAspThrValGluAsnPhe 480  
 DB 494 TATGGAACGTGCTCTAGTTATGTCACAGAGGACTTAGAGACACAGTAGAATTC 553  
 QY 481 AsnProPhe--GlyGluAsnGlyGluGlnGlyThrGlyTrp 493  
 DB 554 AATCCGTACCGCGAAGAGGTAGAGTGAAGGCACCGGTGG 595

# RESULT 12

PCT-US05-47111-476  
 ; Sequence 476, Application PC/TUS0547111  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abad, Mark et al.  
 ; TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits  
 ; FILE REFERENCE: 38-21(53720)B  
 ; CURRENT APPLICATION NUMBER: PCT/US05/47111  
 ; CURRENT FILING DATE: 2005-12-21  
 ; NUMBER OF SEQ ID NOS: 52803  
 ; SOFTWARE: Patentin version 3.3  
 ; SEQ ID NO 476  
 ; LENGTH: 1882  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa  
 PCT-US05-47111-476

Alignment Scores:  
 Pred. No.: 2,75e-71 Length: 1882  
 Score: 789.00 Matches: 178  
 Percent Similarity: 56.3% Conservative: 87  
 Best Local Similarity: 37.8% Mismatches: 172  
 Query Match: 27.3% Indels: 34  
 DB: 1 Gaps: 11

US-10-628-525A-21 (1-539) x PCT-US05-47111-476 (1-1882)  
 QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyIleGlyAsp 69  
 DB 268 ACATAAATTTTATTGCAACTGAATGTCCCATGTGCAAAACCTGGAGCCTCGTGAT 327  
 QY 70 ValCysGlySerLeuProValAlaLeuAlaAArgGlyHisArgValMetValValMet 89  
 DB 328 GTTCTAGGGGAGCTGCCCTCTCTTGTCTCAATGCGGACATCGTGTCTATGACAATAGTT 387  
 QY 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109  
 DB 388 CTTGTTAT-----GATCAATACAAAGATGATGGATACAAATGTC 429  
 QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129  
 DB 430 CTTGTGAGGTCAATATTGTTGTCAGAGGACAGAAACAGTCTGCTTCTCCACTGCTATAAA 489  
 QY 130 AspSerValAspTrpValPheValAspHisProSerTyr-----HisArg 144  
 DB 490 AGGGAGTTGACCGTGTGTTTGTGATCATCTCTATGTTCTTGTGAGAGGTATGGGGCAAG 549  
 QY 145 ProGly---AsnLeuTyrGlyAspLysPheGly---AlaPheGlyAspAsnGlnPheArg 162  
 DB 550 ACTGGACCAAAATTTATCGGTCTTACCCTGAGATGACTACCGGACAAACAGTTGCGG 609  
 QY 163 TyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGlnLeuGlyGly--- 181  
 DB 610 TTTCTGCTTTTATGCTGCTCTTGGAGGCTCCAAGGGTCTCAATCTCAACAATTTCT 669  
 QY 182 ---TyrIle-----TyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAla 197  
 DB 670 GAATATTCTCGGACCATATGTTGAAATGTTGTTCTGTTGCAATGACTGGCACACT 729  
 QY 198 SerLeuValProValLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSer 217  
 DB 730 GGAGTCTCGCATGCTATCTCAAGAGCATCTATCAGGCAAAAGGAATGTATGTGAATGCT 789  
 QY 218 ArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProHisSerThrTyr 237  
 DB 790 AAGTGTGCTTTCTGCATTCAATATGCTTACCAGGGTAGATTTGCCAGAGAAGACTTT 849  
 QY 238 ProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyr 257  
 DB 850 GAACCTCTTAATCTACCGGACAGTTCTGCTTCAATTTGATTTTATGATGGGCAATTT 909  
 QY 258 AlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValVal 277  
 DB 910 AAACCT-----GTAGTAGGTAGAAAGATTAACTGGATGAAGCAGGGATCACT 957  
 QY 278 ThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla--- 296  
 DB 958 GAATGTGATCTGGTTATGACGGTTAGTCCCATTTATGCAAGAACTCGCTTCTGGCCCA 1017  
 QY 297 GluGlyGlyGlnGlyLeuAsnGlnLeuLeuSerArgLysSerValLeuAsnGlyIle 316  
 DB 1018 GATAAAGGTGTGAATTTGATGGCATCTTCCACA---AAGCCCTTGAATGGAATTT 1074  
 QY 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
 DB 1075 GTCAATGGCATGGATGTTTATGAATGGAATCAGCAACAGATCAGTACATCAGCGTGAA 1134  
 QY 337 TyrSerValAspAspLeuSer---GlyLysAlaLysCysLysGlyAlaLeuGlnLysGlu 355  
 DB 1135 TACGATGCAACACCGTAACTGAAGCAGGCACTCAATTAAGGAAATGCTACAGCTGAA 1194  
 QY 356 LeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyr 375  
 DB 1195 GTTGGTGTGCTGTGACTCGAGCATTTCTTTAAATAGTTTGTGGTGTCTTGAAGAG 1254  
 QY 376 GlnLysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGln 395  
 DB 1255 CAGAAAGGGTCAGACATACTAATTGACGCAATTCAGAGTTCGTGGAGGGGAATGTCCAG 1314



Db 1588 GGTTCGTCAATCGAGTCGGAACCTGTTGAT 1620

RESULT 14

US-10-513-024-1373

; Sequence 1373, Application US/10513024

; GENERAL INFORMATION:

; APPLICANT: CHIRON SRL

; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH

; APPLICANT: TELFORD John

; APPLICANT: MARGNANI Vega

; APPLICANT: MARGARIT Y ROS Immaculada

; APPLICANT: GRANDI Guido

; APPLICANT: FRASER Claire

; APPLICANT: TETTELIN Hervé

; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B

; FILE REFERENCE: P030497W0

; CURRENT APPLICATION NUMBER: US/10/513,024

; CURRENT FILING DATE: 2004-11-01

; PRIOR APPLICATION NUMBER: GB-0210128.5

; PRIOR FILING DATE: 2002-05-02

; NUMBER OF SEQ ID NOS: 1373

; SOFTWARE: SeqWin99, version 1.03

; SEQ ID NO 1373

; LENGTH: 2160266

; TYPE: DNA

; ORGANISM: Streptococcus pyogenes

US-10-513-024-1373

Alignment Scores:

Pred. No.: 1,62e-61 Length: 2160266  
Score: 739.50 Matches: 183  
Percent Similarity: 54.4% Conservative: 94  
Best Local Similarity: 36.0% Mismatches: 160  
Query Match: 25.6% Indels: 73  
DB: 15 Gaps: 7

US-10-628-525a-21 (1-539) x US-10-513-024-1373 (1-2160266)

QY 17 IleAlaGluGly---SerIleAspGlnThrValVal-----ValAlaSer 30  
Db 857475 ATCGGAGAGGGGGCAACCACTGATTAATTTGACAAATGCGTTAAGGTTCATCC 857534  
QY 31 -----GluGlnAspSerGluIleValValGlyLys-----GluGln 42  
Db 857535 CGAGTTACATTGAAGGTAGTATGATAAACCCTAGTATGATTCCTAAATTTTCAGGATT 857594  
QY 43 AlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAla 62  
Db 857595 AATGA-GGATATTATACAAATGAAATAATGTTGTCGGCAGAGGGTCTCCCTTTGCT 857653  
QY 63 LysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGly 82  
Db 857654 AAACAGGGTGGTGGGAGATGATGTCGACATCCCAAAATCACTTAGTAAAAAGGT 857713  
QY 83 HisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAla 102  
Db 857714 CATGATGTCGCTGTTGTCATGCCATATTAT-----GATATGGTAGACCAAAATTTGGA 857767  
QY 103 AsnAla-----PheTyrThrGluLysHisIleArgIleProCysPhe 116  
Db 857768 GACCAAAATAGAAAACCTCATGTATTCTATACA----- 857800  
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyr-----Arg 129  
Db 857801 -----GATGTTGGCTGGCGTCATCAATATGTAGGATTAAGAGACTTTCTCAA 857848  
QY 130 AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyr 149  
Db 857849 GATAATGTTACGTTCTTACTTATGATATCAATATATATATTTTATAGAGGTCAATGTCAT 857908  
QY 150 GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla 169  
Db 857909 CGTGAT-----TGGGATGATGGGAGCGTTTGTCTATTTCCAATTAGCT 857953

QY 170 AlaCysGluAlaProIleLeuGluLeuGlyGlyTyrIleTyrClyGlnAsnCysMet 189  
Db 857954 GCTTTAGAG-----TTGATGGAGAAAATCGATTTTATTATCCCGAT-----GTC 857995  
QY 190 PheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyrArg 209  
Db 857996 TTACAGCTCCATGATATCATACAGCAATGATTCCTTCTTATTTGAAAAGAGATACCAC 858055  
QY 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGln 229  
Db 858056 TGGATTCCGGCTATAATAATAAAGAGCAGATTTTACTATTACAAATATGAAATTTCAA 858115  
QY 230 GlyValGluProAlaSerThrTyrProAspLeu---GlyLeuProGluTrpTyr--- 247  
Db 858116 GGGCAGTTGGTCCAGAAATGTTAGGAGATTTATTGGAGTGTGGCGCTCAGAGATATGAA 858175  
QY 248 ---GlyAlaLeuGluTrpValPheProGluTrpAlaArgHisAlaLeuAspLysGly 266  
Db 858176 GATGGAACTCTTAGATGG----- 858196  
QY 267 GluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSer 286  
Db 858197 AATTGCTTAATTTGATGAAGCAGCAATTTCTTACTCAGATAGAGTCAACCGTATCA 858256  
QY 287 LysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeu 306  
Db 858257 CCAAGCTAGCAATGAAATAAAACTCCAGAAATTTGGTAAAGGTTAGATCAAAATATG 858316  
QY 307 SerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsn 326  
Db 858317 CGTATGGAAGCAGGCAAAATTTATCTGGAATTTGAATGTTGATAGCGATTTGTTAAAT 858376  
QY 327 ProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLysSerGlyLysAla 346  
Db 858377 CCAGAAACAGATGCTTTTTCATATCATTTTCAAAAAGCAACTTAGAGGCAAAAT 858436  
QY 347 LysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeu 366  
Db 858437 AAAATAAGTTGGCTTTTACAGGAAATTTGGGCTTACCTCAAGATAAAAATGATACATTA 858496  
QY 367 IleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIle 386  
Db 858497 ATTGCTATTGTTTTCAGGACTTACCGATCAAAAAGGATTTGATATTATTGCTTCTGAAATG 858556  
QY 387 ProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeu 406  
Db 858557 GACAAATATGCTTCAACAAGATATTCAAAATGGTTATTTTAGGAACAGGCTATCACCATTT 858616  
QY 407 GluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGly 426  
Db 858617 GAAGAAAGCTTCTTATTTTGTCTAGTCGTACCTCGTAAATACTATCTGCTAATATTACT 858676  
QY 427 PheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSer 446  
Db 858677 TTTGACTTAAGATTAGCGCAACAGATTTATGGGCTTCAGATATCTTCATGATGCCAGT 858736  
QY 447 ArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProVal 466  
Db 858737 GCTTTTGAACCTTGTGGTCTCTCGCAGATGATGGCTATCAGATATGATGATGCTGCTTG 858796  
QY 467 ValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnPropGlyGluAsn 486  
Db 858797 GTACATGAAGTTGGAGGATTAAGATATCTGTGGTAGCCCTTCATCAATTTGATGTAGT 858856  
QY 487 GlyGluGlnGlyThrGlyTrpAlaPhe 495  
Db 858857 -----GGTACAGGTTTTCATT 858874

RESULT 15

US-11-348-413-6913

; Sequence 6913, Application US/11348413

; GENERAL INFORMATION:



APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
APPLICANT: Murphy, Ellen  
APPLICANT: Olmsted, Stephen  
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
FILE REFERENCE: 031896-084100 (AM 101724)  
CURRENT APPLICATION NUMBER: US/11/348,413  
CURRENT FILING DATE: 2006-02-07  
PRIORITY APPLICATION NUMBER: PCT/US05/035471  
PRIORITY FILING DATE: 2005-10-05  
PRIORITY APPLICATION NUMBER: US 11/243,445  
PRIORITY FILING DATE: 2005-10-05  
PRIORITY APPLICATION NUMBER: US 60/615,573  
PRIORITY FILING DATE: 2004-10-05  
NUMBER OF SEQ ID NOS: 1276209  
SEQ ID NO 6913  
LENGTH: 1431  
TYPE: DNA  
ORGANISM: Streptococcus agalactiae  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(1431)  
OTHER INFORMATION: WANO1UL07; ORF, 00000011100000; Cluster contains WANO1PUHM  
OTHER INFORMATION: SAG0856:glaA-glycogen synthase:2603.NC\_004116.1  
US-11-348-413-6913

Alignment Scores:  
Pred. No.: 1,57e-65 Length: 1431  
Score: 732.00 Matches: 169  
Percent Similarity: 55.5% Conservative: 87  
Best Local Similarity: 36.7% Mismatches: 147  
Query Match: 25.3% Indels: 58  
DB: 11 Gaps: 11

US-10-628-525A-21 (1-539) x US-11-348-413-6913 (1-1431)

QY 51 IleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspVal 70  
Db 7 ATAATGTTGTTGGCGAGAGGTGTCCTCTTTGCTTAAACACAGGTGGTTGGGAGATGTG 66

QY 71 CysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValValMetPro 90  
Db 67 ATTGGGGCACTCCCAAAATCATTAGTAAAGGTCATGATGTCGTTGTGTGTCATGCCA 126

QY 91 ArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAla 104  
Db 127 TATTAT-----GATATGTTAGACCAAAATTTGGAGACCAATAGAAACCTCATGTAT 180

QY 105 PheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhe 124  
Db 181 TTCTATACA-----GATGTTGGCTCG 201

QY 125 PheHisGluTyr-----ArgAspSerValAspTrpValPheVal 137  
Db 202 CGTCATCAATATAGAGTTAAGAGACTTCTCAAGATAAATGTTACGTTCTACTTTATT 261

QY 138 AspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGly 157  
Db 262 GATAATCAATATTATTTTATAGAGTTCATGCTATGTTGAT-----TGG 306

QY 158 AspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeu 177  
Db 307 GATGATGGGAGGCGTTTTCCTTATTCCAAATAGCTGCTTAGAG-----TTGATG 357

QY 178 GluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAla 197  
Db 358 GAGAAATCAATTTTATTCGGAT-----GTCTTACAGCTCCATGATTATCATACA 408

QY 198 SerLeuValProValLeuAlaLysTyrArgProTyrGlyValTyrLysAspSer 217  
Db 409 GCAATGATTCCTTCTTATTGGAAGAGAGATGACCATCGGATTCAGGCCTTATATATATA 468

QY 218 ArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyr 237

Db 469 AGARCAGGTTTTTACTATTCAATAATTTGAATTTCAAGGGCAGTTTGGTCCAGAAATGTTA 528  
QY 238 ProAspLeu---GlyLeuProProGluTyrPhe-----GlyAlaLeuGluTyrValPhe 254  
Db 529 GGAGATTATTGGAGTTGGCGTCGAGAGATATGAAGATCGAACTCTTAGATGG-----582  
QY 255 ProGluTrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274  
Db 583 -----AATAATTGTTCTTAATTGGATCAAGCA 609  
QY 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThr 294  
Db 610 GCAATTCCTTTACTCAGATAGATGCAACCGTATCACAAGCTACGCAAAATGAATAAAA 669  
QY 295 ThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsn 314  
Db 670 ACTCCAGATTGTTAGAGTTTAGATCAAAATTTGCTATGATGAAGCAGGCAAAATTTATCT 729  
QY 315 GlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIlePro 334  
Db 730 GGAATTTGTAATGTTATTGAYAGCGATTGTTAAATCCAGAAACAGATGCTTTTTCGCCA 789  
QY 335 CysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLys 354  
Db 790 TATCATTTTTCRAAAAGCAACTTAGAGGCAAAATTAATAAATTAAGTTGGCTTTACAGAA 849  
QY 355 GluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAsp 374  
Db 850 AATTTGGGCTTACCTCAAGATAAAATGTACCAATTAATTTGTTGTTTCCAGCACTTACC 909  
QY 375 TyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspVal 394  
Db 910 GATCAAAAGGATTTGATATTATTGCTTCTGAATTCGACAAATATGCTTCAACAAGATATT 969  
QY 395 GlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGlu 414  
Db 970 CAAATGGTTATTATTAGAACAGGCTATCACCATTTTTGAAGAAACGTTCTCTTATTTTGTCT 1029  
QY 415 SerIlePheLeuAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArg 434  
Db 1030 AGTCGTTACCTCGAAAAACTATCTGCTAATATATCTTTTGACTTAAGATTAGCGCAACAG 1089  
QY 435 IleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsn 454  
Db 1090 ATTTATGGCGCTTCAGATATCTTCATGATGCCAAGTCTTTTGAACCTTGTGTCTCTCG 1149  
QY 455 GlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArg 474  
Db 1150 CAGATGATGCTATGAGATATGATGCTTGGCTTGGTACATGAAAGTTGGAGGATTAATAA 1209  
QY 475 AspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAla 494  
Db 1210 GATACTGTGTTAGCCTTCAATTTGATGTTAGT-----GGTACAGGTTTTTCA 1260  
QY 495 Phe 495  
Db 1261 TTT 1263

RESULT 16  
US-11-353-150-32824  
; Sequence 32824, Application US/11353150  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Conner, Timothy W.  
; APPLICANT: Lalgudi, Raghunath V.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US  
; CURRENT APPLICATION NUMBER: US/11/353,150  
; CURRENT FILING DATE: 2006-02-14  
; PRIOR APPLICATION NUMBER: 09/565,386  
; PRIOR FILING DATE: 2000-05-04



Qy	71	CysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValValMetPro	90
Db	67	ATTGGGCGATTATCCCGCAGCAAAATCGACAGCGCGTTGACGCTGCGGTACTGTGCGT	126
Qy	91	ArgTyr-----LeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThr	107
Db	127	GCATTTCCCGATATTCGCGGTGGCGTGCACCATGCGCAGGTAGTATCC-----	174
Qy	108	GluLysHisIleAArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlu	127
Db	175	-----CGTGGTGATACCTTCGCCGGA-----CATATCACCGCTGTGTTCGGT	216
Qy	128	TyrArgAspSerValAspTrpValPheValAspHisProSer-----TyrHisArgProGly	146
Db	217	CATTACAAACGGGGTTGGCAATTATCTGATTACGCGCGCATCTCTATGATCGTCCGGGA	276
Qy	147	AsnLeuTyrGlyAsp---LysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeu	165
Db	277	AGCCGGTATCAGATACCAACTATTTCCTATACCGCAACGATTTCGGTTCGCGTGT	336
Qy	166	LeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGly	185
Db	337	CTGGGGTGGGTGGGGCAGAA-----ATGCCACCGGGCTTGACCCATTCTGG	384
Qy	186	GlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAla	205
Db	385	CGTCTGATGTGGTGTCATGCGCAGCACTGGCATGCGAGCCTTGCGCCTCGCTATCTGGCG	444
Qy	206	AlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsn	225
Db	445	CGCGCGCGGGCTCCG-----CGAAGTCGGTGTTCCTGTCGTCACCAAC	486
Qy	226	LeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGlu	245
Db	487	CTGGCCTCATCAAGGCATGTTTATGCAATCATCATGATGATGATCAATTCGCA	540
Qy	246	TrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLys	265
Db	541	-----TGTCATTC-----TTTATATTCATGGCTGGAAATTC	573
Qy	266	GlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrVal	285
Db	574	AACGGACAATCTCTTCTGGAAGCGCGTCTGTACTATGCCGATACATTCACGCGGTC	633
Qy	286	SerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeu	305
Db	634	AGTCCAACTACGCTCGGGAGATCACCGNACCGCAGTTTGCTACGATGTGAAGAGTCTG	693
Qy	306	LeuSerSer-----ArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsn	323
Db	694	TTGCAACAGCGGTCAACCGTGAAGGCGCTTTTCGCGCTACTGAAACGCGGTGACAGAAA	753
Qy	324	AspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSer	343
Db	754	ATCTGGAGTCCAGACGCGACTTACTGTGGCCTCGCGTTCACCCCGCATACGTTGGAA	813
Qy	344	GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp	363
Db	814	GATTAACGGGAAATAAGCGCCAGTTACAAATCCCAATGGGCGCTTAGGTGTGACGATAAA	873
Qy	364	ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln	383
Db	874	GTGCGGCTTTTTCAGTGGTGAGCGGCTCTGACCAACCCAGAAAGGTCTCGACCTGGTCTG	933
Qy	384	LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp	403
Db	934	GAAGCCTTATCGGGTCTCTCTGGACAGCGGGCGGAGCTGGCGCTACTCTCGCGCGCGGCAT	993
Qy	404	ProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGly	423
Db	994	CCGGTCTCGAGGAAGGTTTCCTTTCGGCGGCGGACGGAAATACCCCGGTCAAGTGGCGGT	1053
Qy	424	TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu	443

QY 182 -----TyrIle-----TyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196  
DB 805 AACCCATACTTCTCCGGACCATACGGGAGGAGCGTGTCTGTCGCAACGACGTGGCAC 864  
QY 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
DB 865 ACCGGCCCTCTCTCGTCTACCTCAGAGCAACTACCACTCCACGCGCATCTACAGGAC 924  
QY 217 SerArgSerIleLeuValIleHisLeuAlaHisGlnGlyValGluProAlaSerThr 236  
DB 925 GCAAGACCGCTTCTGCATCCACAACTCTCTACAGGCGCGGTTCGCCCTTCTCCGAC 984  
QY 237 TyrProAspLeuGlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGlu 256  
DB 985 TACCCGGAGCTGAACCTCCCGGAGAGATTCAAGTCGTCTTCGATTTCATC----- 1035  
QY 257 TrpAlaArgHisAlaLeuAspLys-----GlyGluAlaValAsnPheLeuLys 273  
DB 1036 -----GACGGCTACGAGAAGCCGCTGGAGGCGCGGAAGATCAACTCGATGAAG 1083  
QY 274 GlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGlu--- 292  
DB 1084 GCGGGATCTCGAGCGCAGAGGCTCTCAACGTCAGCCCTACTACCCGAGAGCTC 1143  
QY 293 ValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerVal 312  
DB 1144 ATCTCCGGCATCGCCAGGGCTCGGAGCTCGACATCATG-----CGCTCACCGGC 1197  
QY 313 LeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys 332  
DB 1198 ATCAGCGGCATCGTCAACCGCATGAGTGCAGTGCAGGAGTGGACCCAGCAGGACAAAGTAC 1257  
QY 333 IleProCysHisTyrSerValAspAsp---LeuSerGlyIleValAlaLysCysLysGlyAla 351  
DB 1258 ATCGCGCTGAAGTACAGCTGTCGACGCGCGTGGAGGCCAAGCGCTGAAACAGGAGCGG 1317  
QY 352 LeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGly 371  
DB 1318 CTGACGGCGAGTCCGGCTCCGGTGGACCGGAACATCCCGCTGGTGGCTTCATCGGC 1377  
QY 372 ArgLeuAspTyrGlnLysGlyIleAspLeu 381  
DB 1378 AGCGTGAAGACAGAAAGGCCCGCAGCTC 1407

## RESULT 20

US-11-227-183A-29117  
; Sequence 29117, Application US/11227183A  
; GENERAL INFORMATION:  
; APPLICANT: Fisher, Dane K.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US  
; CURRENT APPLICATION NUMBER: US/11/227,183A  
; PRIOR FILING DATE: 2005-09-16  
; PRIOR APPLICATION NUMBER: US 09/619,643  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 29117  
; LENGTH: 374  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: LIB3180-041-P2-M2-H8  
US-11-227-183A-29117

Alignment Scores:  
Pred. No.: 2,348-52 Length: 374  
Score: 597.00 Matches: 120  
Percent Similarity: 96.0% Conservative: 0  
Best Local Similarity: 96.0% Mismatches: 3

Query Match: 20.6% Indels: 2  
DB: 10 Gaps: 0  
US-10-628-525A-21 (1-539) x US-11-227-183A-29117 (1-374)  
QY 263 LeuAspLysGlyGluAlaValAsnPheLeu-LysGlyAlaValValThrAlaAspArgIle 282  
DB 3 CTTCGAAAGGCTGAGGCGAGTTAAATTTGTGGGAAAGGTGCAGTTGTGACAGCGGATCNAAT 62  
QY 282 eValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLe 302  
DB 63 CGTGTCTGTCTAGTAAGGTTATTCGTGGAGGTCAACTGCTGAAGGTGGACAGGCGCT 122  
QY 302 uAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIle 322  
DB 123 CAATGAGCTCTTAAAGTCCAGAAAGAGTGTATTAAACGGAATTTGAAATTTGACAT 182  
QY 322 eAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLe 342  
DB 183 TAATGATTGGAAACCTGCCACAGACAAATGTATCCCTGTCTATTCTCTGTTGATGACCT 242  
QY 342 uSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgPr 362  
DB 243 CTCTGAAAGGCCAAATGTAAAGGTGCATTGCAGAAAGGAGCTGGGTTTACCTATAGGCC 302  
QY 362 cAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln-LysGlyIleAspLeuI 382  
DB 303 TGATGTTCTCTGATTGGCTTTATTGGAAGGTGGATTATCAAAAAGGCGCATTTGATCTCA 362  
QY 382 leGlnLeuIle 385  
DB 363 TTCAACTTATT 373

## RESULT 21

US-11-330-364-17004  
; Sequence 17004, Application US/11330364  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Dubois, Patrice  
; APPLICANT: Mahadeo, Debbie A.  
; APPLICANT: Masucci, James D.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 16517.352 - 38-21(51721)C/US  
; CURRENT APPLICATION NUMBER: US/11/330,364  
; PRIOR FILING DATE: 2006-01-12  
; PRIOR APPLICATION NUMBER: US 09/696,664  
; PRIOR FILING DATE: 2000-10-25  
; PRIOR APPLICATION NUMBER: US 60/161,619  
; PRIOR FILING DATE: 1999-10-26  
; NUMBER OF SEQ ID NOS: 17472  
; SEQ ID NO 17004  
; LENGTH: 635  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3279-215-Q6-K1-C2  
US-11-330-364-17004

## Alignment Scores:

Pred. No.: 2,478-51 Length: 635  
Score: 590.50 Matches: 114  
Percent Similarity: 98.3% Conservative: 0  
Best Local Similarity: 98.3% Mismatches: 1  
Query Match: 20.4% Indels: 2  
DB: 8 Gaps: 1

US-10-628-525A-21 (1-539) x US-11-330-364-17004 (1-635)

QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443  
DB 20 TGG---GGATTTAGTGTTCAGTTTTCCAGTTCACCAAGTAACCTGCGGCTGCATATATTGTTA 76







123 TTTGACTTAT-----GATGGCATGTTAAACCAAGTGGTGGAGGAAA 167  
Qy ValAsnPheLeuTyGlyAlaValThrAlaAspArgIleValThrValSerLyGly 288  
Db ATCAATTGGTGAAGCTGACTTATANAATCATGTTTGTGATACTGTTAGCCCAAN 227  
Qy TySerTrpGlu---ValThrAlaGluGlyGlnGlyLeuAsnGluLeuSer 307  
Db TATGCTAAGAAGCTGGTGTGAGTCCAGACAGAGAGTGAATTTGGACACATCCTT--- 284  
Qy SerArgLys-----SerValLeuAsnGlyIleValAsnGlyIleAsn 323  
Db ---CGCAAAATTGATGATGCTGTTGTTGGAAATTGTGAATGCGATGATGTTGAG 341  
Qy AspTrpAsnProLathrAspLysCysIleProCysHisTySerValAspAsp---Leu 342  
Db GAGTGGAAATCCAACTGACAAATATATAGTGTCAAAATACGATGTTTCAACAGATTTG 401  
Qy SerGlyLysAlaLysCysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgPro 362  
Db GAAGCAAGGCTCTTTTGAAGAAGCCCTCCAGACAGAGTGGATTGGCGGTGACAGA 461  
Qy AspValProLeuIleGlyPheIleGlyArgLeuAspTyGlnLysGlyIleAsnLeu 382  
Db AATATCTCTTATGTTTATGTTTATGTTGAGTGTGAGGACAAAGGTTCTGATATCTT 521  
Qy GlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGly 402  
Db GCAGAAGCTATTTCCCAATTTATCAGGAGAAATGTTGAGTGGTGGCCCTGAGACAGA 581  
Qy AspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArg 422  
Db AAAAAACAAATGGAAGAAACAACTACAGGAATTTGAAATATCATACCTGACAGGCCAGA 641  
Qy GlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeu 442  
Db GGAGTGGCAAAATTCATGTTCCCTTAGCCCAATGATATGTTGAGCTGATTTTATA 701  
Qy LeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyzAlaMetGlnTyGly 462  
Db TTGGTCTTAGCAGATTTGAGCTTGTGCTCTCATTTACGTTACAGCTATGCTATGGA 761  
Qy ThrValProValValHisAlaThrGlyLeuArgAspThrValGluAsnPheAsnPro 482  
Db TCTGTACCAATTTGTTCCCTCAACAGGTGATTTGACACTGCCAAA----- 809  
Qy PheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsn 502  
Db ---GAGGTTTCACTGGATTTTCAGATGGTGGCTTTCAGTGTGTAATGT 854  
Qy MetPheValAspIleAlaAsnCysAsnIleTyzIleGlnGlyThrGln-----Val 519  
Db GATGCTGTGATCCAGCTGA-TGTGATGCTATAGCAAGACTGTCAAAAGGCCCTTGC 913  
Qy LeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHis 534  
Db AGTCTAGGAATCCAGCTTTTACAGAAATATAAAGAAGCTGCAT 958

## RESULT 25

US-10-542-516-5

; Sequence 5, Application US/10542516  
; GENERAL INFORMATION:  
; APPLICANT: Heilm, Ute  
; APPLICANT: Herbers, Karin  
; APPLICANT: Sonnewald, Uwe  
; APPLICANT: Glickmann, Eric  
; TITLE OF INVENTION: Expression cassette with promoters of starch synthesis 3 for the  
; FILE OF INVENTION: expression of nucleic acids in plant tissue containing starch  
; FILE REFERENCE: 13173-00015-US  
; CURRENT FILING DATE: 2005-07-18  
; PRIOR APPLICATION NUMBER: PCT/EP2004/000241

; PRIOR FILING DATE: 2004-01-15  
; PRIOR APPLICATION NUMBER: DE 103 02 324.0  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5

; LENGTH: 3693  
; TYPE: DNA  
; ORGANISM: Solanum tuberosum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3690)  
; OTHER INFORMATION: coding for SSS3  
US-10-542-516-5

## Alignment Scores:

Pred. No.: 2,01e-42 Length: 3693  
Score: 516.00 Matches: 150  
Percent Similarity: 48.0% Conservative: 69  
Best Local Similarity: 32.9% Mismatches: 145  
Query Match: 17.8% Indels: 92  
DB: 7 Gaps: 17

US-10-628-525A-21 (1-539) x US-10-542-516-5 (1-3693)

Qy 51 IleValPheValThrGlyGluAlaSerProTyzAlaLysSerGlyLeuGlyAspVal 70  
Db 2344 ATTGTCCATATTCTCTCGAATGGCACCATTGCAAGGTGGAGGCCTTGGTGAATT 2403  
Qy 71 CysGlySerLeuProValAlaLeuAlaArgGlyHisArgValMetValValMetPro 90  
Db 2404 GTTACTAGTCTTTCCCGTCTGTTCAAGATTAAACCATTAATGTGGATATTATCTTACCT 2463  
Qy 91 ArgTyz-----LeuAsnGlyThrSerAsp-----LysAsnTyzAla 102  
Db 2464 AAGTATGACTGTTGAAGATGAATAATGGAAGGACTTTCGGTTTCACAAAACTAC--- 2520  
Qy 103 AsnAlaPheTyzThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluVal 122  
Db 2521 -----TTTTGGGGTGGGACTGAAATA 2541  
Qy 123 ThrPhePheHisGluTyzArgAspSerValAspTrpValPheValAspHisProSerTyz 142  
Db 2542 AAAGTATGGTTTGGAAAGGTGGAAGGTCTCTCGGTCTATTATTTTGGAG----- 2589  
Qy 143 HisArgProGlyAsn---LeuTyz-----GlyAspLysPheGlyAlaPheGlyAspAsn 159  
Db 2590 -----CCTCAAAACGGGTATTATTTGAAAGGGTGGTCTATGTTGTAGCAATGATGGT 2643  
Qy 160 GlnPheArgTyzThrLeuLeuCysTyzAlaAlaCysGluAlaProLeuIleLeuGluLeu 179  
Db 2644 GAA---CGATTGGTTTCTTCTGTCTCAGCGGCTTTGGAG-----TTTCTTCTGCAA 2691  
Qy 180 GlyGlyTyzIleTyzGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeu 199  
Db 2692 GGTGGATTT-----AGTCCGGATATCATTTTCATTCATGCGATGATGGTCTAGTGTCTCT 2742  
Qy 200 ValProValLeuLeuAlaAlaLysTyzArgProTyzGlyValTyzLysAspSerArgSer 219  
Db 2743 GTTGTCTGGCTCTTTAAGGAACAATATACACTATGGTCTAAGCAAAA---TCTCGTATA 2799  
Qy 220 IleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyzProAsp 239  
Db 2800 GTCTTCAGATACATAATCTTGA-----TTTGGGCA----- 2823  
Qy 240 LeuGlyLeuProGluTrpTyzGlyAlaLeuGluTrpValPheProGluTrpAlaArg 259  
Db 2824 -----TTTGGGCA----- 2832  
Qy 260 ArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAla 279  
Db 2833 -----GATCTCATTTGGGAGACATGACTACGCA 2862



Qy	356	LeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyr	375
Db	2824	CTTGGTTTGAAA---AAAGCTGATCTTCTCTTGGTGAGATTATTACTCGATTGACTCAT	2880
Qy	376	GlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGln	395
Db	2881	CAAAAAGGGATCCATCTCATCAAAATGCCATATGGCGTACCCCTAGAAACGCGGTGGACAG	2940
Qy	396	PheValMetLeuGlySerGly-----AspProGluLeuGluAspTrpMet	410
Db	2941	GTCGTATTACTTGGTTGGCTCTGTATCACCGTATACAAAATGAATTTGTGAATTTGGCC	3000
Qy	411	ArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerValPro	430
Db	3001	AATCAATTGCATTCAGTCATATATGATCGGCAGACATTTGGCTTGATATGATGAACCT	3060
Qy	431	ValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluPro	450
Db	3061	CTTTCCACATGATATATGCTGGTGTGATTTCAATCTTGTTCCCTTCAATCTTTGACCCA	3120
Qy	451	CysGlyLeuAsnGlnLeuTyAlaMetGlnTyArgGlyThrValProValValHisAlaThr	470
Db	3121	TGTGGACTCACTCAACTCACAGCAATGAGATACGGTTCAATACCAATTGTTTCGAAAAACT	3180
Qy	471	GlyGlyLeuArgAspThrVal	477
Db	3181	GGGGGACTTTTATGATACGGTG	3201

```

RESULT 27
US-11-239-591A-7048
; Sequence 7048, Application US/11239591A
; GENERAL INFORMATION:
; APPLICANT: BYRUM, JOSEPH R.
; APPLICANT: HECK, GREGORY R.
; APPLICANT: LA ROSA, THOMAS J.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; TITLE OF INVENTION: WITH PLANTS
; FILE REFERENCE: 16517.338
; CURRENT APPLICATION NUMBER: US/11/239,591A
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: 09/440,687
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 31015
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7048
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Glycine max
US-11-239-591A-7048

```

Alignment Scores:	
Pred. No.:	5,318-42
Score:	498.50
Percent Similarity:	76.0%
Best Local Similarity:	65.1%
Query Match:	17.2%
DB:	8
Length:	436
Matches:	95
Conservative:	16
Mismatches:	32
Indels:	3
Gaps:	1

US-10-628-525A-21 (1-539) x US-11-239-591A-7048 (1-436)

Qy	365	ProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeu	384
		:    :	
Db	2	CCGCCTACTTGGAATTCATTGGAGGCTGGATCAACAGAAGGCCATTGATCTCATAGCCGGG	61
Qy	385	IleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspPro	404
		:    :    :    :	
Db	62	GCGGTTCCTTGGATAAGTGGCCAGCAGTAGTCAGCTAGTTCATGTTGGAACTGGAAGSCCG	121
Qy	405	GluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrp	424
		:    :	
Db	122	GACTTAGAAGATAGTCTTAGGCAAGTTTCAGTCCCAACACCGCTGCAAAAGTCACAGAGATGG	181

Qy	425	ValGlyPheSerValProValSerHisArgIleThrIalaGlyCysAspIleLeuMet	444
Db	182	GTTCGGCTTTTCGGTCAAGATGGCTCCACCGGATAACACAGAGGTGAGACATATTGCTGATG	241
Qy	445	ProSerArgPheGluProCysGlyLeuAsnGlnLeuTyzAlaMetGlnTyzGlyThrVal	464
Db	242	CCATCAGATTTGAGCCCATGTGGATTGATTCNACTCTATGCCATGATTAACGGAAACAATT	301
Qy	465	ProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGly	484
Db	302	CCAGTTGTACATGCTGTGCGTGGATTGAGGATACAGTGAAGCCCTTTTAAATCCATTTGAA	361
Qy	485	GluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPhe	504
Db	362	GAGTCG-----GGCCTGGGTGGACATTTTGACAGTCGTCAGAAACTTAACAAGTTAATA	412
Qy	505	ValAspIleAlaAsnCys	510
Db	413	AATGCATTAGGGAACCTGC	430
RESULT 28			
US-10-542-516-7			
; Sequence 7, Application US/10542516			
; GENERAL INFORMATION:			
; APPLICANT: Heim, Ute			
; APPLICANT: Herbers, Karin			
; APPLICANT: Sonnewald, Uwe			
; APPLICANT: Gluckmann, Eric			
; TITLE OF INVENTION: Expression cassette with promoters of starch synthesis 3 for the			
; TITLE OF INVENTION: expression of nucleic acids in plant tissue containing starch			
; FILE REFERENCE: 13173-00015-US			
; CURRENT APPLICATION NUMBER: US/10/542,516			
; CURRENT FILING DATE: 2005-07-18			
; PRIOR APPLICATION NUMBER: PCT/EP2004/000241			
; PRIOR FILING DATE: 2004-01-15			
; PRIOR APPLICATION NUMBER: DE 103 02 324.0			
; PRIOR FILING DATE: 2003-01-20			
; NUMBER OF SEQ ID NOS: 48			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 7			
; LENGTH: 3078			
; TYPE: DNA			
; ORGANISM: Arabidopsis thaliana			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1)..(3075)			
; OTHER INFORMATION: coding for SSS3			
US-10-542-516-7			

Alignment Scores:		
Pred. No.:	4.26e-40	Length:
Score:	492.50	Matches:
Percent Similarity:	45.7%	Conservative:
Best Local Similarity:	31.7%	Mismatches:
Query Match:	17.0%	Indels:
DB:	7	Gaps:
		3078
		163
		72
		173
		106
		21

US-10-628-525A-21 (1-539) X US-10-542-516-7 (1-3078)

Qy		IleValPheValThrGlyGlualAserProTyAlalysSergLyGlyLeuGiVaspVal	70
Dd	1735	ATTGTTCAATTCCTGTGAATAAGGCACCACCATCGAAGAAGTGGTGCCCTAGGTGATGTT	1794
Qy	71	CyeGLyserProvalLaLauLaalaArGlyHisArgValMetValMetPro	90
Dd	1795	GTCACTAGTCTATCTCGCGCTGTCCAAGATTAAACCATAATGTGGATATAGTTTTCCC	1854
Qy	91	ArgTYr-----LeuaAngLYthrSerAsplysaenTyralaasnAlaphetyr	106
Dd	1855	AAGTATGATTGCATAAGCACAANTTTGTCAAGGAC TTGCCAATTTAACAGAAGCATCAC	1914
Qy	107	ThrglulyshisileargIleProcypesPhgLyglycluhishgluvalthrphephphis	126

Db 1915 -----TGGGGAGGAAGT---GAAATAAAAGTTTGGCAT 1944  
 QY 127 GluTyrArgAspSerValAspTrpValPheValAsp---HisProSerTyrHisArgPro 145  
 Db 1945 GGAAGAGTAGAAGGCGCTTTCGGTTTACTTCTTAGATCCCAAAATGGATGTTTTCAGCGA 2004  
 QY 146 GlyAsnLeuTyrGly-----AspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyr 163  
 Db 2005 GGATGGTTTACGGTGTGCAGATGATGAGGAGATTCGGT----- 2046  
 QY 164 ThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuLeuLeuGluLeuGlyTyrIle 183  
 Db 2047 ---TTCTTCTGTCATGCGGCTCTTGAA-----TTTCTTCTCAGAGGAGTTTCCATCCA 2097  
 QY 184 TyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeu 203  
 Db 2098 GACATTTCTCACTGT-----CATGACTGGTCTAGTGTCCGGTTCATGGTTA 2145  
 QY 204 LeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIle 223  
 Db 2146 TTCAGGATCATATACACAGTACGGTTTAATTA---ACCGTATTGCTTTCACAAAT 2202  
 QY 224 HisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuPro 243  
 Db 2203 CATAAATTTGGAA----- 2214  
 QY 244 ProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeu 263  
 Db 2215 -----TTTGGAGCG----- 2223  
 QY 264 AspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleVal 283  
 Db 2224 -----NATCCCATTTGTAAGCAATGACATTTGCAGCAAAAGCCACA 2265  
 QY 284 ThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsn 303  
 Db 2266 ACCGTTTACCACAACTATGCTAAGGAAGTGTGCGA-----AAC 2304  
 QY 304 GluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsn 323  
 Db 2305 TCTGTAATCTCGCATTTATACAAATTTACGGAATTTATAAACGGGATTCACCCAGAT 2364  
 QY 324 AspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp---Leu 342  
 Db 2365 ATATGGATCCATATAACGATAACTTTATTCCTGACCTTACTTCAGAGAACGTTGTA 2424  
 QY 343 SerGlyLysAlaLysCysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgPro 362  
 Db 2425 GAAAGGCAAAAGAGCAGCCCAAGGAAGATTCGCAAAACAGGCTTGGACTAAAG---AGTGCC 2481  
 QY 363 AspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspIle 382  
 Db 2482 GATTTTCAGTAGTAGGAATTTATACGGCTTTAAACACACAGAGGGAATACATTTGATC 2541  
 QY 383 GlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGly 402  
 Db 2542 AAGCAGCTATTTCGGTACCTTGGACCGATGACAGGTTGCTTTATAGTTTACGCT 2601  
 QY 403 ---AspProGluLeuGlu---AspTrpMetArgSerThrGluSerIlePheLys----- 418  
 Db 2602 CCAGATCTCGGATCCAAATGATTTTGTAAACTTTGGCAACCAATATCTTCTCAT 2661  
 QY 419 ---AspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAla 437  
 Db 2662 GGTGACCGGCTCGGCTTGTCTTAACCTACGATGAACCTCTTTCATTTGATTTATGCT 2721  
 QY 438 GlyCysAspIleLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyr 457  
 Db 2722 GGGGCTGACTTATTCTTGTACCGTGGATTTTGGCCATGTTGACTGACAGCTCAT 2781  
 QY 458 AlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrVal 477  
 Db 2782 GCCATGAGATCGGGGCTGTTCTCTGTTGTAGAAAAAAGTGGAGGACTCTTTGATACGGTT 2841

QY 478 GluAsnPheAsnProPheGlyGluAsnGlyGlu-----GlnGlyThrGlyTyr 493  
 Db 2842 TTTGATGTTGACCCAGCATAAAGAAAGGGCACAAGCTCAAGTTCTAGAACCTAATGGTTTC 2901  
 QY 494 AlaPhe-----AlaProLeuThrThrGluAsnMetPheValAspIleAla-As 509  
 Db 2902 ACCTTCGACGGAGCTGATGCTCT-----GGTGTGATTTATGCTCTC 2943  
 QY 509 nCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArg-- 528  
 Db 2944 AATAGGCGCATATCGCGTGGTACGATGCTAGAGAGTGGTTTAACTCGCTGTGCAAGACG 3003  
 QY 529 -----HisValLysArgLeuHisVal 535  
 Db 3004 GTGATGGAGCAAGACTGGTGCATGGAACCGTCTCGACCTTG 3043  
 RESULT 29  
 US-11-329-388-1791  
 ; Sequence 1791, Application US/11329388  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Andersen, Scott E.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 16517.357 - 38-21(15503)C/US  
 ; CURRENT APPLICATION NUMBER: US/11/329,388  
 ; PRIOR FILING DATE: 2006-01-11  
 ; PRIOR APPLICATION NUMBER: 09/553,094  
 ; FILING DATE: 2000-04-18  
 ; NUMBER OF SEQ ID NOS: 18831  
 ; SEQ ID NO 1791  
 ; LENGTH: 289  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1)..(289)  
 ; OTHER INFORMATION: unsure at all n locations  
 ; OTHER INFORMATION: Clone ID: LIB3061-040-Q1-K1-H2  
 US-11-329-388-1791

Alignment Scores:  
 Pred. No.: 6, 289-40 Length: 289  
 Score: 476.00 Matches: 91  
 Percent Similarity: 97.9% Conservative: 1  
 Beat Local Similarity: 96.8% Mismatches: 2  
 Query Match: 16.5% Indels: 0  
 DB: 8 Gaps: 0

US-10-628-525A-21 (1-539) x US-11-329-388-1791 (1-289)

QY 273 LysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGlu 292  
 Db 7 CGTGGGCGAGTTGTGCAGCATATCGAATCGTACTGTCAAGGGTTATTTCATGGGAG 66  
 QY 293 ValThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerVal 312  
 Db 67 GTCACAACTGCTGAAGGTGGACAGGCGCTCAATGAGCTCTTAAAGCTCCAGAAAGAGTGA 126  
 QY 313 LeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys 332  
 Db 127 TTAACCGAATTTGAATGGAAATGACATTTATGATTGGACCTCCACACAGCAATGT 186  
 QY 333 IleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysGlyGlyAlaLeu 352  
 Db 187 ATCCCTGCTATTATTCGTGTGATGACCTCTCTGAAAGGCCAAATGTAAGGTGCATTG 246  
 QY 353 GlnLysGluLeuGlyLeuProIleArgProAspValProLeu 366  
 Db 247 CAGAAGGAGCTGGGTTTACCTATTAAGGCTGATGTTCTCTG 288  
 RESULT 30

## US-10-542-516-17

Sequence 17, Application US/10542516  
 GENERAL INFORMATION:  
 APPLICANT: Heim, Ute  
 APPLICANT: Herbers, Karin  
 APPLICANT: Sonnewald, Uwe  
 APPLICANT: Gluckmann, Eric  
 TITLE OF INVENTION: Expression cassette with promoters of starch synthesis 3 for the  
 FILE REFERENCE: 13173-00015-US  
 CURRENT FILING DATE: 2005-07-18  
 PRIOR APPLICATION NUMBER: US/10/542,516  
 PRIOR FILING DATE: 2004-01-15  
 PRIOR APPLICATION NUMBER: DE 103 02 324.0  
 PRIOR FILING DATE: 2003-01-20  
 NUMBER OF SEQ ID NOS: 48  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO 17  
 LENGTH: 5025  
 TYPE: DNA  
 ORGANISM: Zea mays  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)..(5022)  
 OTHER INFORMATION: coding for sss3

## US-10-542-516-17

Alignment Scores:  
 Pred. No.: 5e-36 Length: 5025  
 Score: 456.50 Matches: 155  
 Percent Similarity: 45.5% Conservative: 71  
 Best Local Similarity: 31.2% Mismatches: 163  
 Query Match: 15.8% Indels: 109  
 DB: 7 Gaps: 20

## US-10-628-525A-21 (1-539) x US-10-542-516-17 (1-5025)

QY 51 IleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspVal 70  
 DB 3682 ATTGTCACATTGCTGTGAGATGGCCCAATCGCAAGGTTTGAGGCTCTGTGTGATGT 3741  
 QY 71 CysGlySerLeuProValAlaLeuAlaAArgGlyHisArgValMetValMetPro 90  
 DB 3742 GTCACATAGTCTTTCACGCTGCTGCAAGATTAGGACACAAATGTGGAGGTATTCTTCCA 3801  
 QY 91 ArgTyr-----LeuAsnGlyThrSerAspLysAsn-TyrAlaAsnAlaPheTyrThrGl 108  
 DB 3802 AAGTACGGTGTGTTGAACTTAGCAATGTCAGAACTCTAC----- 3841  
 QY 108 uLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyr 128  
 DB 3842 -AAATCCATCAGATTTT-TCTTGGGGTGGTCTGAA-----ATAAATGTGTG 3887  
 QY 128 rArgAspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsnLe 148  
 DB 3888 GCGTGGCAGTAGTCGAAGGCTTTGTGTT-----TACTTCTCGAACCTCMAAAT-- 3936  
 QY 148 uTyrGlyAspLysPheGlyAlaPheGly-----AspAsnGlnPh 161  
 DB 3937 -----GGGATGTTTGGATGCGATATGATATGCGAGGAGCATGACCG 3980  
 QY 161 eArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGly 181  
 DB 3981 CCGATTGGCTTCTTCTGCTGCTCTAGAG-----TTTCTCTCCAAAGTGTATC 4034  
 QY 181 yTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValPr 201  
 DB 4035 TTCTCCGAACATAATACATTGC-----CATGATTGCTCAAGTCTCTCTGTC 4082  
 QY 201 oValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLe 221  
 DB 4083 CTGGCTACACAGGAAACTACCGGAGTCTAGCTTTG-----GCMAACGCGAGGTGTGATT 4139

QY 221 uValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGl 241  
 DB 4140 CACCATCCCAATCTT----- 4155  
 QY 241 yLeuProProGluTyrTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHl 261  
 DB 4156 -----GAATTTGGAGCGCATCA 4172  
 QY 261 sAlaLeuAspLysGlyGluAlaValaAsnPheLeuLysGlyAlaValThrAlaAspAr 281  
 DB 4173 TATT-----GGCAAGCAATGAGATAT-----TGTGATAA 4202  
 QY 281 gIleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlnGl 301  
 DB 4203 AGCAACAACACTGCTCTAATACATATTCAAGGAAGTGTCA-----GGTCATGG 4250  
 QY 301 yLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValaAsnGlyIleAs 321  
 DB 4251 T-----GCCATAGTTCTCTCATCTTGGGAAATTTCTATGGCAATTTCTCAATGGAATTGA 4301  
 QY 321 pIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValaAspAs 341  
 DB 4302 TCCGATATATGGATCCGTACATGACAACTTTATCCCGGTCCACTACACTTGTGTAGAA 4361  
 QY 341 p-----LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIl 360  
 DB 4362 TGTGGTTGAAGGCAAGAGGGCTGCTAAGAGGGCACCTGCAGCAGAAGTTGGGTTCAG-- 4419  
 QY 360 eArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAs 380  
 DB 4420 -CAATTCGATGTCCTCGGTAGGAATCGTACTCGCTCAGACAGCCAAAGGGGTATCCA 4478  
 QY 380 pLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGl 400  
 DB 4479 CTGATCAAGCATGCGATTTACCGTACACTCGAACGAGCAGAGTGTGTTTGTCTGG 4538  
 QY 400 ySerGly-----AspProGluLeuGluAspTrpMetArgSerThrGluSe 415  
 DB 4539 TTCAGCGCGGACTCTCGAATCCAACTGATTTTGTCAACCTGGCGAATACGCTCCACGG 4598  
 QY 415 rIlePheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIl 435  
 DB 4599 CGTAAACCATGGGCAAGTGAGGCTTTCTTGTACCTACGACGAGCCTCTCTCGCATCTGAT 4658  
 QY 435 eThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGl 455  
 DB 4659 ATACGCTGGCTCTGATCTTCTGCTCCATCTATATTGTAGCCTTGGCGCTTAATCTCA 4718  
 QY 455 nLeuTyrAlaMetGlnTyrGlyThrValProValHisAlaThrGlyGlyLeuArgAs 475  
 DB 4719 GCTCGTGGCATGCGGTATGGAACCATCCGATTTGTCGCAAGACTGGAGGCTCTTCGA 4778  
 QY 475 pThrValGluAsnPheAsnProPheGlyGlu-----AsnGlyGluGlnGlyTh 491  
 DB 4779 CACTGTCTTCGATGTGGCAATGACAAGAACGAGCCGAGATCGAGGCTTGGAGCCCAA 4838  
 QY 491 xGlyTrpAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAs 511  
 DB 4839 CCGGTTTAGCTTT-----GACGGAGCTGATAGCAA 4868  
 QY 511 nIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAla 527  
 DB 4869 C-----GGTGTGACTACGCGTGAACAGGGCGATCTCAGCT 4905

Search completed: April 2, 2006, 04:06:40  
 Job time : 1907.01 secs

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GenCore version 5.1.7  
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OM protein - nucleic search, using **same plna p2n model**

Run on: April 1, 2006, 04:29:01 ; Search time 1115.38 Seconds  
(without alignments)  
2853.949 Million cell updates/sec

Title: US-10-628-525a-33

Perfect score: 271

Sequence: 1 MASSMLSSAAVATRTNPAQA.....SRQNLDITSIASNGRVC 56

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:\*  
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2: gb.in:\*  
3: gb.env:\*  
4: gb.om:\*  
5: gb.ov:\*  
6: gb.pat:\*  
7: gb.ph:\*  
8: gb.pr:\*  
9: gb.ro:\*  
10: gb.sts:\*  
11: gb.sy:\*  
12: gb.un:\*  
13: gb.vi:\*  
14: gb.htg:\*  
15: gb.pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	244.5	90.2	806	15	AY220079 Nicotiana
2	240.5	88.7	177	6	I24839 Sequence 8
3	240.5	88.7	177	6	I40228 Sequence 6

4	240.5	88.7	177	6	I72655
5	240.5	88.7	204	6	AR528363
6	240.5	88.7	225	11	ARPRECA2
7	240.5	88.7	499	6	AR205973
8	240.5	88.7	796	15	NSRUB1
9	240.5	88.7	799	15	TORRUBPA
10	240.5	88.7	1314	15	PERBCS11
11	240.5	88.7	2293	15	NPRBCS8B
12	240.5	88.7	2293	15	TORRBCS8B
13	240.5	88.7	2362	15	NTRUBSS
14	237.5	87.6	22574	11	CVR18556
15	234.5	86.5	1629	15	STRBCS2
16	231.5	85.4	1386	15	STRBCS2C
17	231.5	85.4	2242	15	PERBCS08
18	230.5	85.1	1027	15	TOMRBCSC
19	230.5	85.1	1341	15	LERBCS3C
20	230.5	85.1	1520	15	LERBCS3A
21	229.5	84.7	1054	15	LERBCS3B
22	229.5	84.7	4124	15	TOMRBCO
23	228.5	84.3	723	15	SLARBCS
24	228.5	84.3	1703	15	STRBCS2B
25	226	83.4	3323	15	STRBCS1
26	223.5	82.5	599	15	TOMRBCSB
27	223.5	82.5	684	6	AR428736
28	223.5	82.5	684	6	AR455412
29	223.5	82.5	684	6	AX329368
30	223.5	82.5	684	6	AX382258
31	223.5	82.5	742	15	TOMRBCSE
32	223.5	82.5	1097	15	BT013023
33	223.5	82.5	2776	15	LERBCS2
34	217.5	80.3	1261	15	BT012936
35	215.5	79.5	2795	15	NSRUBSSU
36	212	78.2	1337	15	TOMRUBPB
37	210	77.5	546	15	POTRBCS
38	210	77.5	1598	15	STRBCS3
39	208.5	76.9	789	15	AB006080
40	207.5	76.6	546	6	Q0805080
41	207.5	76.6	546	15	AY098970
42	207.5	76.6	577	15	AY051025
43	207.5	76.6	595	15	AY064686
44	207.5	76.6	720	15	AF360124
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47	207.5	76.6	726	6	AX364195
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49	207.5	76.6	764	15	AF462822
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54	206.5	76.2	2006	15	BNRBCSF1
55	206	76.0	778	15	TOMRBCSD
56	206	76.0	1032	15	TOMRBCSA
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59	204.5	75.5	191	6	I06976
60	204.5	75.5	562	15	AY705444
61	204.5	75.5	797	15	HEVRBSS
62	204.5	75.5	1594	15	GRBCS
63	204	75.3	177	6	I06974
64	203.5	75.1	9647	15	ATATSGS
65	202.5	74.7	801	15	AF065615
66	200.5	74.0	1761	15	BNRBCSSW
67	200	73.8	813	15	PYPRBCS
68	199.5	73.6	546	15	AY143814
69	199.5	73.6	652	15	AF410283
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72	199.5	73.6	739	6	AX364175
73	199.5	73.6	2116	15	AY142543
74	199.5	73.6	2714	15	BNRBCS
75	198	73.1	680	15	CIPRBCS2
76	198	73.1	2671	15	CIP2RSS

77	196.5	72.5	812	15	CUSSSU	M15056	Cucumber SS
78	195.5	72.1	704	15	SRRBCS	X06558	Radish mRNA
79	195.5	72.1	3552	15	CIP1RS	L10212	Mesembryant
80	194	71.6	934	6	AX593077	AX593077	Sequence
81	194	71.6	934	6	AX601412	AX601412	Sequence
82	194	71.6	934	15	CAR419826	AJ419826	Coffea ar
83	194	71.6	2034	6	AX593076	AX593076	Sequence
84	194	71.6	2034	6	AX601411	AX601411	Sequence
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86	191.5	70.7	586	15	AY093288	AY093288	Arabidops
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89	191.5	70.7	587	15	BT003356	BT003356	Arabidops
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91	191.5	70.7	721	15	AY062543	AY062543	Arabidops
92	191.5	70.7	728	15	AY062437	AY062437	Arabidops
93	191.5	70.7	758	15	AY059939	AY059939	Arabidops
94	191.5	70.7	776	15	CIPRBC	M31640	Ice plant r
95	191.5	70.7	780	15	AF1011228	AF101228	Manihot e
96	191.5	70.7	780	15	AF101233	AF101233	Manihot e
97	191.5	70.7	811	15	AF101230	AF101230	Manihot e
98	191.5	70.7	824	15	AF101231	AF101231	Manihot e
99	191.5	70.7	1093	15	MNRUBISCO	M96583	Manihot esc
100	191.5	70.7	1162	15	MNRUBCSA	M95930	Manihot esc
101	190.5	70.3	853	15	AF008214	AF008214	Musa acum
102	189.5	69.9	144	15	POTRBCSB	M79357	Potato rbcS
103	189.5	69.9	803	15	BRPBCSSU	Y07779	Betula pend
104	189	69.7	844	15	PYPRECO	D05572	Pyrus pyrif
105	186.5	68.8	144	15	POTRBCSD	M79359	Potato rbcS
106	186.5	68.8	70687	15	AP06376	AP006376	Lotus cor
107	186	68.6	853	15	MSCARB	X65494	Malus (unid
108	185.5	68.5	751	15	SORBCS2	X97600	S.oleracea
109	184.5	68.1	692	15	S1PRUBPCS	M16888	White camp
110	184.5	68.1	726	15	BNRBCSSU	X07367	B.napus mRNA
111	184.5	68.1	763	9	BC038257	BC038257	Mus muscu
112	183.5	67.7	144	15	POTRBCSC	M79358	Potato rbcS
113	183.5	67.7	793	15	AF101232	AF101232	Manihot e
114	183.5	67.7	3024	15	C1P6RSS	L10213	Mesembryant
115	181.5	67.0	174	6	AR229546	AR229546	Sequence
116	181.5	67.0	178	6	AR260582	AR260582	Sequence
117	181.5	67.0	249	15	AJ609388	AJ609388	Arabidops
118	181.5	67.0	264	6	AR229543	AR229543	Sequence
119	181.5	67.0	268	6	AR260581	AR260581	Sequence
120	181.5	67.0	279	6	AR016596	AR016596	Sequence
121	181.5	67.0	279	6	I15329	I15329	Sequence 9
122	181.5	67.0	296	11	SNATS1A	X68342	Synthetic D
123	181.5	67.0	355	6	AR007589	AR007589	Sequence
124	181.5	67.0	355	6	I18862	I18862	Sequence 5
125	181.5	67.0	355	6	I36788	I36788	Sequence 5
126	181.5	67.0	355	6	I55992	I55992	Sequence 5
127	181.5	67.0	355	6	AR301815	AR301815	Sequence
128	181.5	67.0	355	6	AR301833	AR301833	Sequence
129	181.5	67.0	543	15	AY097366	AY097366	Arabidops
130	181.5	67.0	583	15	AY093380	AY093380	Arabidops
131	181.5	67.0	583	15	AY093388	AY093388	Arabidops
132	181.5	67.0	583	15	BT000362	BT000362	Arabidops
133	181.5	67.0	583	15	BT002076	BT002076	Arabidops
134	181.5	67.0	617	15	AY065101	AY065101	Arabidops
135	181.5	67.0	696	6	AR229544	AR229544	Sequence
136	181.5	67.0	702	15	AY054581	AY054581	Arabidops
137	181.5	67.0	711	15	AY054188	AY054188	Arabidops
138	181.5	67.0	721	15	AY059940	AY059940	Arabidops
139	181.5	67.0	720	15	AY062612	AY062612	Arabidops
140	181.5	67.0	752	15	AF410291	AF410291	Arabidops
141	181.5	67.0	754	15	AF325004	AF325004	Arabidops
142	181.5	67.0	772	15	AY062711	AY062711	Arabidops
143	181.5	67.0	788	15	AY058831	AY058831	Arabidops
144	181.5	67.0	825	15	AF325011	AF325011	Arabidops
145	181.5	67.0	1630	6	AR229553	AR229553	Sequence 1
146	181.5	67.0	1631	6	A59869	A59869	Sequence 1
147	181.5	67.0	2821	15	ATRBCSA	X13611	Arabidops
148	181.5	67.0	3162	15	AY050459	AY050459	Arabidops
149	181.5	67.0	5560	6	A60112	A60112	Sequence 5
c 150	181.5	67.0	5560	6	AR098311	AR098311	Sequence
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RESULT 1							
AY220079	806 bp	mRNA	linear	PLN 16-APR-2003			
LOCUS	Nicotiana tabacum putative ribulose biphosphate carboxylase small						
DEFINITION	subunit protein precursor, mRNA, complete cds; nuclear gene for						
ACCESSION	AY220079						
VERSION	AY220079.1	GI:30013662					
KEYWORDS	Nicotiana tabacum (common tobacco)						
SOURCE	Nicotiana tabacum						
REFERENCE	1 (bases 1 to 806)						
AUTHORS	Tang, L., Dollins, C., Erra, S. and Petracek, M.						
TITLE	Phycosynthetic Control of Nuclear mRNA Gene Expression in Tobacco						
JOURNAL	Unpublished						
AUTHORS	2 (bases 1 to 806)						
TITLE	Direct Submission						
JOURNAL	Submitted (15-JAN-2003) Biochemistry and Molecular Biology,						
OK 74078, USA	Oklahoma State University, 246 Noble Research Center, Stillwater,						
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	TERGFVYRNKSPCYDGRYTWKMLPMFGCTDATQVLAIEVGEAKKAYPEAWIRIIG						
	FDNVRQVCISFIAYKPEGY"						
ORIGIN							
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Query Match:	90.2%	Indels:	1				
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US-10-628-525A-33 (1-56) x AY220079 (1-806)							
QY	1	MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla	20				
Db	61	ATGGCTTCCTCTGTTCTTTCTCTGAGCAGTTGCCACTCGCACCACCAATGTTGCTCAAGCT	120				
QY	21	SerMetValAlaProPheThrGlyLeuYsSerAlaAla---	39				
Db	121	AAATGAGTGTGACCTTTTCACTGGTCTTAAGTCAGCTGCCTCCTGTTTCAAGGAG	180				
QY	40	GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys	56				
Db	181	CAAAACCTTGACATCACTTCCATTGCTAGCANTGGTGGAGATGCAATGC	231				
RESULT 2							
I24839							
LOCUS	I24839	177 bp	DNA	linear	PAT 07-OCT-1996		

DEFINITION Sequence 8 from patent US 5545816.  
ACCESSION I24839  
VERSION I24839.1 GI:1604709  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 177)  
AUTHORS Ausich,R.L., Brinkhaus,F.L., Mukharji,I., Proffitt,J., Yarger,J. and Yen,H.-C.B.  
TITLE Phytoene biosynthesis in genetically engineered hosts  
JOURNAL Patent: US 5545816-A 8 13-AUG-1996;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 1.23e-20 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x I24839 (1-177)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
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Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 61 AACATGGTGGCGCTTTCCTCTGCGAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 120

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 171

RESULT 3  
LOCUS I40228  
DEFINITION Sequence 6 from patent US 5618988.  
ACCESSION I40228  
VERSION I40228.1 GI:2083233  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 177)  
AUTHORS Hauptmann,R., Eschenfeldt,W.H., English,J. and Brinkhaus,F.L.  
TITLE Enhanced carotenoid accumulation in storage organs of genetically engineered plants  
JOURNAL Patent: US 5618988-A 6 08-APR-1997;  
FEATURES Location/Qualifiers  
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ORIGIN

Alignment Scores:  
Pred. No.: 1.23e-20 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x I40228 (1-177)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 1 ATGGCTTCCTCAGTTCTTCTCTGCGAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60

Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 61 AACATGGTGGCGCTTTCCTCTGCGAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 120

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 171

RESULT 4  
LOCUS I72655  
DEFINITION Sequence 12 from patent US 5684238.  
ACCESSION I72655  
VERSION I72655.1 GI:3008794  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 177)  
AUTHORS Ausich,R.L., Brinkhaus,F.L., Mukharji,I., Proffitt,J.H., Yarger,J.G. and Yen,H.-C.B.  
TITLE Biosynthesis of zeaxanthin and glycosylated zeaxanthin in genetically engineered hosts  
JOURNAL Patent: US 5684238-A 12 04-NOV-1997;  
FEATURES Location/Qualifiers  
source 1..177  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 1.23e-20 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x I72655 (1-177)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 1 ATGGCTTCCTCAGTTCTTCTCTGCGAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60

Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 61 AACATGGTGGCGCTTTCCTCTGCGAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 120

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 171

RESULT 5  
LOCUS AR528363  
DEFINITION Sequence 3 from patent US 6723895.  
ACCESSION AR528363  
VERSION AR528363.1 GI:53916426  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 204)  
AUTHORS DeBonte,L.R. and Shorrosh,B.S.  
TITLE Plants containing a cytosolic acetyl CoA-carboxylase nucleic acid  
JOURNAL Patent: US 6723895-A 3 20-APR-2004;  
FEATURES Location/Qualifiers  
source 1..204  
/organism="unknown"  
/mol\_type="genomic DNA"

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 1 ATGGCTTCCTCAGTTCTTCTCTGCGAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60

Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 61 AACATGGTGGCGCTTTCCTCTGCGAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 120

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 171

## ORIGIN

Alignment Scores:	1.44e-20	Length:	204
Pred. No.:	240.50	Matches:	52
Score:	96.5%	Conservative:	3
Percent Similarity:	91.2%	Mismatches:	1
Best Local Similarity:	91.2%	Indels:	1
Query Match:	88.7%	Gaps:	1
DB:	6		

US-10-628-525A-33 (1-56) X AR528363 (1-204)

## RESULT 6

APRECA2	APRECA2	Hybrid rbc-preSS-CAT gene (CAT=chloramphenicol acetyltransferase).	225 bp	DNA	linear	SYN 18-APR-1995
LOCUS	X05923	X05923.1	GI:58130			
DEFINITION		artificial gene; chloramphenicol acetyltransferase; ribulose				
ACCESSION		bisphosphate carboxylase; transit peptide.				
VERSION		synthetic construct				
KEYWORDS		synthetic construct				
SOURCE		other sequences; artificial sequences.				
ORGANISM		1 (bases 1 to 225)				
REFERENCE		Boutry, M., Nagy, F., Poulsen, C., Aoyagi, K. and Chua, N.H.				
AUTHORS		Targeting of bacterial chloramphenicol acetyltransferase to				
TITLE		mitochondria in transgenic plants				
		Nature 328 (6128), 340-342 (1987)				
JOURNAL		3474528				
PUBMED		bacterial CAT coding sequence was fused to the chloroplast				
COMMENT		transit sequence of rbcS8B from <i>Nicotiana plumbaginifolia</i> .				

## ORIGIN

**Alignment Scores:**

Pred. No.:	1.6e-20	Length:	225
Score:	240.50	Matches:	52
Percent Similarity:	96.5%	Conservative:	3
Best Local Similarity:	91.2%	Mismatches:	1
Query Match:	88.7%	Indels:	1
DB:	11	Gaps:	1

US-10-628-525A-33 (1-56) x ARPREC2 (1-225)

## RESULT 7

```

AR205973
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
AR205973
Sequence 41 from patent US 6369296.
AR205973
AR205973.1 GI:21503691
.
Unknown.
SOURCE
Unknown.
Unclassified.
1 (bases 1 to 499)
Ratcliff,F.Giles., Martin-Hernandez,A.Montserrat. and
Baulcombe,D.Charles
Recombinant plant viral vectors
Patent: US 6369296-A 41 09-APR-2002;
Location/Qualifiers
1. .499
/organism="unknown"
/mol type="unassigned DNA"

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## ORIGIN

Alignment Scores:		
Pred. No.:	3.9e-20	499
Score:	240.50	52
Percent Similarity:	96.5%	3
Best Local Similarity:	91.2%	1
Query Match:	88.7%	1
DB:	6	1
Length:		
Matches:		
Conservative:		
Mismatches:		
Indels:		
Gaps:		

US-10-628-525A-33 (1-56) x AR205973 (1-499)

1	MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProIleAla	20
	:::::	
8	ATGGCTTCTCAGTTCTTCTCTGCGACGAGTTGCCACCGCAAGAATGTGTCTCAAGCT	67
21	SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys	39
	:::	
68	AACATGTTGTGCACCTTTCACTGGCGTTTAAGTCAGCTGCCTCATTTCCCTGTTTCAAGGAAG	127
40	GlnAsnLeuAspIleThrSerIleAlaSerAsnGlycylArgValGlnCys	56
128	CAAACACTTGACATCACTTCATTGCGCAGCAACGGCGGAAGAGTGCAGAAATGC	178

## RESULT 8

NSRUB1	NSRUB1	796 bp	mRNA	linear	PLN 18-APR-2005
LOCUS	Nicotiana glauca silvestris mRNA for the small subunit of ribulose				
DEFINITION	biphosphate carboxylase.				
ACCESSION	X01722				
VERSION	X01722.1				
KEYWORDS	GI:19759				
	carboxylase; ribulose biphosphate carboxylase.				

SOURCE Nicotiana sylvestris (wood tobacco)  
 ORGANISM Nicotiana sylvestris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
 REFERENCE 1 (bases 1 to 796)  
 AUTHORS Pinck, M., Guillevey, E., Durr, A., Hoff, M., Pinck, L. and Fleck, J.  
 TITLE Complete sequence of one of the mRNAs coding for the small subunit of ribulose biphosphate carboxylase of Nicotiana sylvestris  
 JOURNAL Biochimie 66 (7-8), 539-545 (1984)  
 PUBMED 6549380  
 COMMENT Data kindly reviewed (22-JUL-1985) by J. Fleck.  
 FEATURES  
 source  
 1..796  
 /organism="Nicotiana sylvestris"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4096"  
 misc\_feature  
 1..60  
 /note="5' untranslated region"  
 repeat\_region  
 19..25  
 /note="direct repeat 1"  
 21..46  
 /note="pot. stem and loop structure"  
 misc\_feature  
 27..33  
 /note="direct repeat 1"  
 repeat\_region  
 53..61  
 /note="direct repeat 2"  
 61..603  
 /note="unnamed protein product; small subunit protein precursor"  
 /codon\_start=1  
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 /db\_xref="UniProt/Swiss-Pro: P69250"  
 /translation="MASSVLSAAVATRSNVAQNVAPFTGLKSAASPPVSRKQNLID ITSANGRGVQCMQWPPINKKYETLSVLPDLSQEQLLSEVEYLLKNGWVPCLEF TEHGIVRENNKSPGYDGRYTWKLPMPFGCTDATQVLAEEVEANKAYPQAWIRIIG FDNVRQVCISFIAPYPEGY"  
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 61..231  
 /note="transit peptide (aa -57 to -1)"  
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 232..600  
 /product="mature small subunit protein (aa 1-123)"  
 repeat\_region  
 249..257  
 /note="direct repeat 2"  
 misc\_feature  
 601..796  
 /note="3' untranslated region"  
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 /note="polyA site"  
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 Alignment Scores:  
 Pred. No.: 6,56e-20 Length: 796  
 Score: 240.50 Matches: 52  
 Percent Similarity: 96.5% Conservative: 3  
 Best Local Similarity: 91.2% Mismatches: 1  
 Query Match: 88.7% Indels: 1  
 DB: 15 Gaps: 1  
 US-10-628-525A-33 (1-56) x NSRUB1 (1-796)  
 QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAenProAlaGlnAla 20  
 DB 61 ATGGCTTCCTCAGTCTCTTCTCTGCGAGCATGTCACCGCGAGCAATGTTGCTCAAGCT 120  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 DB 121 AACATGGTTGCACCTTTTCACTGGCCCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAA 180  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 DB 181 CAAACCTTGACATCACTTCCATTGCGAGCAACGCGGAAGAGTGCATATGC 231

RESULT 9  
 TOBRUBPA  
 LOCUS  
 DEFINITION Tobacco ribulose-1,5-bisphosphate carboxylase small subunit gene, exons 1 and 2, clone TSSU3-8.  
 ACCESSION M32419.1 GI:170327  
 VERSION  
 KEYWORDS ribulose 1,5-bisphosphate carboxylase.  
 SOURCE Nicotiana tabacum (common tobacco)  
 ORGANISM Nicotiana tabacum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
 REFERENCE 1 (bases 1 to 979)  
 AUTHORS O'Neal, J.K., Pokalsky, A.R., Kiehne, K.L. and Shewmaker, C.K.  
 TITLE Isolation of tobacco SSU genes: characterization of a transcriptionally active pseudogene  
 JOURNAL Nucleic Acids Res. 15 (21), 8661-8677 (1987)  
 PUBMED 3684569  
 COMMENT  
 FEATURES  
 source  
 1..979  
 /organism="Nicotiana tabacum"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4097"  
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 /notes="precursor"  
 /codon\_start=1  
 /product="ribulose-1,5-bisphosphate carboxylase small subunit"  
 /protein\_id="AAA34116.1"  
 /db\_xref="GI:170328"  
 /translation="MASSVLSAAVATRSNVAQNVAPFTGLKSAASPPVSRKQNLID ITSANGRGVQCMQWPPINKKYETLSVLPDLSQEQLLSEVEYLLKNGWVPCLEF" 584..757  
 /notes="ribulose-1,5-bisphosphate carboxylase small subunit signal peptide"  
 mat\_peptide  
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 /product="ribulose-1,5-bisphosphate carboxylase small subunit"  
 <584..760  
 /note="ribulose-1,5-bisphosphate carboxylase small subunit precursor"  
 /number=1  
 761..853  
 /note="ribulose-1,5-bisphosphate carboxylase small subunit"  
 /number=1  
 854..>979  
 /note="ribulose-1,5-bisphosphate carboxylase small subunit; putative"  
 /number=2  
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 Pred. No.: 8,26e-20 Length: 979  
 Score: 240.50 Matches: 52  
 Percent Similarity: 96.5% Conservative: 3  
 Best Local Similarity: 91.2% Mismatches: 1  
 Query Match: 88.7% Indels: 1  
 DB: 15 Gaps: 1  
 US-10-628-525A-33 (1-56) x TOBRUBPA (1-979)  
 QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAenProAlaGlnAla 20  
 DB 584 ATGGCTTCCTCAGTCTCTTCTCTGCGAGCATGTCACCGCGAGCAATGTTGCTCAAGCT 643  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 DB 644 AACATGGTTGCACCTTTTCACTGGCCCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAA 703

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QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
|
|
|
Db 704 CAAACCTTGACATCACTTCATTCGACGACGCGGAGAGTGCAATGC 754
|
|
|
RESULT 10
PERBCS11
LOCUS Petunia x hybrida rbcS gene (ssu11a) for ribulose 1,5-bisphosphate
DEFINITION carboxylase small subunit.
ACCESSION X03821
VERSION X03821.1 GI:20492
SOURCE ribulose biphosphate carboxylase.
ORGANISM Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Petunia.
1 (bases 1 to 1314)
Tumer,N.E., Clark,W.G., Tabor,G.J., Hironaka,C.M., Fraley,R.T. and
Shah,D.M.
The genes encoding the small subunit of ribulose-1,5-bisphosphate
carboxylase are expressed differentially in petunia leaves
Nucleic Acids Res. 14 (8), 3325-3342 (1986)
3010233
REFERENCE 2
AUTHORS Dean,C., Favreau,M., Dunsmuir,P. and Bedbrook,J.
TITLE Confirmation of the relative expression levels of the Petunia
(Mitchell) rbcS genes
Nucleic Acids Res. 15 (11), 4655-4668 (1987)
3588304
PUBMED
COMMENT *source strain=Mitchell.
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/organism="Petunia x hybrida"
/mol_type="genomic DNA"
/cultivar="Mitchell"
/db_xref="taxon:4102"
107..111
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186..193
TATA_signal
213..215
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/note="put. transcription initiation region"
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Join(279..455,673..807,958..1188)
CDS
/gene="rbcS"
/EC_number="4.1.1.39"
/codon_start=1
/product="ribulose 1,5-bisphosphate carboxylase"
/protein_id="CAA27445.1"
/db_xref="GI:20493"
/db_xref="GOA:P04715"
/db_xref="UniProt/Swiss-Prot:P04715"
/translation="MASSVMSSAAVATSTNAQASMVAFPTGLKSAASFPVSRKQNLID
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exon
<279..455
/gene="rbcS"
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intron
456..672
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exon
673..807
/gene="rbcS"
/number=2
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808..957
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exon
958..>1188
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/number=3
ORIGIN

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Alignment Scores:
Pred. No.: 1,15e-19 Length: 1314
Score: 240.50 Matches: 52
Percent Similarity: 94.7% Conservative: 2
Best Local Similarity: 91.2% Mismatches: 2
Query Match: 88.7% Indels: 1
DB: 15 Gaps: 1
US-10-628-525A-33 (1-56) x PERBCS11 (1-1314)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
|
|
|
Db 279 ATGGCTTCCTCAGTGATGTCCTCAGCTGCAGTTGCCACAGCACCACCAATGCTGCTCAAGCC 338
|
|
|
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
|
|
|
Db 339 AGCATGGTTGCAACCTTCACCTGCCTCAGTCTGAGCTGCAGCCCTCCCTCTTTCCAGGAAA 398
|
|
|
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
|
|
|
Db 399 CAGAACCTTGACATTCATTCCATTGCTAGCAATGGTGAAGAGTTCAATGC 449
|
|
|
RESULT 11
PERBCS8B
LOCUS Nicotiana plumbaginifolia rbcS-8B gene for ribulose biphosphate
DEFINITION carboxylase small subunit.
ACCESSION X13711
VERSION X13711.1 GI:19705
KEYWORDS enhancer-like sequence; rbcS gene; ribulose biphosphate
carboxylase.
SOURCE Nicotiana plumbaginifolia (curled-leaved tobacco)
ORGANISM Nicotiana plumbaginifolia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 2293)
Poulsen,C., Fluhr,R., Kauffman,J.M., Boutry,M. and Chua,N.H.
Characterization of an rbcS gene from Nicotiana plumbaginifolia and
expression of an rbcS-CAT chimeric gene in homologous and
heterologous nuclear background
Mol. Gen. Genet. 205, 193-200 (1986)
REFERENCE 2 (bases 1 to 1130)
Poulsen,C. and Chua,N.H.
Dissection of 5' upstream sequences for selective expression of the
Nicotiana plumbaginifolia rbcS-8B gene
Mol. Gen. Genet. 214 (1), 16-23 (1988)
JOURNAL
PUBMED 3226423
FEATURES
source
1..2293
/organism="Nicotiana plumbaginifolia"
/mol_type="genomic DNA"
/db_xref="taxon:4092"
/clone_lib="EMBL4"
1..450
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/note="enhancer-like sequence"
complement(403..410)
misc_feature
/note="SV40 enhancer core similarity"
435..892
misc_feature
/note="SV40 enhancer core similarity"
885..892
misc_feature
/note="SV40 enhancer core similarity"
911..915
CAAT_signal
927..931
CAAT_signal
945..949
TATA_signal
1008..1015
misc_feature
1035
/note="alternative transcriptional start"
1039..2171
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/note="primary transcript"
1039..1289
exon
/number=1
1049..1051
misc_feature

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Alignment Scores:		2.13e-19	Length:	2293
Pred. No.:		240.50	Matches:	52
Score:		96.5%	Conservative:	3
Percent Similarity:		91.2%	Mismatches:	1
Best Local Similarity:		88.7%	Indels:	1
Query Match:		15	Gaps:	1
DB:				
US-10-628-525A-33 (1-56) x TORBSC8B (1-2293)				
QY	1	MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThrAsnProAlaGlnAla	20	
Db	1113	ATGGCTTCCTCAGTCTTCTCTGAGCAGTGCCACCGCAGCAATGTTGCTCAAGCT	1172	
QY	21	SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys	39	
Db	1173	AACATGGTTGCACCTTTCATGCTGCTTAAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG	1232	
QY	40	GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys	56	
Db	1233	CAAAACCTTGACATACTTCCATTGCCAGACGGCGGAAGAGTGCATGTC	1283	
RESULT 13				
NTRUBSS				
LOCUS				
DEFINITION				
Tobacco gene for ribulose 1,5-bisphosphate carboxylase small subunit.				
ACCESSION				
X02353				
VERSION				
X02353.1 GI:20023				
KEYWORDS				
ribulose biphosphate carboxylase.				
SOURCE				
Nicotiana tabacum (common tobacco)				
ORGANISM				
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.				
REFERENCE				
1 (bases 1 to 2362)				
Mazur, B.J. and Chui, C.F.				
AUTHORS				
Sequence of a genomic DNA clone for the small subunit of ribulose bis-phosphate carboxylase-oxygenase from tobacco				
Nucleic Acids Res. 13 (7), 2373-2386 (1985)				
JOURNAL				
PUBMED				
4000958				
FEATURES				
source				
1..2362				
Location/Qualifiers				
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/mol_type="genomic DNA"				
/db_xref="taxon:4097"				
46..111				
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repeat_unit				
57..63				
/note="put. regulatory sequence"				
repeat_region				
93..406				
/note="series of 43 bp imp. tandem direct repeats"				
repeat_unit				
389..454				
/note="inverted repeat A"				
misc_signal				
435..442				
/note="put. regulatory sequence"				
misc_signal				
586..592				
/note="put. regulatory sequence"				
misc_signal				
830..837				
/note="put. regulatory sequence"				
misc_signal				
857..862				
/note="put. regulatory sequence"				
promoter				
873..878				
/note="put. CAAT-box"				
misc_signal				
891..896				
/note="put. regulatory sequence"				
promoter				
955..962				
/note="put. TATA-box"				
CDS				
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/codon_start=1				
/product="small subunit ribulose 1,5-bisphosphate				
carboxylase"				
protein_id="CAA26208.1"				
/db_xref="GI:20024"				
/db_xref="GOA:P69249"				
/db_xref="InterPro:IPR000894"				
/db_xref="UniProt/Swiss-Prot:P69249"				
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TEHGFVRENNKSPGYIDGRYTWIMKLPFMFGCTDATQVLAEEVEAKKAYPQAWIRIIG				
FDNRVQCISFIAYKEGY"				
1048..1218				
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mat_peptide				
/product="small subunit ribulose 1,5-bisphosphate				
carboxylase"				
/EC_number="4.1.1.39"				
intron				
/note="intron I"				
misc_signal				
1307..1313				
/note="put. regulatory sequence"				
intron				
1453..1608				
/note="intron II"				
intron				
1662..1806				
/note="intron III"				
misc_signal				
1672..1678				
/note="put. regulatory sequence"				
misc_feature				
2145..2153				
/note="pot. polyA signal"				
polyA_site				
2175				
/note="put. polyA site"				
ORIGIN				
Alignment Scores:				
Pred. No.:	2.21e-19	Length:	2362	
Score:	240.50	Matches:	52	
Percent Similarity:	96.5%	Conservative:	3	
Best Local Similarity:	91.2%	Mismatches:	1	
Query Match:	88.7%	Indels:	1	
DB:	15	Gaps:	1	
US-10-628-525A-33 (1-56) x NTRUBSS (1-2362)				
QY	1	MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThrAsnProAlaGlnAla	20	
Db	1048	ATGGCTTCCTCAGTCTTCTCTGAGCAGTGCCACCGCAGCAATGTTGCTCAAGCT	1107	
QY	21	SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys	39	
Db	1108	AACATGGTTGCACCTTTCATGCTGCTTAAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG	1167	
QY	40	GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys	56	
Db	1168	CAAAACCTTGACATACTTCCATTGCCAGACGGCGGAGAGTGCATGTC	1218	
RESULT 14				
CVE18556				
LOCUS				
DEFINITION				
Cloning vector pSLJ8313, T-DNA region.				
ACCESSION				
Y18556				
VERSION				
Y18556.1 GI:4191249				
KEYWORDS				
cloning vector; T-DNA.				
SOURCE				
Cloning vector pSLJ8313				
ORGANISM				
Other sequences; artificial sequences; vectors.				
REFERENCE				
1				
Ratet, P. and Rippe, S.				
AUTHORS				
Unpublished				
JOURNAL				
REFERENCE				
2 (bases 1 to 22574)				
Ratet, P.				
AUTHORS				
Direct Submission				
TITLE				
Submitted (21-DEC-1998) P. Ratet, Institut des Sciences Vegetales				
(ISV), CNRS, Avenue de la Terrasse, Bat 23, 91198 Gif sur Yvette				
cedex, FRANCE				
REMARK				
Revised by author				

```

COMMENT      Related sequences X00493, M32238, X03820, X79465, M25427, M19104,
X01077, X05822, M35007, A00196, V00087.
FEATURES
  source      Cloning vector constructed by Tissier A. and Jones J.D.G.
              Location/Qualifiers
                1..22574
                  /organism="Cloning vector pSLJ8313"
                  /mol_type="other DNA"
                  /db_xref="taxon:86981"
                  /lab_host="Escherichia coli"
                  /focus
  source      join(1..890,16711..17439,22291..22574)
                  /organism="Agrobacterium tumefaciens"
                  /mol_type="other DNA"
                  /db_xref="taxon:358"
                  /plasmid="pTI15955"
  source      join(891..2488,3713..5272)
                  /organism="Petunia sp."
                  /mol_type="other DNA"
                  /db_xref="taxon:4104"
                  /focus
  source      2489..3703
                  /organism="Streptomyces griseolus"
                  /mol_type="other DNA"
                  /db_xref="taxon:1909"
  source      join(5273..5482,13154..14507)
                  /organism="Cauliflower mosaic virus"
                  /mol_type="other DNA"
                  /db_xref="taxon:10641"
  source      join(5483..13153,14596..15589,19205..20106)
                  /organism="Zea mays"
                  /mol_type="other DNA"
                  /db_xref="taxon:4577"
  source      join(14508..14595,16075..16146)
                  /organism="Tobacco mosaic virus"
                  /mol_type="other DNA"
                  /db_xref="taxon:12242"
  source      join(15790..16074,22003..22290)
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                  /mol_type="other DNA"
                  /db_xref="taxon:358"
                  /plasmid="pTI137"
                  /db_xref="taxon:16147..16698"
  source      /organism="Streptomyces hygroscopicus"
                  /mol_type="other DNA"
                  /db_xref="taxon:1912"
  source      join(17944..19204,20121..21944)
                  /organism="Escherichia coli"
                  /mol_type="other DNA"
                  /db_xref="taxon:562"
  misc_feature 299..323
                  /notes="T-DNA left border"
  misc_feature 322..22574
                  /notes="T-DNA region"
  gene          891..5272
                  /gene="cytochrome P450, artificial"
  misc_feature 891..5272
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                  /notes="artificial cytochrome P450 gene"
  promoter      891..2446
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                  /notes="source: rbcS gene, Petunia sp."
  CDS           2447..3703
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                  /codon_start=1
                  /transl_table=11
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                  /protein_id="CAA77215.1"
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                  /translation="MQVPPYGGKKYDTPATTPQTTDAPFPSSNRCSPYQLPDGYAQ
LRDTPGLHRVLYDGRQAVVYTKHEARKLGDPRLSNRTDDNFPATSPRFEAVRE
SPQAFGLDPHPHGRRTMTIGFTVKRIKGRPEVEVVHGFGLDMLAAGTADIVS
QPALPVSMVI CRLLGVPVADHEFPQDASKRLVQSDAQASALTARNDLAGYLDGLITQ
FQTEPGAGLVGLVQDLQANGIDREELISTAMLLLIAGHTASMTLSLSVITLLDHP
EQTAALRADRSVPGAVESLLRYLAADIAGGRVATADIEVEGHLIRAGEGIVVNSI
ANRDGTYVEDPDALDIHRSARHHLAFQGVHQCILGQNLARLELEVLNLMALMDRVPTLR
LAYVEQLVLRPGTTIQGVNELPVTW"
  sig_peptide   2447..2488
                  /genes="cytochrome P450, artificial"
                  /note="source: rbcS gene, Petunia sp."
  mat_peptide   2489..3700
                  /genes="cytochrome P450, artificial"
                  /product="source: suac gene, Streptomyces griseolus"
  misc_signal   3713..5272
                  /genes="cytochrome P450, artificial"
                  /note="contains polyA signal from rbcS, Petunia sp."
  misc_feature 5273..13153
                  /notes="chimaeric En/Spm TnpAD locus"
  promoter      5273..5482
                  /notes="source: Cauliflower mosaic virus"
  misc_feature 5483..13153
                  /note="En/Spm TnpAD locus
source: Zea mays"
  promoter      13154..14507
                  /notes="source: Cauliflower mosaic virus"
  misc_feature 14508..14595
                  /notes="5' leader sequence, Tobacco mosaic virus"
  misc_feature 14596..20106
                  /notes="En/Spm transposable element, defective"
  misc_feature 15790..17439
                  /notes="artificial bar gene"
  gene          15790..16698
                  /gene="bar, artificial"
  promoter      15790..16074
                  /gene="bar, artificial"
                  /notes="source: nopaline synthase gene, Agrobacterium
tumefaciens, plasmid pTi137"
  CDS           16147..16698
                  /gene="bar, artificial"
                  /notes="source: Streptomyces hygroscopicus"
                  /codon_start=1
                  /transl_table=11
                  /product="phosphothicin acetyl transferase"
                  /protein_id="CAA77216.1"
                  /db_xref="GI:4191251"
                  /translation="MSPERPADIRRATEADPAVCTIVNHYIETSTVNRTRPQBPO
EWTDDLVRURERYPMLVAVDGEVAGIAYAGPWKARNAYDWTAEYSTVYSPRRTGSL
GSTLYTHLLKSLEAQGKSVAVIGLNPDPVSRMHEALGYAPRGLRAAGFKHGNWHD
VGFWQLDFSLPVPVPPRPVLPVTET"
  misc_signal   16711..17439
                  /notes="contains polyA signal
source: octopine synthase gene, Agrobacterium tumefaciens,
plasmid pTI15955"
  CDS           17944..18954
                  /note="source: Escherichia coli"
                  /codon_start=1
                  /transl_table=11
                  /product="adenyl transferase"
                  /protein_id="CAA77217.1"
                  /db_xref="GI:4191252"
                  /translation="NRSNRWSTLTERSGNGAVAFVMACYDCFFGVQSNPRASKQQA
RYAVGRCMLWSSNDVDTQGSRPKTKLNMREAVIAEVSTQSLSEVVGVLEHLEPTLL
AVHLVGSADVGGIKSHSDIDLAVTVYRLDETTRRALINDLETSAPESEILRAVE
VTIVVHDDILPWRYPAKRELQFGQWRNDILAGIFEFPATIDIDLALLTKAREHVAL
PKGAAABELPDPVPEQDLFEALNETLTWNSSPPDWAGDERNVLTLSRIWYSVATGKIA
VQDAADWAMERLPAQYQPVILEARQAYLGQBEDRLASRADQLEEFVHYVKGITKV
GK"
  misc_feature 20107..22290
                  /note="chimeric uidA (gus) gene"
  gene          20121..21944
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  CDS           20121..21944
                  /gene="gus"
                  /note="source: Escherichia coli"
                  /codon_start=1
                  /transl_table=11
                  /product="beta-glucuronidase"
                  /protein_id="CAA77218.1"

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/db_xref="GI:4191253"
/translation="MGQSLMRPVEPTTPEIKKLDGLWAFSLDRENCGLDQWWSAL
QSSRAIVPGSFNDPADADIRNYAGNVQREVFIPKQAGQRIVLRFDAETHYGVK
WYNNQVMEHQGGTPEADVPYVIAGSRVITVCVNNELNWTIPPGWVITDENGK
KKQSPHDFPNVAGIHRSTYTPNTWDDITVTVHVAQDCNHSVQVQVWGDVS
VELRDADQVATQGSTGLQVNPPLWQPGEGYELCVTAKSQTECDIYPLRVGI
RSPVYAEMLDWADEHIGVITDETAAGFNLGSGIGFEAGNKKPKLYSBEAVNGTQQA
HYVAKELIARDKHPSPVVMSTANEPDTPQVHGNISPLAENRKLDPTRITCVNV
MFCDAHTIDISLFDVLCLNRYGYWTVQSGDLEAKVLEKLLAWQEKLRQPIITE
YGVDTIAGLHSTWDSBEEYQACMLDMYHRVDFRVSAAVVGQVWVNFADFATFSQGLR
VGGNKGIPTDRDKPFSAAFLQKRWTGNMFKEKQQQGGK"
22003..22290
/note="region containing polyA signal
source: nopaline synthase gene, Agrobacterium tumefaciens,
plasmid pTi337"
22291..22574
/note="Agrobacterium tumefaciens, plasmid pTi15955 T_DNA,
right border region"
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## misc\_signal

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Alignment Scores:
Pred. No.: 6,37e-18 Length: 22574
Score: 237.50 Matches: 51
Percent Similarity: 94.7% Conservative: 3
Best Local Similarity: 89.5% Mismatches: 2
Query Match: 87.6% Indels: 1
DB: 11 Gaps: 1
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## ORIGIN

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US-10-628-525A-33 (1-56) x CVE18556 (1-22574)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2276 ATGGCTTCTCTGTGATTCCTCTGCAGCTGTGCTACTCGCACTAATGTGCTCAAGCT 2335
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSerArgLys 39
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2336 AGCATGGTTGCACCTTTTAATGGCTTAAAGTCTGCTGTCTCTCCACGTTTCAAGGAG 2395
QY 40 GlnAnLeuAspIleThrSerIleAlaSerAnGlyGlyArgValGlnCys 56
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2396 CAAAACCTTGACATCACTTCCATTGCTAGCAATGGTGAAGAGTCCAATGC 2446
```

## RESULT 15

```
STRBCS2 1629 bp DNA linear PLN 09-OCT-1996
LOCUS S.tuberosum rbcS2 gene for ribulose-(1,5)-bisphosphate
cardoxylase/oxygenase small subunit.
```

```
ACCESSION X69760.1 GI:21564
VERSION chloroplast; gene expression; gene family; photosynthesis; protein
KEYWORDS transport; rbcS2a gene.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum.
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```
REFERENCE 1 (bases 1 to 1629)
AUTHORS Fritz,C.C., Wolter,F.P., Schenkemeyer,V., Herget,T. and
Schreier,P.H.
TITLE The gene family encoding the ribulose-(1,5)-bisphosphate
cardoxylase/oxygenase (Rubisco) small subunit of potato
```

```
JOURNAL Gene 137 (2), 271-274 (1993)
PUBMED 8299958
AUTHORS Schreier,P.H.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-1992) P.H. Schreier, Bayer AG, PF-E/FU Gebaeude
6240, 5090 Leverkusen-Bayerwerk, FRG
COMMENT Related sequence: Fritz, C.C., Proc. Natl. Acad. Sci. 88:4458-4462
(91).
```

## FEATURES

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source Location/Qualifiers
1..1629
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/organism="Solanum tuberosum"
/mol_type="genomic DNA"
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/chromosomes="II"
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1..1629
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1..629
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Join(630..806,896..1030,1116..1346)
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/codon_start=1
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/protein_id="CAA49414.1"
/db_xref="GI:21565"
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/translation="MASSVMSSAAVATRGNGAQASVAPFTGLKSAASPPVSRKQNLID
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TEHGFVYRENNKSPGYIDGRYWTMMKLPFMFGCTDATQVLAEEVEAKKAYPQAWIRIIG
FDNVQVQCISFIAYKPEGY"
630..806
/gene="rbcS2a"
/product="ribulose biphosphate carboxylase"
/number=1
/number=1
/EC_number="4.1.1.39"
807..895
/gene="rbcS2a"
/number=1
896..1030
/gene="rbcS2a"
/product="ribulose biphosphate carboxylase"
/number=2
/EC_number="4.1.1.39"
1031..1115
/gene="rbcS2a"
/number=2
1116..1346
/gene="rbcS2a"
/product="ribulose biphosphate carboxylase"
/number=3
/EC_number="4.1.1.39"
1347..1629
/gene="rbcS2a"
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## ORIGIN

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Alignment Scores:
Pred. No.: 7,91e-19 Length: 1629
Score: 234.50 Matches: 51
Percent Similarity: 94.7% Conservative: 3
Best Local Similarity: 89.5% Mismatches: 2
Query Match: 86.5% Indels: 1
DB: 15 Gaps: 1
US-10-628-525A-33 (1-56) x STRBCS2 (1-1629)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 630 ATGGCTTCTTTCAGTGATGTCTTCAGCAGCTGTTCGCCGCCGCCGCAATGGTGCAAGCC 689
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAa---PheProValSerArgLys 39
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 690 AGCATGGTTGCACCTCTTCACTGGACTTAAGTCCGCCGCTCTTCCCTGTTTCAAGGAAG 749
QY 40 GlnAnLeuAspIleThrSerIleAlaSerAnGlyGlyArgValGlnCys 56
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 750 CAAAACCTTGACATCACTTCCATTGCTAGCAATGGTGAAGAGTCAAGTGC 800
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## RESULT 16

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STRBCS2C
LOCUS STRBCS2C 1386 bp DNA linear PLN 09-OCT-1996
```

DEFINITION S.tuberosum rbcS2c gene for ribulose-(1,5)-bisphosphate carboxylase/oxygenase small subunit.

ACCESSION X69762

VERSION X69762.1 GI:21568

KEYWORDS chloroplast; gene expression; gene family; photosynthesis; protein transport; rbcS2c gene.

SOURCE Solanum tuberosum (potato)

ORGANISM Solanum tuberosum

REFERENCE 1 (bases 1 to 1386)

AUTHORS Fritsch, C.C., Wolter, P.P., Schenkemeyer, V., Herget, T. and Schreier, P.H.

TITLE The gene family encoding the ribulose-(1,5)-bisphosphate carboxylase/oxygenase (Rubisco) small subunit of potato

JOURNAL Gene 137 (2), 271-274 (1993)

PUBMED 8299958

REFERENCE 2 (bases 1 to 1386)

AUTHORS Schreier, P.H.

TITLE Direct Submission

JOURNAL Submitted (01-DEC-1992) P.H. Schreier, Bayer AG, PF-E/FU Gebaeude 6240, 5090 Leverkusen-Bayerwerk, FRG

COMMENT Related sequence: Fritz, C.C., Proc. Natl. Acad. Sci. 88:4458-4462 (91).

FEATURES

source

1. .1386

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/mol\_type="genomic DNA"

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/chromosome="II"

/clone\_lib="phage lambda"

1. .1386

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1. 428

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/codon\_start=1

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/protein\_id="CA49416.1"

/db\_xref="GI:21569"

/db\_xref="GOA:P26577"

/db\_xref="UniProt/Swiss-Prot:P26577"

/translations="MASSVMSAAVATRGNGAASVAPPTGLKSTASFPVSRKQNLID ITSIAAGGVRCVQWPPINMKYETLSVLPDLSDEQLLKEVEYLLKNGWVPCLEFE TEHGFTYRNNKSPGYDGRYTWMLKPLMPFGCTDQVLAEBEAKKAYPQAWIRIIG FDNVRQVCISFIAYKPEG"

429..605

/genes="rbcS2c"

/product="ribulose biphosphate carboxylase"

/number=1

/EC\_number="4.1.1.39"

606..694

/genes="rbcS2c"

/number=1

695..829

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/product="ribulose biphosphate carboxylase"

/number=2

/EC\_number="4.1.1.39"

830..914

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/number=2

915..1145

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1146..1386

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ORIGIN

Alignment Scores:

Pred. No.: 1,54e-18 Length: 1386

Score: 231.50 Matches: 50

Percent Similarity: 94.7% Conservative: 4

Best Local Similarity: 87.7% Mismatches: 2

Query Match: 85.4% Indels: 1

DB: 15 Gaps: 1

US-10-628-525A-33 (1-56) x STRBCS2C (1-1386)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20

Db 429 ATGGCTTCTTCAATGCTCTCAGCAGCTGTGGCCACCGCGCAATGGTGCACAAGCC 488

Qy 21 SerMetValAlaProPheThrGlyLeuLeuSer---AlaAlaPheProValSerArgGly 39

Db 489 AGCATGGTTGCACCCCTTCACCTGCGCTCAAGTCCACCGCCCTCTTCCCTGTTTCAAGGAAG 548

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

Db 549 CAAAACCTTGACATTACCTCCATTGCTAGCAATGGTGAAGAGTCAGATGC 599

RESULT 17

PERBCS08

LOCUS 2242 bp DNA linear PLN 09-JUN-1999

DEFINITION Petunia x hybrida rbcS gene (ssu8) for ribulose 1,5-bisphosphate carboxylase small subunit.

ACCESSION X03820

VERSION X03820.1 GI:20490

KEYWORDS rbcS gene; ribulose biphosphate carboxylase.

SOURCE Petunia x hybrida

ORGANISM Petunia x hybrida

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanales; Solanales; Petunia.

REFERENCE 1 (bases 1 to 2242)

AUTHORS Tumer, N.E., Clark, W.G., Tabor, G.J., Hironaka, C.M., Fraley, R.T. and Shah, D.M.

TITLE The genes encoding the small subunit of ribulose-1,5-bisphosphate carboxylase are expressed differentially in petunia leaves

JOURNAL Nucleic Acids Res. 14 (8), 3325-3342 (1986)

PUBMED 3010233

COMMENT \*source

FEATURES

source

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/mol\_type="genomic DNA"

/cultivar="Mitchell"

/db\_xref="taxon:4102"

280..288

/notes="enhancer-like sequence"

319..323

CAAT\_signal

399..404

TATA\_signal

432..661

exon

/number=1

misc\_feature

432

/notes="put. transcription initiation site"

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/db\_xref="GI:20491"

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/db\_xref="UniProt/Swiss-Prot:P04714"

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AUTHORS	Manzara,T.
TITLE	Direct Submission
JOURNAL	Submitted (09-AUG-1989)
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	/clone="RbcS3"
enhancer	122..134
old_sequence	130..132
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promoter	/citation=[2]
	139..147
	/note="regulatory sequence"
CAAT_signal	174..184
misc_feature	236..244
	/note="regulatory sequence"
TATA_signal	247..254
exon	281..474
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gene	298..1019
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CDS	join(298..474,567..701,789..1019)
	/genes="rbcS3C"
	/codon_start=1
	/product="ribulose 1,5-bisphosphate carboxylase/oxygenase"
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	/db_xref="GI:19338"
	/db_xref="GOA:P07180"
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	298..468
sig_peptide	/genes="rbcS3C"
mat_peptide	join(467..474,567..701,789..1013)
	/genes="rbcS3C"
	/product="ribulose 1,5-bisphosphate carboxylase/oxygenase"
intron	475..566
	/genes="rbcS3C"
	/number=1
exon	567..701
	/genes="rbcS3C"
	/number=2
intron	702..788
	/genes="rbcS3C"
	/number=2
exon	789..>1016
	/genes="rbcS3C"
	/number=3
polyA_signal	1125..1130
polyA_signal	1128..1133
polyA_signal	1137..1142
ORIGIN	
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Pred. No.:	1 97e-18 Length: 1341
Score:	230.50 Matches: 50
Percent Similarity:	93.0% Conservative: 3
Best Local Similarity:	87.7% Mismatches: 3
Query Match:	Indels: 1
DB:	Gaps: 1
US-10-628-525A-33 (1-56) x LERBCS3C (1-1341)	
Oy	1 MetAlaSerSerMetLeuSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db	298 ATGGCTTCTTCAGTAATGCTCCACAGCGCTGTTCGCCCGGGCAATGGTGACAGCT 357
Oy	21 SerMetValAlaProPhoThrGlyLeuIysSer----AlaAlaPheProValSerArgIys 39



Unpublished  
JOURNAL Submitted (13-May-1992) to DDBJ by:  
COMMENT Mamoru Sugiura  
Center for Gene Research  
Nagoya University  
Chikusa-ku, Nagoya 464-01  
Japan  
Phone: 052-781-5111 x3453  
Fax: 052-782-3849  
Location/Qualifiers  
1. 4124  
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/db\_xref="taxon:4081"  
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2498..2734  
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TATA\_signal 3310..3317  
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exon 3620..3754  
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ORIGIN  
Alignment Scores:  
Pred. No.: 9,13e-18 Length: 4124  
Score: 229.50 Matches: 50  
Percent Similarity: 93.0% Conservatives: 3  
Best Local Similarity: 87.7% Mismatches: 3

Query Match: 84.7% Indels: 1  
DB: 15 Gaps: 1  
US-10-628-525A-33 (1-56) x TOMERBCO (1-4124)  
Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
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Db 3351 ATGGCTTTCCTATAGTTTCTTCAGCTGCTGTGGCCACCGCGCAATGGTGCAAGCT 3410  
Qy 21 SerMetValAlaProPheThrGlyLeuLysSer---AlaAlaPheProValSerArgLys 39  
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Db 3411 AGCATGGTTGCACCTTCCTGACTCACTGCTCTTCCTGTTTCAAGGAAG 3470  
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
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Db 3471 CAAACCTTGACATTACCTCCATTGCTAGCACCGTGGAGAGAGTCAGTTGC 3521

RESULT 23  
SLARBCS 723 bp mRNA linear PLN 30-JUN-1995  
LOCUS Stellaria longipes ribulose-1,5-bisphosphate carboxylase/oxygenase  
DEFINITION (rbcS) mRNA, complete cds.  
ACCESSION L26605  
VERSION L26605.1 GI:556417  
KEYWORDS rbcS gene; ribulose 1,5-bisphosphate carboxylase/oxygenase small  
subunit.  
SOURCE Stellaria longipes  
ORGANISM Stellaria longipes  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
Caryophyllales; Caryophyllaceae; Stellaria.  
REFERENCE 1 (bases 1 to 723)  
AUTHORS Zhang,X.-H., Muhammad,N. and Chinnappa,C.C.  
TITLE Characterization and evolution of a cDNA encoding the small subunit  
of ribulose-1,5-bisphosphate carboxylase/oxygenase (rbcS) of  
Stellaria longipes (Caryophyllaceae)  
JOURNAL Plant Species Biol. 10, 39-51 (1995)  
AUTHORS Zhang,X.-H.  
TITLE Direct Submission  
JOURNAL Submitted (04-OCT-1994) Xing-Hai Zhang, Department of Biological  
Sciences, University of Calgary, Alberta, Canada  
COMMENT Original source text: Stellaria longipes cDNA to mRNA.  
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ORIGIN	/gene="rbcs"			
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Score:	228.50	Matches: 49		
Percent Similarity:	94.7%	Conservative: 5		
Best Local Similarity:	86.0%	Mismatches: 2		
Query Match:	84.3%	Indels: 1		
DB:	15	Gaps: 1		
US-10-628-525A-33 (1-56) x SLABCS (1-723)				
Qy	1	MetAlaSerSerMetLeuSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20		
Db	33	ATGGCTTCTCAATATGTCATCGCAGCTGTGTGTACACGACCAATGGTCTCAGCT 92		
Qy	21	SerMetValAlaProPheThrGlyLeuIysSer---AlaAlaPheProValSerArgLys 39		
Db	93	AGCATGTGCGACCCCTCACTGGTCTCAAGTCTAACGCTTCTTTCTCTGTTTCAAGGAAG 152		
Qy	40	GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56		
Db	153	ACAACCTTGACATTACTTCCATTGCTAGCAATGGTGGACGATCAGATGC 203		
RESULT 24				
STRBCS2B	1703 bp	DNA linear PLN 09-OCT-1996		
LOCUS	S.tuberosum rbcS2b gene for ribulose-(1,5)-bisphosphate			
DEFINITION	carboxylase/oxygenase small subunit.			
ACCESSION	X69761.1			
VERSION	GI:21566			
KEYWORDS	chloroplast; gene expression; gene family; photosynthesis; protein transport; rbcS2b gene.			
SOURCE	Solanum tuberosum (potato)			
ORGANISM	Solanum tuberosum [Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Solanum.			
REFERENCE	1 (bases 1 to 1703)			
AUTHORS	Fritz,C.C., Wolter,F.P., Schenkemeyer,V., Herget,T. and Schreier,P.H.			
TITLE	The gene family encoding the ribulose-(1,5)-bisphosphate carboxylase/oxygenase (Rubisco) small subunit of potato			
JOURNAL	Gene 137 (2), 271-274 (1993)			
PUBMED	8299958			
REFERENCE	2 (bases 1 to 1703)			
AUTHORS	Schreier,P.H.			
TITLE	Direct Submission			
JOURNAL	Submitted (01-DEC-1992) P.H. Schreier, Bayer AG, PF-E/FU Gebaeude 6240, 5090 Leverkusen-Bayerwerk, FRG			
COMMENT	Related sequence: Fritz, C.C., Proc. Natl. Acad. Sci. 88:4458-4462 (1991).			
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	/chromosomes="II"			
	/clone_lib="phage lambda"			
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	/gene="rbcs2b"			
5'UTR	1. .733			
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	/codon_start=1			
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	/protein_id="CAA49415.1"			
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Pred. No.: 4,51e-18 Length: 1703				
Score: 228.50 Matches: 49				
Percent Similarity: 93.0% Conservative: 4				
Best Local Similarity: 86.0% Mismatches: 3				
Query Match: 84.3% Indels: 1				
DB: 15 Gaps: 1				
US-10-628-525A-33 (1-56) x STRBCS2B (1-1703)				
Qy	1	MetAlaSerSerMetLeuSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20		
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Qy	21	SerMetValAlaProPheThrGlyLeuIysSer---AlaAlaPheProValSerArgLys 39		
Db	794	AGCATGTGGGCGCCCTTCACTGGACTCAAGTCCACCGCCTCTTTCCCTGTTTCAAGGAAG 853		
Qy	40	GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56		
Db	854	CAAAACCTTGACATTACTTCCATTGCTAGCAATGGTGGAGAGTCAGATGC 904		
RESULT 25				
STRBCS1	3323 bp	DNA linear PLN 09-OCT-1996		
LOCUS	S.tuberosum rbcS1 gene for ribulose-(1,5)-bisphosphate			
DEFINITION	carboxylase/oxygenase small subunit.			
ACCESSION	X69759.1			
VERSION	GI:21562			
KEYWORDS	chloroplast; gene expression; gene family; photosynthesis; protein transport; rbcS1 gene.			







SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE 1  
 AUTHORS Flint, D., Meyer, K. and Viitanen, P.V.  
 TITLE Sinapolyglucose:malate sinapolytransferase form malate conjugates  
 JOURNAL Patent: WO 0204653-A 16 17-JAN-2002;  
 FEATURES E.I. DUPONT DE NEMOURS AND COMPANY (US)  
 source Location/Qualifiers  
 1. .684  
 /organism="synthetic construct"  
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ORIGIN

Alignment Scores:

Pred. No.:	6.68e-18	Length:	684
Score:	223.50	Matches:	47
Percent Similarity:	93.0%	Conservative:	6
Best Local Similarity:	82.5%	Mismatches:	3
Query Match:	82.5%	Indels:	1
DB:	6	Gaps:	1

US-10-628-525A-33 (1-56) x AX382258 (1-684)

Qy 1 MetAlaSerSerMetLeuSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
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 Db 1 ATGGCTTCCTCTGTCATTTCTTACGACGCTGTTGCCACGCGCAATGTTACACAGCT 60  
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 Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
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 Db 61 AGCATGGTTGCACCTTTCACTGGTCTCAATCTTCAGCCACTTTCCCTGTTACAAGAG 120  
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 Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
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 Db 121 CAAACCTTGACATCACTTCCATTGCTAGCAATGGTGAAGAGTTAGCTGC 171  
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Search completed: April 1, 2006, 15:15:59  
 Job time : 1122.38 secs

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 00:15:06 ; Search time 131.845 Seconds  
(without alignments)  
2830.777 Million cell updates/sec

Title: US-10-628-525A-33

Perfect score: 271

Sequence: 1 MASSMLSSAAVATRTNPAQA.....SRKQNLDTITSASNGRGVOC 56

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-Q=/abas/ABSSWEB spool/US10628525/runat\_31032006\_095109\_16557/app query.fasta\_1  
-DB=N Geneseg -QMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=pcio -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abes06h  
-USER=US10628525 @CGN\_1\_1\_1404 @runat\_31032006\_095109\_16557 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSBBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseg 21.\*

1: geneseqn1980s.\*  
2: geneseqn1990s.\*  
3: geneseqn2000s.\*  
4: geneseqn2001as.\*  
5: geneseqn2001bs.\*  
6: geneseqn2002as.\*  
7: geneseqn2002bs.\*  
8: geneseqn2003as.\*  
9: geneseqn2003bs.\*  
10: geneseqn2003cs.\*  
11: geneseqn2003ds.\*  
12: geneseqn2004as.\*  
13: geneseqn2004bs.\*  
14: geneseqn2005as.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	240.5	88.7	171	2	AAT66535
2	240.5	88.7	174	8	ABX93949
3	240.5	88.7	177	2	AAT27129
4	240.5	88.7	177	2	AAT40794

5	240.5	88.7	177	2	AAT37096
6	240.5	88.7	177	2	AAT41744
7	240.5	88.7	177	2	AAT91545
8	240.5	88.7	204	6	AAT70688
9	240.5	88.7	297	10	ADK59826
10	240.5	88.7	377	10	ADK56121
11	240.5	88.7	489	10	ADK56120
12	240.5	88.7	492	10	ADK76164
13	240.5	88.7	499	6	ADK35635
14	240.5	88.7	504	10	ADK59824
15	240.5	88.7	581	10	ADK75089
16	240.5	88.7	608	10	ADK76944
17	240.5	88.7	614	10	ADK76956
18	240.5	88.7	615	10	ADK76949
19	240.5	88.7	632	10	ADK76953
20	240.5	88.7	684	10	ADK76948
21	240.5	88.7	718	10	ADK58382
22	240.5	88.7	736	10	ADK54321
23	240.5	88.7	736	10	ADK57660
24	240.5	88.7	841	11	ADM44879
25	240.5	88.7	847	11	ADM45447
26	240.5	88.7	859	11	ADM45065
27	240.5	88.7	924	10	ADK75566
28	240.5	88.7	958	10	ADK76165
29	240.5	88.7	1442	2	AAQ92327
30	236.5	87.3	619	11	ADM45158
31	236.5	87.3	668	11	ADM45687
32	236.5	87.3	668	11	ADM45687
33	235.5	86.9	177	2	AAQ13721
34	235.5	86.9	609	10	ADK76965
35	230.5	85.1	171	14	ABE04209
36	230.5	85.1	171	14	ABE04212
37	226.5	83.6	169	8	ABA257803
38	223.5	82.5	684	6	ABA91838
39	223.5	82.5	684	6	ABK47712
40	223.5	82.5	684	10	ADC25988
41	223.5	82.5	684	14	ADV91622
42	221	81.5	714	10	ADK54320
43	221	81.5	725	11	ADM44821
44	221	81.5	736	10	ADK57661
45	221	81.5	741	11	ADM45450
46	219.5	81.0	171	3	AAA54025
47	218.5	80.6	194	13	ADV04451
48	218	80.4	683	10	ADK54330
49	218	80.4	737	10	ADK57662
50	218	80.4	737	10	ADK58383
51	218	80.4	789	11	ADM44820
52	218	80.4	806	11	ADM45686
53	215	79.3	655	11	ADM45154
54	215	79.3	738	10	ADK54333
55	215	79.3	753	10	ADK58381
56	215	79.3	754	10	ADK57645
57	215	79.3	811	11	ADM45377
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59	209.5	77.3	385	12	ADP92165
60	207.5	76.6	315	11	ADM45114
61	207.5	76.6	444	3	AAC37666
62	207.5	76.6	447	11	ADM45105
63	207.5	76.6	450	11	ADM45121
64	207.5	76.6	477	3	AAC37237
65	207.5	76.6	546	12	ADN73596
66	207.5	76.6	599	3	AAC47674
67	207.5	76.6	639	11	ADM45122
68	207.5	76.6	639	11	ADM45116
69	207.5	76.6	724	6	ABK30640
70	207.5	76.6	724	6	ABL49453
71	207.5	76.6	726	6	ABK30788
72	207.5	76.6	727	11	ADM44972
73	207.5	76.6	741	11	ADM45551
74	207.5	76.6	745	11	ADM45553
75	207.5	76.6	771	6	ABN99150
76	207.5	76.6	1205	6	ABN98273
77	206	76.0	654	10	ADK57659

1 240.5 88.7 171 2 AAT66535  
2 240.5 88.7 174 8 ABX93949  
3 240.5 88.7 177 2 AAT27129  
4 240.5 88.7 177 2 AAT40794

78	205.5	75.8	151	9	ACC85002	Acc85002 Tobacco r
79	204.5	75.5	191	1	AA95096	Aa95096 Transit p
80	204.5	75.5	191	3	Az98882	Aa98882 Small sub
81	204.5	75.5	191	4	AA165715	Aa165715 Nucleotid
82	204.5	75.5	1084	6	AA31813	Aa31813 Gossypium
83	204	75.3	177	1	AA95095	Aa95095 Transit p
84	204	75.3	177	3	Az98881	Aa98881 Small sub
85	204	75.3	177	4	AA165714	Aa165714 Nucleotid
86	200.5	74.0	675	13	ADV04475	Adv04475 Nucleotid
87	199.5	73.6	263	6	ABQ85598	Abq85598 Arabidops
88	199.5	73.6	364	11	ADM45548	Adm45548 Insect re
89	199.5	73.6	546	3	AAC48433	Aac48433 Arabidops
90	199.5	73.6	700	11	ADM45118	Adm45118 Insect re
91	199.5	73.6	700	11	ADM44971	Adm44971 Insect re
92	199.5	73.6	711	6	ABK30617	Abk30617 Plant dwa
93	199.5	73.6	711	6	ABL49430	AbL49430 Sequence
94	199.5	73.6	737	11	ADM45549	Adm45549 Insect re
95	199.5	73.6	739	6	ABK30768	Abk30768 Plant dwa
96	199.5	73.6	1036	13	ADT17269	Adt17269 Plant cdn
97	199.5	73.6	2581	13	ADT15847	Adt15847 Plant cdn
98	197	72.7	240	3	AAA31345	Aaa31345 Plant mic
99	197	72.7	256	3	AAA31405	Aaa31405 Plant mic
100	197	72.7	339	3	AAA31255	Aaa31255 Plant mic
101	197	72.7	341	3	AAA31253	Aaa31253 Plant mic
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103	197	72.7	351	3	AAA31294	Aaa31294 Plant mic
104	197	72.7	363	3	AAA31381	Aaa31381 Plant mic
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108	197	72.7	403	3	AAA31288	Aaa31288 Plant mic
109	197	72.7	407	3	AAA31390	Aaa31390 Plant mic
110	197	72.7	410	3	AAA31259	Aaa31259 Plant mic
111	197	72.7	412	3	AAA31387	Aaa31387 Plant mic
112	197	72.7	413	3	AAA31410	Aaa31410 Plant mic
113	197	72.7	423	3	AAA31314	Aaa31314 Plant mic
114	197	72.7	426	3	AAA31403	Aaa31403 Plant mic
115	197	72.7	430	3	AAA31336	Aaa31336 Plant mic
116	197	72.7	433	3	AAA31284	Aaa31284 Plant mic
117	197	72.7	457	3	AAA31269	Aaa31269 Plant mic
118	197	72.7	479	3	AAA32042	Aaa32042 Plant mic
119	197	72.7	479	3	AAA31291	Aaa31291 Plant mic
120	197	72.7	484	3	AAA31305	Aaa31305 Plant mic
121	197	72.7	502	3	AAA31309	Aaa31309 Plant mic
122	197	72.7	570	3	AAA32041	Aaa32041 Plant mic
123	197	72.7	606	3	AAA32043	Aaa32043 Plant mic
124	197	72.7	2586	14	ADW16694	Adw16694 Eucalyptu
125	195.5	72.1	752	13	ADV04474	Adv04474 Nucleotid
126	195.5	72.1	767	6	ABN99163	Abn99163 Arabidops
127	195.5	72.1	780	6	ABN99112	Abn99112 Arabidops
128	194	71.6	934	8	ABQ83212	Abq83212 Coffee rb
129	194	71.6	2034	8	ABQ83211	Abq83211 Coffee rb
130	193.5	71.4	329	13	ADT16033	Adt16033 Plant cdn
131	193.5	71.4	1000	13	ADT16035	Adt16035 Plant cdn
132	193	71.2	350	3	AAA31396	Aaa31396 Plant mic
133	192.5	71.0	363	6	ABQ85593	Abq85593 Arabidops
134	192.5	71.0	392	8	ABX62856	Abx62856 Arabidops
135	191.5	70.7	386	3	AAC37628	Aac37628 Arabidops
136	191.5	70.7	546	3	AAC48432	Aac48432 Arabidops
137	191	70.5	240	3	AAA31368	Aaa31368 Plant mic
138	190	70.1	481	3	AAA31306	Aaa31306 Plant mic
139	190	70.1	764	10	ADK56736	Adk56736 Plant DNA
140	188	69.4	215	3	AAA31341	Aaa31341 Plant mic
141	188	69.4	424	10	ADK57649	Adk57649 Plant DNA
142	188	69.4	424	10	ADK54327	Adk54327 Plant DNA
143	188	69.4	424	11	ADM45552	Adm45552 Insect re
144	188	69.4	450	3	AAA31250	Aaa31250 Plant mic
145	188	69.4	1299	10	ADK54308	Adk54308 Plant DNA
146	186	68.6	618	10	ADC76975	Adc76975 DNA homol
147	186	68.6	618	10	ADC75104	Adc75104 Poppy phy
148	186	68.6	618	10	ADC75565	Adc75565 DNA homol
149	186	68.6	677	11	ADM45205	Adm45205 Insect re
150	185	68.3	629	10	ADK52842	Adk52842 Plant DNA

ALIGNMENTS

RESULT 1		
AAT66535		
ID	AAT66535 standard; DNA; 171 BP.	
XX		
AC	AAT66535;	
XX		
DT	27-AUG-2003 (revised)	
DT	22-JUL-1997 (first entry)	
XX		
DE	Plastid targetting signal.	
XX		
KW	Transgenic plant; selectable marker; carotenoid; pigment;	
KW	plastid targetting signal; RUBISCO; phytoene synthase; plasmid pET0203;	
SS		
OS	Unidentified.	
XX		
PN	WO9714807-AL.	
XX		
PD	24-APR-1997.	
XX		
PF	29-MAR-1996; 96WO-US004313.	
XX		
PR	16-OCT-1995; 95US-00543608.	
XX		
PA	(SEMI-) SEMINIS VEGETABLES.	
PI	Trulson AJ, Braun CJ;	
XX		
DR	WPI; 1997-245122/22.	
XX	P-PSDB; AAW16493.	
PT	Visual identification of transgenic plant material - from production of	
PT	carotenoid pigment encoded by cassette containing Erwinia phytoene	
XX	synthase gene, useful for selecting material for regeneration.	
PS	Example; Page 36; 62pp; English.	
CC	A plastid targetting signal (AAT66535) is obt'd. from the small subunit of	
CC	the ribulose-1,4-bisphosphate carboxylase oxygenase (RUBISCO). It can be	
CC	used to target the Erwinia herbicola phytoene synthase crtB gene (see	
CC	also AAT66534) to plant plastids, where expression of the gene results in	
CC	carotenoid biosynthesis. The construct is a component of pET0203 (ATCC	
CC	97282), a binary vector used in a method for the visual identification of	
CC	transgenic plant material. The vector includes an expression cassette	
CC	comprising the tomato E8 promoter (see also AAT66533), the plastid	
CC	targetting signal fused to the crtB gene, and a 3' non-translated region	
CC	(AAT66536). Transgenic plant cells and tissues are identified by the	
CC	appearance of orange colour. (Updated on 27-AUG-2003 to correct OS	
CC	field.)	
XX		
Sequence	171 BP; 38 A; 52 C; 37 G; 44 T; 0 U; 0 Other;	
Alignment Scores:		
Pred. No.:	2.03e-24	Length: 171
Score:	240.50	Matches: 52
Percent Similarity:	96.5%	Conservative: 3
Best Local Similarity:	91.2%	Mismatches: 1
Query Match:	88.7%	Indels: 1
DB:	2	Gaps: 1
US-10-628-525A-33 (1-56) x AAT66535 (1-171)		
Oy	1 MetalaserSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla	20
Db	1 ATGGCTTCTCAGTTCCTTCCTGACAGTTCACCCGACGACATGTGCTCAAGCT	60
Oy	21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys	39
	:::	

Db 61 AACATGTTGGCGCTTTCACTGGCTTAAGTCAGCTGCCTCACTTCCTCTGTTCAAGGAG 120

Qy 40 GlnAenLeuAspIleThrSerIleAlaSerAenGlyArgValGlnCys 56  
|||||

Db 121 CAAACCTTGACATCACTTCATTGCCAGCAACGGCGGAGAGTGCAATGC 171  
|||||

RESULT 2

ABX93949

ID ABX93949 standard; DNA; 174 BP.

XX AC

XX AC ABX93949;

DT 04-JUN-2003 (first entry)

XX

DE DNA encoding small sub-unit of pea rubisco prSS.

XX

KW Plastid transit peptide; Cuphea acyl-ACP thioesterase;

KW protein translocation; plastid; transgenic; plant;

KW modified fatty acid composition; oilseed crop; transformation;

KW medium chain specific condensing enzyme; modified oil content;

KW small sub-unit of pea rubisco; prSS; ds; Pea.

XX

OS Pisum sativum.

XX

PH Key Location/Qualifiers

FT CDS 1..174

FT /\*tag= a

FT /product= "Plastid transit peptide"

FT /partial

FT /note= "No stop codon given"

XX

PN US2002178467-A1.

XX

XX 28-NOV-2002.

XX

XX 11-MAY-2001; 2001US-00854286.

XX

XX 12-MAY-2000; 2000US-0203618P.

XX

XX (DEHE/) DEHESH K.

XX

XX Dehesh K;

XX

DR WPI; 2003-352617/33.

XX

XX P-PSDB; ABU08651.

XX

PT New recombinant DNA construct for modifying the fatty acid composition of

PT a plant cell, comprises a promoter that functions in plant cells, linked

PT to a heterologous DNA encoding a plastid transit peptide of Cuphea acyl-

PT ACP thioesterase.

XX

XX Disclosure; Page 19; 32pp; English.

XX

XX The invention describes a recombinant DNA construct (I) comprising a

XX promoter that functions in plant cells, operably linked to a heterologous

XX DNA molecule encoding a plastid transit peptide (PTP) of a Cuphea acyl-

XX ACP thioesterase (AT), operably linked to a heterologous DNA encoding a

XX protein, operably linked to a DNA molecule providing 3' termination

XX functions. (I) is useful in an improved method for translocating a

XX protein to a crop plant cell plastid, by introducing (I) into a crop

XX plant cell, and regenerating the crop plant cell into a transgenic crop

XX plant. (I) is useful for producing a modified fatty acid composition of

XX an oilseed crop, by transforming a plant cell of an oil seed crop with

XX (I) and a DNA construct that provides expression of a medium chain

XX specific condensing enzyme, regenerating the plant cell into a transgenic

XX oil seed crop plant, planting seeds of the transgenic oil seed crop

XX plant, harvesting seeds from the transgenic oil seed crop plant and

XX processing the seeds for purification of a modified oil content. This

XX sequence encodes the small sub-unit of pea rubisco, prSS, a transit

XX peptide of the invention

XX

XX Sequence 174 BP; 40 A; 52 C; 37 G; 45 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 2,08e-24 Length: 174

Score: 240.50 Matches: 52

Percent Similarity: 96.5% Conservative: 3

Best Local Similarity: 91.2% Mismatches: 1

Query Match: 88.7% Indels: 1

DB: 8 Gaps: 1

US-10-628-525A-33 (1-56) x ABX93949 (1-174)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAenProAlaGlnAla 20  
|||||

Db 1 ATGGCTTCCTCAGTCTTTCTCTGAGCAGTGTGCCACCCGACGCAATGTTGCTCAAGCT 60  
|||||

Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
:::|||||

Db 61 AACATGTTGCACCTTTCATGCGCTTAAGTCAGCTGCCTTCCTCTGTTCAAGGAG 120  
|||||

Qy 40 GlnAenLeuAspIleThrSerIleAlaSerAenGlyArgValGlnCys 56  
|||||

Db 121 CAAACCTTGACATCACTTCATTGCCAGCAACGGCGGAGAGTGCAATGC 171  
|||||

## RESULT 3

AATZ7129

ID AATZ7129 standard; DNA; 177 BP.

XX

AC AATZ7129;

DT 17-DEC-1996 (first entry)

XX

DE Modified RUBISCO signal peptide coding sequence.

XX

KW Ribulose bis-phosphate carboxylase-oxygenase; RUBISCO; signal peptide;

KW plastid transit peptide; non-higher plant; phytoene synthase; carotenoid;

KW ss.

XX

OS Nicotiana tabacum.

XX

PH Key Location/Qualifiers

FT mutation 69

FT /\*tag= a

FT /note= "T>G change"

FT mutation 72

FT /\*tag= b

FT /note= "A>G change"

XX

PN WO9613149-A1.

XX

XX 09-MAY-1996.

XX

XX 27-OCT-1995; 95WO-US013937.

XX

XX 28-OCT-1994; 94US-00331004.

XX

XX (STAD ) AMOCO CORP.

XX

XX Hauptmann R, Eschenfeldt WH, English J, Brinkhaus FL;

XX

XX WPI; 1996-239176/24.

XX

XX Accumulating coloured native carotenoid(s) in transgenic plants -

XX comprises transforming plants with DNA encoding non-higher plant phytoene

XX synthase and promoter driving storage organ expression of the enzyme.

XX

XX Example 1; Page 79; 103pp; English.

XX

XX This sequence represents a modified version of the ribulose bis-phosphate

XX carboxylase-oxygenase (RUBISCO) signal peptide coding sequence. This

XX sequence contains two changes compared to the wild type coding sequence.

XX Two cytidine residues were added to the 5' end to create a NcoI

XX restriction site. The second change introduces an Nari site that cleaves

XX between bases 73 and 74. This change constituted a G for T replacement at

XX position 69 and a G for A replacement at position 72. Both of these

CC changes left the encoded amino acid sequence unchanged. The final two  
 CC residues at the 3' end were deleted to maintain the fragment length of  
 CC 177 bp and to provide the natural SphI restriction site sticky end. This  
 CC sequence was used in the preparation of a chimeric DNA molecule encoding  
 CC a protein having an N-terminal plastid transit peptide portion whose C-  
 CC terminus is bonded to the N-terminus of a non-higher plant phytoene  
 CC synthase enzyme. This construct allows the accumulation of carotenoids  
 XX  
 SQ Sequence 177 BP; 40 A; 53 C; 39 G; 45 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2,13e-24 Length: 177  
 Score: 240.50 Matches: 52  
 Percent Similarity: 96.5% Conservative: 3  
 Best Local Similarity: 91.2% Mismatches: 1  
 Query Match: 88.7% Indels: 1  
 DB: 2 Gaps: 1

US-10-628-525A-33 (1-56) x AAT27129 (1-177)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 |||||  
 Db 1 ATGGCTTCCTCAGTTCTTCTCTGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60  
 |||||  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 ::|||  
 Db 61 AACATGGTGGCGCTTTCAGTGGCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 120  
 |||||  
 QY 40 GlnAnLeuAspIleThrSerIleAlaSerAnGlyGlyArgValGlnCys 56  
 |||||  
 Db 121 CAAACCTTGCATCACTTCCATTCGCCACGCGGAAGAGTGCATATGC 171  
 |||||

#### RESULT 4

AAT40794  
 ID AAT40794 standard; DNA; 177 BP.

XX  
 AC AAT40794;  
 DT 25-MAR-2003 (revised)  
 DT 10-DEC-1996 (first entry)  
 XX Chloroplast transit peptide coding sequence.  
 DE  
 XX GGPP synthase; lycopene cyclase; phytoene synthase; beta-carotene;  
 KW phytoene dehydrogenase-4H; carotenoid; C40; zeaxanthin; diglucoside;  
 KW pigment; food colourant; chloroplast transit peptide; increase yield;  
 KW tobacco ribulose bis-phosphate carboxylase-oxygenase; ss.  
 XX  
 OS Nicotiana tabacum.

Key Location/Qualifiers  
 FH misc\_difference 69  
 FT /\*tag= a  
 FT /note= "replacement of native T with G"  
 FT misc\_difference 72  
 FT /\*tag= b  
 FT /note= "replacement of native A with G"

US5530188-A.

25-JUN-1996.

21-JUL-1993; 93US-00095726.

02-MAR-1990; 90US-00487613.

18-MAY-1990; 90US-00525551.

03-AUG-1990; 90US-00562674.

28-FEB-1991; 91US-00662921.

30-OCT-1991; 91US-00785566.

(STAD ) AMOCO CORP.

Yen HB, Brinkhaus FL, Proffitt J, Mukharji I, Yarger J;

PI Ausich RL;

XX WPI; 1996-308823/31.

DR P-PSDB; AAW01124.

XX

PT Increasing prodn. of total carotenoid(s) in a higher plant - by  
 PT transforming with vector encoding chloroplast transit peptide operably  
 PT linked to the Erwinia herbicola lycopene cyclase structural gene.

XX Example 2; Fig 17; 99pp; English.

XX The present sequence encodes a chloroplast transit peptide (AAW01124) of  
 CC the tobacco ribulose bis-phosphate carboxylase-oxygenase gene which can  
 CC be operatively linked in frame to the 5' end of the lycopene cyclase  
 CC structural gene (AAT40795). This leads to increased production of total  
 CC carotenoids in the chloroplast of transformed plants as compared to  
 CC native, non-transformed plants of the same type. Other enzymes involved  
 CC in the carotenoid biosynthesis pathway include geranylgeranyl  
 CC pyrophosphate (AAW01119), phytoene synthase (W01121) and phytoene  
 CC dehydrogenase-4H (AAW01122). Beta-carotene is an effective and apparently  
 CC harmless food colourant and is also in the pathway for biological  
 CC synthesis of further C40 carotenoids such as zeaxanthin and zeaxanthin  
 CC diglucoside. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 177 BP; 40 A; 53 C; 39 G; 45 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 2,13e-24 Length: 177  
 Score: 240.50 Matches: 52  
 Percent Similarity: 96.5% Conservative: 3  
 Best Local Similarity: 91.2% Mismatches: 1  
 Query Match: 88.7% Indels: 1  
 DB: 2 Gaps: 1

US-10-628-525A-33 (1-56) x AAT40794 (1-177)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 |||||  
 Db 1 ATGGCTTCCTCAGTTCTTCTCTGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60  
 |||||  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 ::|||  
 Db 61 AACATGGTGGCGCTTTCAGTGGCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 120  
 |||||  
 QY 40 GlnAnLeuAspIleThrSerIleAlaSerAnGlyGlyArgValGlnCys 56  
 |||||  
 Db 121 CAAACCTTGCATCACTTCCATTCGCCACGCGGAAGAGTGCATATGC 171  
 |||||

#### RESULT 5

AAT37096

ID AAT37096 standard; DNA; 177 BP.

XX

AC AAT37096;

DT 25-MAR-2003 (revised)

DT 18-OCT-1996 (first entry)

XX Ribulose bis-phosphate carboxylase-oxygenase signal peptide.

XX E. herbicola; geranylgeranyl pyrophosphate synthase; pARC376;  
 KW GGPP synthase; biosynthesis; carotenoid; lycopene;  
 KW farnesyl pyrophosphate; phytoene; FPP; isopentenyl pyrophosphate; IPP;  
 KW tail to tail dimerisation; phytoene synthase; phytoene dehydrogenase-4H;  
 KW food colourant; herbicide; norflurazon; ss.

XX Nicotiana tabacum.

OS

PN US5530189-A.

XX

PD 25-JUN-1996.

XX

PF 22-JUL-1993; 93US-00096043.

XX



```

PR 02-MAR-1990; 90US-00487613.
PR 18-MAY-1990; 90US-00525551.
PR 03-AUG-1990; 90US-00562674.
PR 28-FEB-1991; 91US-00662921.
PR 30-OCT-1991; 91US-00785568.
XX (STAD ) AMOCO CORP.
PA
XX
XX Yen HB, Brinkhaus FL, Proffitt J, Mukharji I, Yarger J;
PI Ausich RL;
XX
XX WPI; 1996-308824/31.
XX P-PSDB; AAW00175.
XX
XX DNA encoding Erwinia herbicola phytoene dehydrogenase-4H - used for
XX prodn. of lycopene, and to produce transgenic plants resistant to
XX norflurazon.
XX
XX Example 3; Fig 17; 87pp; English.
XX
XX This sequence is based on the nucleotide sequence encoding the Nicotiana
XX tabacum ribulose bis-phosphate carboxylase-oxygenase signal peptide. Two
XX changes were made to the wild type sequence in the production of this
XX sequence. Firstly, two cytidine residues were added at the 5' end to
XX create a NcoI site. Secondly, an XbaI site that cleaves between bases 73
XX and 74 was introduced. This change was a G for a T replacement at
XX position 69 and a G for A replacement at position 72, both of which
XX changes left the amino acid sequence unchanged. This sequence was
XX generated using the double stranded fragments given in AAT37097-100. This
XX signal peptide sequence was used in the expression of geranylgeranyl
XX pyrophosphate (GGPP) synthase in higher plants. GGPP synthase is an
XX enzyme which is involved in the biosynthesis of carotenoids, esp.
XX lycopene, from the ubiquitous precursor, farnesyl pyrophosphate. In E.
XX herbicola, phytoene has been found to be formed biosynthetically in a two
XX step process. The initial step is the condensation of farnesyl
XX pyrophosphate (FPP) and isopentenyl pyrophosphate (IPP) to form GGPP. This
XX reaction is catalysed by GGPP synthase. This first step is immediately
XX followed by a tail to tail dimerisation of GGPP, catalysed by the enzyme
XX phytoene synthase, to form phytoene. Lycopene is produced from phytoene
XX by the catalytic action of phytoene dehydrogenase-4H. The genes encoding
XX components of the lycopene biosynthesis pathway may be used to transform
XX a host cell for the commercial production of lycopene which is used as a
XX food colourant. Plants transformed with the phytoene dehydrogenase-4H
XX coding sequence are protected from the herbicide norflurazon. (Updated on
XX 25-MAR-2003 to correct PF field.)
XX
XX Sequence 177 BP; 40 A; 53 C; 39 G; 45 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.13e-24 Length: 177
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 2 Gaps: 1

US-10-628-525A-33 (1-56) x AAT37096 (1-177)

QY 1 MetAlaSerSerMetLeuSerAlaAlaValAlaThrArgThrAenProAlaGlnAla 20
DB 1 ATGGCTTCCTCAGTCTTTCTCTGACGAGTGGCCACCGCAGCAATGTTGCTCAAGCT 60
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
DB 61 AACATGGTGGCGCTTTTCACTGGCTTAAGTCAGTCGCTCATTCCTGTTTCAAGGAG 120

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56
DB 121 CAAAACCTTGACATCATCTTCATTGCCAGCAGCAACGGCGGAGAGTGCAATGC 171

RESULT 6
AAT41744
ID AAT41744 standard; DNA; 177 BP.

```

```

XX AAT41744;
XX
XX 25-MAR-2003 (revised)
XX 10-DEC-1996 (first entry)
XX
XX Tobacco transit peptide coding sequence.
XX
XX Wild type; N-terminally truncated; geranylgeranyl pyrophosphate; GGPP;
XX GGPP synthase; phytoene synthase; carotenoid; phytoene; PARC306A;
XX PARC489D; transit peptide; tobacco; chloroplast; skin disorder; ss.
XX
XX Nicotiana tabacum.
XX
XX US5545816-A.
XX
XX 13-AUG-1996.
XX
XX 19-JUL-1993; 93US-00093557.
XX
XX 02-MAR-1990; 90US-00487613.
XX 18-MAY-1990; 90US-00525551.
XX 03-AUG-1990; 90US-00562674.
XX 28-FEB-1991; 91US-00662921.
XX 30-OCT-1991; 91US-00785569.
XX
XX (STAD ) AMOCO CORP.
XX
XX Yen HB, Brinkhaus FL, Proffitt J, Mukharji I, Yarger J;
XX Ausich RL;
XX
XX WPI; 1996-383742/38.
XX P-PSDB; AAW00344.
XX
XX Transformed plants containing DNA encoding Erwinia herbicola enzymes -
XX esp. geranylgeranyl pyrophosphate synthase and phytoene synthase, allows
XX large scale production of phytoene.
XX
XX Example 3; Col 61-62; 61pp; English.
XX
XX This sequence encodes the tobacco transit peptide which allows transport
XX of proteins into the chloroplasts of the plant. This sequence may be
XX attached to the phytoene synthase or geranylgeranyl pyrophosphate (GGPP)
XX synthase coding sequences, for transport into tobacco chloroplasts. This
XX allows the tobacco plants to produce high levels of phytoene for use in
XX the treatment of skin disorders. Phytoene synthase and GGPP synthase (see
XX also AAT41741-43) are enzymes which catalyse the formation of
XX carotenoids, particularly phytoene. An N-terminally truncated form of
XX GGPP synthase which has the first thirteen amino acids replaced by four
XX heterologous amino acids derived from the plasmid PARC306A was found to
XX be about twice as active as the wild type enzyme. A C-terminal truncated
XX protein was found to have even higher activity and was cloned into
XX plasmid PARC489D. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 177 BP; 40 A; 53 C; 39 G; 45 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.13e-24 Length: 177
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 2 Gaps: 1

US-10-628-525A-33 (1-56) x AAT41744 (1-177)

QY 1 MetAlaSerSerMetLeuSerAlaAlaValAlaThrArgThrAenProAlaGlnAla 20
DB 1 ATGGCTTCCTCAGTCTTTCTCTGACGAGTGGCCACCGCAGCAATGTTGCTCAAGCT 60
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
DB 61 AACATGGTGGCGCTTTTCACTGGCTTAAGTCAGTCGCTCATTCCTGTTTCAAGGAG 120

```

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyValGlnCys 56  
ID AAT91545  
DB 121 CAAAACCTTGACATCATCTTCATTGTCAGCAGCACGGCGGAAGAGTGCAATGC 171

RESULT 7  
AAI70688  
ID AAT91545 standard; DNA; 177 BP.  
XX AAT91545;  
XX 25-MAR-2003 (revised)  
DT 15-JAN-1998 (first entry)  
XX Phytoene dehydrogenase-4H transit peptide encoding DNA.  
XX Geranylgeranyl pyrophosphate synthase; Erwinia herbicola; GGPP;  
KW lycopene cyclase; recombinant enzyme; transgenic organism; beta-carotene;  
KW yeast; plant; vitamin A; cancer; ss.  
XX Synthetic.  
XX Key Location/Qualifiers  
FH 1. .177  
FT /\*tag= a  
FT /product= "Transit peptide"  
FT /note= "No stop codon given"  
XX US5656472-A.  
XX 12-AUG-1997.  
XX 07-JUN-1995; 95US-00473512.  
XX 02-MAR-1990; 90US-00487613.  
PR 18-MAY-1990; 90US-00525551.  
PR 03-AUG-1990; 90US-00562674.  
PR 28-FEB-1991; 91US-00662921.  
PR 21-JUL-1993; 93US-00095726.  
XX (STAD ) AMOCO CORP.  
PA Mukharji I, Proffitt J, Ausich RL, Yarger J, Yen HB;  
PI Brinkhaus FL;  
XX WPI; 1997-414592/38.  
DR P-PSDB; AAW32473.  
XX DNA encoding Erwinia herbicola lycopene cyclase - for producing  
PT recombinant enzyme, and transgenic organisms with increased beta-carotene  
PT levels.  
XX Example 3; Fig 17; 102pp; English.  
XX A novel DNA molecule has been isolated which encodes an Erwinia herbicola  
CC lycopene cyclase enzyme that converts lycopene to beta- carotene. The DNA  
CC molecule comprises at least 1125 bp and is present in the plasmids  
CC pARC147, pARC1509, pARC1510 and pARC1520. The present sequence encodes a  
CC transit peptide which can be attached to the 5'-end of phytoene  
CC dehydrogenase-4H, for transport into plant chloroplasts. The new DNA  
CC molecule can be used to produce the recombinant enzyme and transgenic  
CC organisms, e.g. yeasts or plants, with increased beta- carotene levels.  
CC Beta-carotene is used as a colourant in margarine and butter and as an  
CC intermediate for vitamin A, and may prevent cancer. (Updated on 25-MAR-  
CC 2003 to correct PF field.)  
XX Sequence 177 BP; 40 A; 53 C; 39 G; 45 T; 0 U; 0 Other;  
SQ

Alignment Scores:  
Pred. No.: 2.13e-24 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1

Query Match: 88.7% Indels: 1  
DB: 2 Gaps: 1  
US-10-628-525A-33 (1-56) x AAT91545 (1-177)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
DB 1 ATGGCTTCCTCAGTTCTTCTCTGCGAGTGGCCACCGCAGCAATGTTGCTCAAGCT 60  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
DB 61 AACATGGTGGCGCTTTCACCTGGCTTAACTGAGCTGCCTCATTCCTGTTTCAGGAAG 120  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyValGlnCys 56  
DB 121 CAAAACCTTGACATCATCTTCATTGCCAAGCGGGAAGAGTGCAATGC 171

RESULT 8  
AAI70688  
ID AAI70688 standard; DNA; 204 BP.  
XX AAI70688;  
XX 04-FEB-2002 (first entry)  
DT Tobacco Rubisco transit peptide small subunit DNA.  
DE Tobacco; Rubisco; ribulosebiphosphate carboxylase; transit peptide;  
KW acetyl-CoA carboxylase; transgenic plant; oilseed; vegetable oil;  
KW Brassica; soybean; ds.  
XX Nicotiana tabacum.  
XX Key Location/Qualifiers  
FH transit\_peptide 1. .171  
FT /\*tag= a  
FT mat\_peptide 172. .204  
FT /\*tag= b  
FT /note= "5' end of mature protein coding sequence"  
XX WO200181604-A1.  
XX 01-NOV-2001.  
XX 20-APR-2001; 2001WO-US012928.  
XX 20-APR-2000; 2000US-0198794P.  
XX (CRGI ) CARGILL INC.  
XX Shorrosh BS, Debonte LR;  
XX WPI; 2002-041417/05.  
DR P-PSDB; AAM50331.  
XX Using Nucleic acids encoding alfalfa cytosolic Acetyl-Coenzyme A  
PT Carboxylase (ACCase; EC 6.4.1.2) to increase the oil content of Soybean  
PT and Brassica seeds.  
XX Disclosure; Fig 1; 62pp; English.  
XX The present sequence is that of DNA encoding the tobacco small subunit  
CC Rubisco transit peptide and the 5' portion of the mature small subunit  
CC Rubisco protein (see AAM50331). Nucleic acid constructs of the invention  
CC include a nucleic acid encoding a cytosolic acetyl-CoA carboxylase (EC-  
CC 6.4.1.2) and a promoter, and may also include a nucleic acid encoding the  
CC tobacco small subunit Rubisco transit peptide. Such constructs can be  
CC introduced into soybean and Brassica plants (especially Brassica napus  
CC (oilseed rape), Brassica rapa (turnip), Brassica juncea, Brassica  
CC carinata, Brassica nigra (black mustard) and Brassica oleracea  
CC (cauliflower, sprout, cabbage, broccoli)) to increase the oil content of  
CC their seeds from about 5% to about 25% greater on a dry weight basis  
CC (claimed)

XX  
SQ Sequence 204 BP; 50 A; 60 C; 43 G; 51 T; 0 U; 0 Other;

Alignment Scores:  

Pred. No.:	2-58e-24	Length:	204
Score:	240.50	Matches:	52
Percent Similarity:	96.5%	Conservative:	3
Best Local Similarity:	91.2%	Mismatches:	1
Query Match:	88.7%	Indels:	1
DB:	6	Gaps:	1

US-10-628-525A-33 (1-56) x AA170688 (1-204)

Oy 1 MetAlaSerSerMetLeuSerGerXLaLaValAlaThArGrThrAsnProAlaGlnAla 20  
| | | | | : | : | : | | | | | : | : | |  
Db 1 ATGGCTTCCTCAGTCTTTCCCTCGCAGCATGTGCACGCCGAGCAATGTTGCTCAAAGCT 60  
| | | | | : | : | : | | | | | : | : | |  
Oy 21 SerWetValAlaProPhenThrGlyIeuLyvSerLala---PheProValSerArgLys 39  
| | | | | : | : | : | | | | | : | : | |  
Db 61 AACATGGTGCCACTTTCATTGACCTTAAGTCAGCTGCCTCATTTCCCCTGTTTCAAGGAAG 120  
| | | | | : | : | : | | | | | : | : | |  
Oy 40 GlnAsnLeuAspileThrSerileAlaSerAnGlyGlyArgValGlnCys 56  
| | | | | : | : | : | | | | | : | : | |  
Db 121 CAARACTTGACATCTCTTCATTGCCAGCACGCCGAGAGTGCAATGC 171  
| | | | | : | : | : | | | | | : | : | |

RESULT 9  
ADK59826  
ID ADK59826 standard; DNA; 297 BP.

XX AC ADK59826;  
XX DT  
XX DE O6-MAY-2004 (first entry)  
XX DE Plant DNA sequence which confers altered metabolic characteristic #7209.  
XX KW altered metabolic characteristic; plant; acid metabolism;  
KW alcohol metabolism; fatty acid metabolism;  
KW branched fatty acid metabolism; alkaloid metabolism;  
KW amino acid metabolism; ester metabolism; glyceride metabolism;  
KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;  
KW terpene metabolism; isoprenoid metabolism; alkene metabolism;  
KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;  
KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.  
OS Unidentified.  
OS WC2003020936-A1.  
PN  
PD 13-MAR-2003.  
XX  
XX PF 30-AUG-2002; 2002WO-US027884.  
XX PR 31-AUG-2001; 2001US-0316471P.  
XX PA (DOWC ) DOW CHEM CO.  
PA (DOWC ) DOW AGROSCIENCES LLC.  
XX  
PI Weglarz T, Gachotte D, Blakelee B, McCreary DA, Pell RJ;  
PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;  
XX WPI; 2003-313091/30.  
XX  
XX Novel genes that confer altered metabolic characteristics in Nicotiana benthamiana plants, useful for altering the levels of metabolites e.g. acids, fatty acids, amino acids, carbohydrates, hydrocarbons and steroids.  
PS Claim 1; SEQ ID NO 7209; 2576bp; English.  
XX  
XX The invention comprises DNA sequences which confer an altered metabolic characteristic when they are expressed in a plant. The DNA sequences of the invention are useful for producing plants with an altered metabolic characteristic, such as: altered acid metabolism, alcohol metabolism, fatty acid metabolism, branched fatty acid metabolism, alkaloid or other

CC base metabolism, altered amino acid metabolism, altered ester metabolism,  
CC altered glyceride metabolism, altered phenolic metabolism, altered  
CC carbohydrate metabolism, altered sterol, oxygenated terpene, or  
CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon  
CC metabolism, ketone or quinone metabolism. The DNA sequences of the  
CC invention may be used to provide disease resistance in a plant and gene  
CC shuffling or sexual PCR procedures. The present nucleic acid represents a  
CC DNA sequence of the invention.

XX  
SQ Sequence 297 BP; 83 A; 70 C; 70 G; 74 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.:            4,29e-24            Length:            297  
Score:                 240.50            Matches:            52  
Percent Similarity:    96.5%            Conservative:        3  
Best Local Similarity: 91.2%            Mismatches:          1  
Query Match:           88.7%           Indels:              1  
DB:                    10                Gaps:                1

US-10-628-525A-33 (1-56) x ADK59826 (1-297)

Qy 1 MetAlaSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProHlaGlnAla 20  
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Qy 97 ATGGCTTCCTCAGTCTTTCTCTCAGCAGGTGCACCCCGCAGCAATGTTCTCAAGCT 156  
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db ::|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 157 AACATGGTTGCACCTTTCACAGGCTTAAGTCGTGCTCATTCCTGTTTCAAGAAAG 216  
Qy 40 GlnAnLeuAspIleThrSerIleAlaSerAnGlyGlyArgValGlnCys 56  
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 217 CAATACTTGACATCACATTCCATTGCCAGCAACGGCGGAAGAGTGCATGC 267

RESULT 10  
ADK56121  
ID ADK56121 standard; DNA; 377 BP.  
XX  
XX AC ADK56121;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Plant DNA sequence which confers altered metabolic characteristic #3504.  
XX  
KW altered metabolic characteristic; plant; acid metabolism;  
KW alcohol metabolism; fatty acid metabolism;  
KW amended fatty acid metabolism; alkaloid metabolism;  
KW amino acid metabolism; ester metabolism; glyceride metabolism;  
KW phenolic metabolism; carbohydrate metabolism; steroid metabolism;  
KW terpene metabolism; isoprenoid metabolism; alkene metabolism;  
KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;  
KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.  
OS Unidentified.  
XX  
XX WO2003020936-A1.  
XX  
PD 13-MAR-2003.  
XX  
PF 30-AUG-2002; 2002WO-US027884.  
XX  
XX 31-AUG-2001; 2001US-0316471P.  
XX  
XX (DOWC ) DOW CHEM CO.  
PA (DOWC ) DOW AGROSCIENCES LLC.  
XX  
XX Weglazz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;  
PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;  
XX WPI; 2003-313091/30.  
XX

Novel genes that confer altered metabolic characteristics in Nicotiana benthamiana plants, useful for altering the levels of metabolites e.g. acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.

XX Claim 1; SEQ ID NO 3504; 2576pp; English.

XX The invention comprises DNA sequences which confer an altered metabolic

CC characteristic when they are expressed in a plant. The DNA sequences of

CC the invention are useful for producing plants with an altered metabolic

CC characteristic, such as: altered acid metabolism, alcohol metabolism,

CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other

CC base metabolism, altered amino acid metabolism, altered ester metabolism,

CC altered glyceride metabolism, altered phenolic metabolism, altered

CC carbohydrate metabolism, altered sterol, oxygenated terpene, or

CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon

CC metabolism, ketone or quinone metabolism. The DNA sequences of the

CC invention may be used to provide disease resistance in a plant and gene

CC shuffling or sexual PCR procedures. The present nucleic acid represents a

CC DNA sequence of the invention.

XX SQ Sequence 377 BP; 103 A; 89 C; 86 G; 99 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5 93e-24 Length: 377

Score: 240.50 Matches: 52

Percent Similarity: 96.5% Conservative: 3

Best Local Similarity: 91.2% Mismatches: 1

Query Match: 88.7% Indels: 1

DB: 10 Gaps: 1

US-10-628-525A-33 (1-56) x ADK56121 (1-377)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20

ADK56120

DB 68 ATGGCTTCCTCAGTCTTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 127

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39

DB 128 AACATGGTTGCACCTTTCCAGGCTCTTAAGTCTGCTGCCTCATTCCTGTTTCAAGAAAG 187

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

ADK56120

DB 188 CAAAACCTTGACATCACTTCCATTGCGAGGAGGAGGAGTGCATGTC 238

RESULT 11

ID ADK56120 standard; DNA; 489 BP.

XX ADK56120;

XX 06-MAY-2004 (first entry)

XX Plant DNA sequence which confers altered metabolic characteristic #3503.

XX altered metabolic characteristic; plant; acid metabolism;

KW alcohol metabolism; fatty acid metabolism;

KW branched fatty acid metabolism; alkaloid metabolism;

KW amino acid metabolism; ester metabolism; glyceride metabolism;

KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;

KW terpene metabolism; isoprenoid metabolism; alkene metabolism;

KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;

KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.

XX Unidentified.

OS WO2003020936-A1.

PN 13-MAR-2003.

XX 30-AUG-2002; 2002WO-US027884.

XX 31-AUG-2001; 2001US-0316471P.

XX (DOWC ) DOW CHEM CO.

PA (DOWC ) DOW AGROSCIENCES LLC.

XX

PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;

PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;

XX WPI; 2003-313091/30.

XX Novel genes that confer altered metabolic characteristics in Nicotiana

PT benchamiana plants, useful for altering the levels of metabolites e.g.

PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.

XX Claim 1; SEQ ID NO 3503; 2576pp; English.

XX The invention comprises DNA sequences which confer an altered metabolic

CC characteristic when they are expressed in a plant. The DNA sequences of

CC the invention are useful for producing plants with an altered metabolic

CC characteristic, such as: altered acid metabolism, alcohol metabolism,

CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other

CC base metabolism, altered amino acid metabolism, altered ester metabolism,

CC altered glyceride metabolism, altered phenolic metabolism, altered

CC carbohydrate metabolism, altered sterol, oxygenated terpene, or

CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon

CC metabolism, ketone or quinone metabolism. The DNA sequences of the

CC invention may be used to provide disease resistance in a plant and gene

CC shuffling or sexual PCR procedures. The present nucleic acid represents a

CC DNA sequence of the invention.

XX SQ Sequence 489 BP; 136 A; 113 C; 114 G; 126 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8 43e-24 Length: 489

Score: 240.50 Matches: 52

Percent Similarity: 96.5% Conservative: 3

Best Local Similarity: 91.2% Mismatches: 1

Query Match: 88.7% Indels: 1

DB: 10 Gaps: 1

US-10-628-525A-33 (1-56) x ADK56120 (1-489)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20

ADK56120

DB 79 ATGGCTTCCTCAGTCTTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 138

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39

DB 139 AACATGGTTGCACCTTTCCAGGCTCTTAAGTCTGCTGCCTCATTCCTGTTTCAAGAAAG 198

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

ADK56120

DB 199 CAAAACCTTGACATCACTTCCATTGCGAGGAGGAGGAGTGCATGTC 249

RESULT 12

ID ADC76164 standard; DNA; 492 BP.

XX ADC76164;

XX 01-JAN-2004 (first entry)

XX DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1433.

DE rice; yeast; poppy; plant; disease resistance; anti-fungal;

KW phytopathogen; gene shuffling; ds.

KW Unidentified.

OS WO2003020905-A2.

PN 13-MAR-2003.

XX 30-AUG-2002; 2002WO-US027883.

XX 31-AUG-2001; 2001US-0316392P.

XX (DOWC ) DOW CHEM CO.

PA

XX Shukla V, Butler H, Larrinua I, Reddy AS;  
XX WPI; 2003-290185/28.  
XX Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae  
XX sativa, Saccharomyces cerevisiae, Trichoderma harzianum and Papaver  
XX rhoes, useful for conferring disease resistance in plants.  
XX Claim 1; SEQ ID NO 1433; 617pp; English.  
XX The invention relates to a novel isolated nucleic acid derived from  
XX Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae  
XX (yeast), Trichoderma harzianum (Hypocrea lixi) and Papaver rhoes  
XX (poppy) and a sequence that hybridises to them under conditions of low  
XX stringency, where expression of the nucleic acid in a plant results in a  
XX disease resistance phenotype. The polynucleotides of the invention  
XX demonstrate anti-fungal activity and may be useful in conferring disease  
XX resistance in a plant against phytopathogen such as Aspergillus flavus,  
XX Gibberella fujikuroi and Gibberella zeae. Furthermore, the  
XX polynucleotides may be useful to retrieve unknown sequences and in gene  
XX shuffling or sexual PCR procedures. The current sequence is that of the  
XX DNA of the invention which is homologous to that of the phytopathogen  
XX resistance-related contig cDNAs.  
SQ Sequence 492 BP; 140 A; 115 C; 111 G; 126 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.5e-24 Length: 492  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 10 Gaps: 1

US-10-628-525A-33 (1-56) x ADC76164 (1-492)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraThrArgThrAenProAlaGlnAla 20  
Db 66 ATGGCTTCCTCAGTTCTTCTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 125  
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 126 AACATGGTTGCACCTTTCACTGCTCTTAAGTCTGCTGCCTCATTCCTGTTTCAAGGAAG 185  
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 186 CAAACCTTGACATCACTTCATTCGCGACGACGGCGGAGAGTGCAATGC 236

RESULT 13  
AAD35635  
ID AAD35635 standard; cDNA; 499 BP.  
XX  
XX AAD35635;  
XX  
XX  
XX

DT 26-JUL-2002 (first entry)

XX Nicotiana benthamiana rubisco partial cDNA sequence.

XX Nucleic acid vector; tobacco rattle virus; virus induced gene silencing;  
XX TRV; VIGS; ribulose-1,5-bisphosphate carboxylase oxygenase; rubisco;  
XX transgenic plant; enzyme; ss.

XX Nicotiana benthamiana.

XX US6369296-B1.

XX 09-APR-2002.

XX 01-FEB-2000; 2000US-00495797.

XX 01-FEB-2000; 2000US-00495797.

XX

(PLAN-) PLANT BIOSCIENCE LTD.

XX Ratcliff FG, Martin-Hernandez AM, Baulcombe DC;

XX WPI; 2002-337969/37.

XX Novel nucleic acid vector, useful for producing transgenic plants,  
XX comprises a plant active promoter linked to a recombinant tobacco rattle  
XX virus cDNA.

XX Example 2; Col 37-38; 32pp; English.

XX The invention relates to a nucleic acid vector. The vector comprises a  
XX plant active promoter operably linked to a recombinant tobacco rattle  
XX virus (TRV) cDNA which includes cis acting elements of TRV RNA permitting  
XX in the presence of replicase, replication of the cDNA, a viral subgenomic  
XX promoter operably linked to a sequence encoding a TRV coat protein, and a  
XX heterologous sequence, and border sequences for transfer into a plant  
XX genome. The vector is useful for producing genetically engineered plant  
XX cells or transgenic plants. The nucleic acids are used to initiate  
XX virus induced gene silencing (VIGS). The present sequence is Nicotiana  
XX benthamiana ribulose-1,5-bisphosphate carboxylase oxygenase (rubisco)  
XX partial cDNA related to the invention

SQ Sequence 499 BP; 132 A; 120 C; 123 G; 124 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.67e-24 Length: 499  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x AAD35635 (1-499)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraThrArgThrAenProAlaGlnAla 20  
Db 8 ATGGCTTCCTCAGTTCTTCTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 67  
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 68 AACATGGTTGCACCTTTCACTGCTCTTAAGTCTGCTGCCTCATTCCTGTTTCAAGGAAG 127

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 128 CAAACCTTGACATCACTTCATTCGCGACGACGGCGGAGAGTGCAATGC 178

RESULT 14  
ADK59824

ID ADK59824 standard; DNA; 504 BP.

XX  
XX ADK59824;

DT 06-MAY-2004 (first entry)

XX Plant DNA sequence which confers altered metabolic characteristic #7207.

XX altered metabolic characteristic; plant; acid metabolism;

XX alcohol metabolism; fatty acid metabolism;

XX amino acid metabolism; ester metabolism; glyceride metabolism;

XX phenolic metabolism; carboxylate metabolism; sterol metabolism;

XX terpene metabolism; isoprenoid metabolism; alkene metabolism;

XX alkyne metabolism; hydrocarbon metabolism; ketone metabolism;

XX quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.

XX Unidentified.

XX WO2003020936-A1.

XX 13-MAR-2003.

XX

PF 30-AUG-2002; 2002WO-US027884.  
XX  
PR 31-AUG-2001; 2001US-0316471P.  
XX  
XX (DOWC ) DOW CHEM CO.  
PA (DOWC ) DOW AGROSCIENCES LLC.  
XX  
XX  
PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;  
PI Oriado JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;  
XX  
XX WPI; 2003-313091/30.  
XX  
XX Novel genes that confer altered metabolic characteristics in Nicotiana  
PT benthamiana plants, useful for altering the levels of metabolites e.g.  
PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and steroids.  
XX  
XX Claim 1; SEQ ID NO 7207; 2576pp; English.  
XX  
XX The invention comprises DNA sequences which confer an altered metabolic  
CC characteristic when they are expressed in a plant. The DNA sequences of  
CC the invention are useful for producing plants with an altered metabolic  
CC characteristic, such as: altered acid metabolism, alcohol metabolism,  
CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other  
CC base metabolism, altered amino acid metabolism, altered ester metabolism,  
CC altered glyceride metabolism, altered phenolic metabolism, altered  
CC carbohydrate metabolism, altered sterol, oxygenated terpene, or  
CC isoprenoid metabolism, alkene or alkynyl metabolism, hydrocarbon  
CC metabolism, ketone or quinone metabolism. The DNA sequences of the  
CC invention may be used to provide disease resistance in a plant and gene  
CC shuffling or sexual PCR procedures. The present nucleic acid represents a  
CC DNA sequence of the invention.  
XX  
XX SQ Sequence 504 BP; 139 A; 117 C; 118 G; 130 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.78e-24 Length: 504  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 10 Gaps: 1

US-10-628-525A-33 (1-56) x ADK59824 (1-504)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 78 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCCGCGCAATGTTGCTCAAGCT 137  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 138 AACATGGTTGCACCTTTTCACAGGCTTAAGTCTGCTGCTCATCTCCCTGTTTCAGGAAG 197  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 198 CAAAACCTTGCATCATCTCCATTCGACGACGCGGGAAGAGTGCAATGC 248

RESULT 15  
ADC75089  
ID ADC75089 standard; cDNA; 581 BP.  
XX  
XX AC ADC75089;  
XX  
XX DT 01-JAN-2004 (first entry)  
XX  
XX DE N benthamiana phytopathogen resistance-related contig cDNA - SEQ ID 13.  
XX  
XX KW rice; yeast; poppy; plant; disease resistance; anti-fungal;  
KW phytopathogen; gene shuffling; ss.  
XX  
XX OS Nicotiana benthamiana.  
XX  
XX FN WO2003020905-A2.  
XX

PD 13-MAR-2003.  
XX  
PF 30-AUG-2002; 2002WO-US027883.  
XX  
PR 31-AUG-2001; 2001US-0316392P.  
XX  
XX (DOWC ) DOW CHEM CO.  
PA  
XX Shukla V, Butler H, Larrinua I, Reddy AS;  
PI WPI; 2003-290185/28.  
XX  
XX Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae  
PT sativa, Saccharomyces cerevisiae, Trichoderma harzianum and Papaver  
PT rhoeas, useful for conferring disease resistance in plants.  
XX  
XX Claim 1; SEQ ID NO 13; 617pp; English.  
XX  
XX The invention relates to a novel isolated nucleic acid derived from  
CC Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae  
CC (yeast), Trichoderma harzianum (Hypocrea lixii) and Papaver rhoeas  
CC (poppy) and a sequence that hybridises to them under conditions of low  
CC stringency, where expression of the nucleic acid in a plant results in a  
CC disease resistance phenotype. The polynucleotides of the invention  
CC demonstrate anti-fungal activity and may be useful in conferring disease  
CC resistance in a plant against phytopathogen such as Aspergillus flavus,  
CC Gibberella fujikuroi and Gibberella zeae. Furthermore, the  
CC polynucleotides may be useful to retrieve unknown sequences and in gene  
CC shuffling or sexual PCR procedures. The current sequence is that of the  
CC phytopathogen resistance-related contig cDNA of the invention.  
XX  
XX SQ Sequence 581 BP; 162 A; 132 C; 143 G; 144 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.06e-23 Length: 581  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 10 Gaps: 1

US-10-628-525A-33 (1-56) x ADC75089 (1-581)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 63 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCCGCGCAATGTTGCTCAAGCT 122  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 123 AACATGGTTGCACCTTTTCACAGGCTTAAGTCTGCTGCTCATCTCCCTGTTTCAGGAAG 182  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 183 CAAAACCTTGCATCATCTCCATTCGACGACGCGGGAAGAGTGCAATGC 233

RESULT 16  
ADC76944  
ID ADC76944 standard; DNA; 608 BP.  
XX  
XX AC ADC76944;  
XX  
XX DT 01-JAN-2004 (first entry)  
XX  
XX DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1213.  
XX  
XX KW rice; yeast; poppy; plant; disease resistance; anti-fungal;  
KW phytopathogen; gene shuffling; ds.  
XX  
XX OS Unidentified.  
XX  
XX FN WO2003020905-A2.  
XX  
XX PD 13-MAR-2003.





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XX 30-AUG-2002; 2002WO-US027883.
XX PF
XX 31-AUG-2001; 2001US-0316392P.
XX PR
XX (DOWC ) DOW CHEM CO.
XX PA
XX Shukla V, Butler H, Larrinua I, Reddy AS;
XX WPI; 2003-290185/28.
XX DR
XX Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae
PT sativa, Saccharomyces cerevisiae, Trichoderma harzianum and Papaver
PT rhoas, useful for conferring disease resistance in plants.
XX
XX Claim 1; SEQ ID NO 1218; 617pp; English.
XX
XX The invention relates to a novel isolated nucleic acid derived from
CC Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae
CC (yeast), Trichoderma harzianum (Hypocrea lixii) and Papaver rhoas
CC (poppy) and a sequence that hybridises to them under conditions of low
CC stringency, where expression of the nucleic acid in a plant results in a
CC disease resistance phenotype. The polynucleotides of the invention
CC demonstrate anti-fungal activity and may be useful in conferring disease
CC resistance in a plant against phytopathogen such as Aspergillus flavus,
CC Gibberella fujikuroi and Gibberella zeae. Furthermore, the
CC polynucleotides may be useful to retrieve unknown sequences and in gene
CC shuffling or sexual PCR procedures. The current sequence is that of the
CC DNA of the invention which is homologous to that of the phytopathogen
CC resistance-related contig cDNAs.
XX
XX Sequence 615 BP; 168 A; 144 C; 146 G; 156 T; 0 U; 1 Other;
SQ
Alignment Scores:
Pred. No.: 1.15e-23 Length: 615
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 10 Gaps: 1
US-10-628-525A-33 (1-56) x ADC76949 (1-615)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThraAsnProAlaGlnAla 20
DB 47 ATGGCTTCTCAGTCTTTCTCAGCAGCAGTTCGCCCGCAGCAATGTTGCTCAAGCT 106
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
DB 107 AACATGGTTGCACCTTTTCACAGTCTTAAGTCTGCTGCCTCATTCCTCTGTTCAAGAAAG 166
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB 167 CAAACCTTTGACATCACTTCCATTGCGCAGCAACGGCGGAAGAGTGCAATGC 217
RESULT 19
ADC76953
ID ADC76953 standard; DNA; 632 BP.
XX
XX ADC76953;
XX
XX 01-JAN-2004 (first entry)
XX
XX DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1222.
DE
XX rice; yeast; poppy; plant; disease resistance; anti-fungal;
XX phytopathogen; gene shuffling; ds.
XX
XX Unidentified.
XX
XX WO2003020905-A2.
XX
XX 13-MAR-2003.
XX

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XX 30-AUG-2002; 2002WO-US027883.
XX PF
XX 31-AUG-2001; 2001US-0316392P.
XX PR
XX (DOWC ) DOW CHEM CO.
XX PA
XX Shukla V, Butler H, Larrinua I, Reddy AS;
XX WPI; 2003-290185/28.
XX DR
XX Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae
PT sativa, Saccharomyces cerevisiae, Trichoderma harzianum and Papaver
PT rhoas, useful for conferring disease resistance in plants.
XX
XX Claim 1; SEQ ID NO 1222; 617pp; English.
XX
XX The invention relates to a novel isolated nucleic acid derived from
CC Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae
CC (yeast), Trichoderma harzianum (Hypocrea lixii) and Papaver rhoas
CC (poppy) and a sequence that hybridises to them under conditions of low
CC stringency, where expression of the nucleic acid in a plant results in a
CC disease resistance phenotype. The polynucleotides of the invention
CC demonstrate anti-fungal activity and may be useful in conferring disease
CC resistance in a plant against phytopathogen such as Aspergillus flavus,
CC Gibberella fujikuroi and Gibberella zeae. Furthermore, the
CC polynucleotides may be useful to retrieve unknown sequences and in gene
CC shuffling or sexual PCR procedures. The current sequence is that of the
CC DNA of the invention which is homologous to that of the phytopathogen
CC resistance-related contig cDNAs.
XX
XX Sequence 632 BP; 177 A; 146 C; 149 G; 160 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.19e-23 Length: 632
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 10 Gaps: 1
US-10-628-525A-33 (1-56) x ADC76953 (1-632)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThraAsnProAlaGlnAla 20
DB 52 ATGGCTTCTCAGTCTTTCTCAGCAGCAGTTCGCCCGCAGCAATGTTGCTCAAGCT 111
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
DB 112 AACATGGTTGCACCTTTTCACAGTCTTAAGTCTGCTGCCTCTCCCTGTTCAAGGAAG 171
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB 172 CAAACCTTTGACATCACTTCCATTGCGCAGCAACGGCGGAAGAGTGCAATGC 222
RESULT 20
ADC76948
ID ADC76948 standard; DNA; 684 BP.
XX
XX ADC76948;
XX
XX 01-JAN-2004 (first entry)
XX
XX DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1217.
DE
XX rice; yeast; poppy; plant; disease resistance; anti-fungal;
XX phytopathogen; gene shuffling; ds.
XX
XX Unidentified.
XX
XX WO2003020905-A2.
XX
XX 13-MAR-2003.
XX

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XX 30-AUG-2002; 2002WO-US027883.  
 XX  
 XX 31-AUG-2001; 2001US-0316392P.  
 XX  
 XX (DOWC ) DOW CHEM CO.  
 XX  
 XX Shukla V, Butler H, Larrinua I, Reddy AS;  
 XX  
 XX WPI; 2003-290185/28.  
 XX  
 XX Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae  
 XX sativa, Saccharomyces cerevisiae, Trichoderma harzianum and Papaver  
 XX rhoeas, useful for conferring disease resistance in plants.  
 XX  
 XX Claim 1; SEQ ID NO 1217; 617pp; English.  
 XX  
 XX The invention relates to a novel isolated nucleic acid derived from  
 XX Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae  
 XX (yeast), Trichoderma harzianum (Hypocrea lixi) and Papaver rhoeas  
 XX (poppy) and a sequence that hybridizes to them under conditions of low  
 XX stringency, where expression of the nucleic acid in a plant results in a  
 XX disease resistance phenotype. The polynucleotides of the invention  
 XX demonstrate anti-fungal activity and may be useful in conferring disease  
 XX resistance in a plant against phytopathogen such as Aspergillus flavus,  
 XX Gibberella fujikuroi and Gibberella zeae. Furthermore, the  
 XX polynucleotides may be useful to retrieve unknown sequences and in gene  
 XX shuffling or sexual PCR procedures. The current sequence is that of the  
 XX DNA of the invention which is homologous to that of the phytopathogen  
 XX resistance-related contig cDNAs.  
 XX  
 XX Sequence 684 BP; 181 A; 155 C; 160 G; 188 T; 0 U; 0 Other;  
 XX  
 XX Alignment Scores:  
 XX Pred. No.: 1.33e-23 Length: 684  
 XX Score: 240.50 Matches: 52  
 XX Percent Similarity: 96.5% Conservative: 3  
 XX Best Local Similarity: 91.2% Mismatches: 1  
 XX Query Match: 88.7% Indels: 1  
 XX DB: 10 Gaps: 1  
 XX  
 XX US-10-628-525A-33 (1-56) x ADC76948 (1-684)  
 QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20  
 Db 47 ATGGCTTCTCAGTCTTTCTCAGCAGCAGTGTGCCACCGCAGCAATGTGTCTCAAGCT 106  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 Db 107 AACATGTTGCACCTTTTCACAGGTCTTAAAGTCTGCTGCCTCCTTCCTGTTTCAAGAAAG 166  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 167 CAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCATATGC 217  
 RESULT 21  
 ID ADK58382  
 XX ADK58382 standard; DNA; 718 BP.  
 XX  
 XX AC ADK58382;  
 XX  
 XX DT 06-MAY-2004 (first entry)  
 XX  
 XX Plant DNA sequence which confers altered metabolic characteristic #5765.  
 XX  
 XX altered metabolic characteristic; plant; acid metabolism;  
 XX alcohol metabolism; fatty acid metabolism; alkaloid metabolism;  
 XX branched fatty acid metabolism; alkaloid metabolism;  
 XX amino acid metabolism; ester metabolism; glyceride metabolism;  
 XX phenolic metabolism; carbohydrate metabolism; sterol metabolism;  
 XX terpene metabolism; isoprenoid metabolism; alkene metabolism;  
 XX alkyne metabolism; hydrocarbon metabolism; ketone metabolism;  
 XX quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.

XX Unidentified.  
 XX OS  
 XX PN WO2003020936-A1.  
 XX  
 XX PD 13-MAR-2003.  
 XX  
 XX 30-AUG-2002; 2002WO-US027884.  
 XX  
 XX 31-AUG-2001; 2001US-0316471P.  
 XX  
 XX (DOWC ) DOW CHEM CO.  
 XX (DOWC ) DOW AGROSCIENCES LLC.  
 XX  
 XX Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;  
 XX Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;  
 XX WPI; 2003-313091/30.  
 XX  
 XX Novel genes that confer altered metabolic characteristics in Nicotiana  
 XX benthamiana plants, useful for altering the levels of metabolites e.g.  
 XX acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.  
 XX  
 XX Claim 1; SEQ ID NO 5765; 2576pp; English.  
 XX  
 XX The invention comprises DNA sequences which confer an altered metabolic  
 XX characteristic when they are expressed in a plant. The DNA sequences of  
 XX the invention are useful for producing plants with an altered metabolic  
 XX characteristic, such as: altered acid metabolism, alcohol metabolism,  
 XX fatty acid metabolism, branched fatty acid metabolism, alkaloid or other  
 XX base metabolism, altered amino acid metabolism, altered ester metabolism,  
 XX carbohydrate metabolism, altered phenolic metabolism, altered  
 XX isoprenoid metabolism, altered sterol, oxygenated terpene, or  
 XX metabolism, ketone or quinone metabolism. The DNA sequences of the  
 XX invention may be used to provide disease resistance in a plant and gene  
 XX shuffling or sexual PCR procedures. The present nucleic acid represents a  
 XX DNA sequence of the invention.  
 XX  
 XX SQ Sequence 718 BP; 190 A; 162 C; 162 G; 204 T; 0 U; 0 Other;  
 XX  
 XX Alignment Scores:  
 XX Pred. No.: 1.42e-23 Length: 718  
 XX Score: 240.50 Matches: 52  
 XX Percent Similarity: 96.5% Conservative: 3  
 XX Best Local Similarity: 91.2% Mismatches: 1  
 XX Query Match: 88.7% Indels: 1  
 XX DB: 10 Gaps: 1  
 XX  
 XX US-10-628-525A-33 (1-56) x ADK58382 (1-718)  
 QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20  
 Db 45 ATGGCTTCTCAGTCTTTCTCAGCAGCAGTGTGCCACCGCAGCAATGTGTCTCAAGCT 104  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 Db 105 AACATGTTGCACCTTTTCACAGGTCTTAAAGTCTGCTGCCTCCTTCCTGTTTCAAGAAAG 164  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 165 CAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCATATGC 215  
 RESULT 22  
 ID ADK54321  
 XX ADK54321 standard; DNA; 736 BP.  
 XX  
 XX AC ADK54321;  
 XX  
 XX DT 06-MAY-2004 (first entry)  
 XX  
 XX Plant DNA sequence which confers altered metabolic characteristic #1704.  
 XX



Db 123 AACATGTTGACCTTTCACCTGCTTAACTCAGTCCTCGTTCCTGTTTCAAGGAG 182

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
|||||

Db 183 CAAACCTTGACATCACTTCCATTCGACGCAACGCGGAAGAGTGCAATGC 233  
|||||

RESULT 24

ADM44879

ID ADM44879 standard; DNA; 841 BP.

XX

AC ADM44879;

DT 03-JUN-2004 (first entry)

XX

DE Insect resistance associated DNA sequence SeqID286.

XX

KW insect resistant phenotype; plant protectant; gene therapy;

KW Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;

KW Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.

XX

OS Unidentified.

XX

PN WO2003020025-A2.

XX

PD 13-MAR-2003.

XX

PF 30-AUG-2002; 2002WO-US027882.

XX

PR 31-AUG-2001; 2001US-0316319P.

XX

PA (DOWC ) DOW CHEM CO.

XX

PI Shukla V, Meade T, Larrinua I;

XX

DR WPI; 2003-290133/28.

XX

PT New isolated nucleic acid having expression that results in an insect resistant phenotype, useful for conferring insect resistance and for producing insect-resistant plants.

XX

PS Claim 1; SEQ ID NO 286; 396pp; English.

XX

CC This invention relates to a novel isolated nucleic acid comprising, or hybridizing under low stringent conditions to, any of the 1214 nucleic acid sequences given in the specification, where the expression of the nucleic acid in a plant results in an insect resistant phenotype. The invention may be useful as a plant protectant or for gene therapy. The genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza sativa and Papaver rhoeas. The isolated nucleic acid and vector are useful for conferring insect resistance and for producing insect-resistant plants. The present sequence is that of a DNA sequence of the invention which may confer insect resistance to plants.

XX

SQ Sequence 841 BP; 218 A; 174 C; 187 G; 262 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.76e-23 Length: 841

Score: 240.50 Matches: 52

Percent Similarity: 96.5% Conservative: 3

Best Local Similarity: 91.2% Mismatches: 1

Query Match: 88.7% Indels: 1

DB: 11 Gaps: 1

US-10-628-525A-33 (1-56) x ADM44879 (1-841)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
|||||

Db 57 ATGGCTTCTCAGTCTTTCTTCAGCAGAGTTCACCCGCAATGTTGCTCAAGCT 116  
|||||

Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
|||||

Db 117 AACATGTTGACCTTTCACCTGCTTAACTCAGTCCTCGTTCCTGTTTCAAGGAG 176  
|||||

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
|||||

Db 177 CAAACCTTGACATCACTTCCATTCGACGCAACGCGGAAGAGTGCAATGC 227  
|||||

RESULT 25

ADM45447

ID ADM45447 standard; DNA; 847 BP.

XX

AC ADM45447;

DT 03-JUN-2004 (first entry)

XX

DE Insect resistance associated DNA sequence SeqID854.

XX

KW insect resistant phenotype; plant protectant; gene therapy;

KW Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;

KW Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.

XX

OS Unidentified.

XX

PN WO2003020025-A2.

XX

PD 13-MAR-2003.

XX

PF 30-AUG-2002; 2002WO-US027882.

XX

PR 31-AUG-2001; 2001US-0316319P.

XX

PA (DOWC ) DOW CHEM CO.

XX

PI Shukla V, Meade T, Larrinua I;

XX

DR WPI; 2003-290133/28.

XX

PT New isolated nucleic acid having expression that results in an insect resistant phenotype, useful for conferring insect resistance and for producing insect-resistant plants.

XX

PS Claim 1; SEQ ID NO 854; 396pp; English.

XX

CC This invention relates to a novel isolated nucleic acid comprising, or hybridizing under low stringent conditions to, any of the 1214 nucleic acid sequences given in the specification, where the expression of the nucleic acid in a plant results in an insect resistant phenotype. The invention may be useful as a plant protectant or for gene therapy. The genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza sativa and Papaver rhoeas. The isolated nucleic acid and vector are useful for conferring insect resistance and for producing insect-resistant plants. The present sequence is that of a DNA sequence of the invention which may confer insect resistance to plants.

XX

SQ Sequence 847 BP; 221 A; 174 C; 189 G; 263 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.77e-23 Length: 847

Score: 240.50 Matches: 52

Percent Similarity: 96.5% Conservative: 3

Best Local Similarity: 91.2% Mismatches: 1

Query Match: 88.7% Indels: 1

DB: 11 Gaps: 1

US-10-628-525A-33 (1-56) x ADM45447 (1-847)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
|||||

Db 63 ATGGCTTCTCAGTCTTTCTTCAGCAGAGTTCACCCGCAATGTTGCTCAAGCT 122  
|||||

Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
|||||

Db 123 AACATGTTGACCTTTCACCTGCTTAACTCAGTCCTCGTTCCTGTTTCAAGGAG 182  
|||||

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
|||||

Db 183 CAAAACCTTGACATCATCTTCCATTGCCAGCAACGGCGGAAGAGTGCAATGC 233

## RESULT 26

ADW45065  
ID ADM45065 standard; DNA; 859 BP.

XX AC ADM45065;  
XX ADW45065;

XX 03-JUN-2004 (first entry)

XX Insect resistance associated DNA sequence SeqID472.

XX insect resistant phenotype; plant protectant; gene therapy;  
KW Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;  
KW Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.  
OS Unidentified.

XX WO2003020025-A2.  
XX 13-MAR-2003.

XX 30-AUG-2002; 2002WO-US027882.  
XX 31-AUG-2001; 2001US-0316319P.

XX (DOWC ) DOW CHEM CO.  
XX Shukla V, Meade T, Larrinua I;

XX WPI; 2003-290133/28.

XX New isolated nucleic acid having expression that results in an insect  
PT resistant phenotype, useful for conferring insect resistance and for  
PT producing insect-resistant plants.  
XX Claim 1; SEQ ID NO 472; 396pp; English.

XX This invention relates to a novel isolated nucleic acid comprising, or  
CC hybridising under low stringent conditions to, any of the 1214 nucleic  
CC acid sequences given in the specification, where the expression of the  
CC nucleic acid in a plant results in an insect resistant phenotype. The  
CC invention may be useful as a plant protectant or for gene therapy. The  
CC genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza  
CC sativa and Papaver rhoeas. The isolated nucleic acid and vector are  
CC useful for conferring insect resistance and for producing insect-  
CC resistant plants. The present sequence is that of a DNA sequence of the  
CC invention which may confer insect resistance to plants.

XX SQ Sequence 859 BP; 219 A; 177 C; 194 G; 269 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.81e-23 Length: 859  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 11 Gaps: 1

US-10-628-525A-33 (1-56) x ADM45065 (1-859)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20

Db 79 ATGGCTTCTCTAGTCTTTCTTCAGCAGCAGTTCGCCAGCGAGCAAGTGTCTCAAGCT 138

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39

Db 139 AACATGGTGTGCACCTTTTCACAGGCTTAAAGTCTGCTGCCTCATCTCCCTGTTTCAAGAAAG 198

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

Db 199 CAAAACCTTGACATCATCTTCCATTGCCAGCAACGGCGGAAGAGTGCAATGC 249

## RESULT 27

ADC75566  
ID ADC75566 standard; DNA; 924 BP.

XX AC ADC75566;  
XX ADW75566;

XX 01-JAN-2004 (first entry)

XX DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 490.  
XX rice; yeast; poppy; plant; disease resistance; anti-fungal;  
KW phytopathogen; gene shuffling; ds.

XX Unidentified.  
OS WO2003020905-A2.

XX 13-MAR-2003.

XX 30-AUG-2002; 2002WO-US027883.  
XX 31-AUG-2001; 2001US-0316392P.

XX (DOWC ) DOW CHEM CO.  
XX Shukla V, Butler H, Larrinua I, Reddy AS;

XX WPI; 2003-290185/28.

XX Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryza  
PT sativa, Saccharomyces cerevisiae, Trichoderma harzianum and Papaver  
PT rhoeas, useful for conferring disease resistance in plants.  
XX Claim 1; SEQ ID NO 490; 617pp; English.

XX The invention relates to a novel isolated nucleic acid derived from  
CC Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae  
CC (yeast), Trichoderma harzianum (Hypocrea lixi) and Papaver rhoeas  
CC (poppy) and a sequence that hybridises to them under conditions of low  
CC stringency, where expression of the nucleic acid in a plant results in a  
CC disease resistance phenotype. The polynucleotides of the invention  
CC demonstrate anti-fungal activity and may be useful in conferring disease  
CC resistance in a plant against phytopathogen such as Aspergillus flavus,  
CC Gibberella fujikuroi and Gibberella zeae. Furthermore, the  
CC polynucleotides may be useful to retrieve unknown sequences and in gene  
CC shuffling or sexual PCR procedures. The current sequence is that of the  
CC DNA of the invention which is homologous to that of the phytopathogen  
CC resistance-related contig cDNAs.

XX SQ Sequence 924 BP; 257 A; 189 C; 186 G; 292 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 2e-23 Length: 924  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 10 Gaps: 1

US-10-628-525A-33 (1-56) x ADC75566 (1-924)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20

Db 56 ATGGCTTCTCTAGTCTTTCTTCAGCAGCAGTTCGCCAGCGAGCAAGTGTCTCAAGCT 115

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39

Db 116 AACATGGTGTGCACCTTTTCACAGGCTTAAAGTCTGCTGCCTCATCTCCCTGTTTCAAGGAAG 175

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

Db 176 CAAAACCTTGACATCATCTTCCATTGCCAGCAACGGCGGAAGAGTGCAATGC 226



```
RESULT 28
ADC76165
ID ADC76165 standard; DNA; 958 BP.
XX AC
XX ADC76165;
XX
XX 01-JAN-2004 (first entry)
XX
XX DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1434.
XX rice; poppy; plant; disease resistance; anti-fungal;
XX phytopathogen; gene shuffling; ds.
XX
XX Unidentified.
XX WO2003020905-A2.
XX
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WO-US027883.
XX
XX 31-AUG-2001; 2001US-0316392P.
XX (DOWC ) DOW CHEM CO.
XX
XX Shukla V, Butler H, Larrinua I, Reddy AS;
XX WPI; 2003-290185/28.
XX
XX Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryza
XX sativa, Saccharomyces cerevisiae, Trichoderma harzianum and Papaver
XX rhoeas, useful for conferring disease resistance in plants.
XX
XX Claim 1; SEQ ID NO 1434; 617pp; English.
XX
XX The invention relates to a novel isolated nucleic acid derived from
XX Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae
XX (yeast), Trichoderma harzianum (Hypocrea lixii) and Papaver rhoeas
XX (poppy) and a sequence that hybridises to them under conditions of low
XX stringency, where expression of the nucleic acid in a plant results in a
XX disease resistance phenotype. The polynucleotides of the invention
XX demonstrate anti-fungal activity and may be useful in conferring disease
XX resistance in a plant against phytopathogen such as Aspergillus flavus,
XX Gibberella fujikuroi and Gibberella zeae. Furthermore, the
XX polynucleotides may be useful to retrieve unknown sequences and in gene
XX shuffling or sexual PCR procedures. The current sequence is that of the
XX DNA of the invention which is homologous to that of the phytopathogen
XX resistance-related contig cDNAs.
XX
XX Sequence 958 BP; 265 A; 195 C; 199 G; 299 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 2 1e-23 Length: 958
XX Score: 240.50 Matches: 52
XX Percent Similarity: 96.5% Conservative: 3
XX Best Local Similarity: 91.2% Mismatches: 1
XX Query Match: 88.7% Indels: 1
XX DB: 10 Gaps: 1
XX
XX US-10-628-525A-33 (1-56) x ADC76165 (1-958)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
DB 90 ATGGCTTCCTCAGTCTTTCTCAGCAGCAGTGTGCCACCGCAGCAATGTTGCTCAAGCT 149
QY 21 SerMetValAlaProPheThrGlyLeuYysSerAlaAla---PheProValSerArgGly 39
DB 150 AACATGGTTCACCTTTCACCTGCTCTTAAGTTCAGCTGCCTCGCTTCCTGTTTCAGGAA 209
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB 210 CAACACCTTGACATCACTTCCATTGTCAGCAGCAGCGGAGAGATGTCATATGC 260
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```
RESULT 29
AAQ92327
ID AAQ92327 standard; DNA; 1442 BP.
XX AC
XX AAQ92327;
XX
XX 25-MAR-2003 (revised)
XX 11-NOV-1995 (first entry)
XX
XX Chloroplast transit peptide, tyrosinase activator protein and tyrosinase
XX gene fusion.
XX
XX Tyrosinase; tyrosinase activator protein; fusion enzyme;
XX Streptomyces antibioticus; ORF438; Chloroplast transit peptide; tobacco;
XX ribulosebiphosphate-carboxylase; transgenic plant; vector; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 9..1442
XX FT /tag= a
XX FT /product= "Chloroplast transit peptide, tyrosinase"
XX FT misc_difference 396..398
XX FT /tag= b
XX FT /codon= seq:CAC, aa:Asp
XX FT misc_difference 1083..1085
XX FT /tag= c
XX FT /codon= seq:CAG, aa:Glu
XX FT misc_difference 1386..1388
XX FT /tag= d
XX FT /codon= seq:CAC, aa:Asp
XX
XX WO9513386-A2.
XX
XX 18-MAY-1995.
XX
XX 08-NOV-1994; 94WO-US012857.
XX
XX 12-NOV-1993; 93US-00152483.
XX (BIOS-) BIOSOURCE TECHNOLOGIES INC.
XX
XX Della-Cioppa G, Kumagai MH;
XX WPI; 1995-194104/25.
XX P-PSDB; AAR74174.
XX
XX DNA encoding fusion enzyme including tyrosinase and tyrosinase activator
XX protein - useful for in vivo or in vitro prodn. of melanin(s).
XX
XX Example 6; Page 36-37; 54pp; English.
XX
XX The sequence encodes a fusion protein of a tyrosinase, tyrosinase
XX activator protein and a chloroplast transit peptide (CTP) from tobacco
XX ribulosebiphosphate-carboxylase. The CTP gene is fused to the N-terminal
XX SpH1 site of ORF438 (containing a tyrosinase activator protein gene). The
XX resulting fusion is exchanged in plasmid Bluescript containing the ORF438
XX -tyrosinase gene fusion. The gene fusion allows import of the protein
XX into higher plant chloroplasts, followed by transit peptide cleavage to
XX give an active enzyme. Expression gives a melanin-positive phenotype.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 1442 BP; 220 A; 538 C; 465 G; 219 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 3.65e-23 Length: 1442
XX Score: 240.50 Matches: 52
XX Percent Similarity: 96.5% Conservative: 3
XX Best Local Similarity: 91.2% Mismatches: 1
XX Query Match: 88.7% Indels: 1
XX DB: 2 Gaps: 1
XX
XX US-10-628-525A-33 (1-56) x AAQ92327 (1-1442)
```

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 Db 9 ATGGCTTCCTCAGTCTTTCTCTGACAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 68  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 Db 69 AACATGGTTGCACCTTTTCACTGGCCTTAAGTCAGTCGCTCATTCCTGTTTCAAGGAAG 128  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 129 CAAACCTTGACATCATCTTCCATTGCCAAGCGCGGAAGAGTGCAATGC 179

RESULT 30

ADM45158  
 ID ADM45158 standard; DNA; 619 BP.  
 XX  
 AC ADM45158;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Insect resistance associated DNA sequence SeqID565.  
 XX  
 KW Insect resistant phenotype; plant protectant; gene therapy;  
 KW Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;  
 KW Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003020025-A2.  
 XX  
 PD 13-MAR-2003.  
 XX  
 PF 30-AUG-2002; 2002WO-US027882.  
 XX  
 PR 31-AUG-2001; 2001US-0316319P.  
 XX  
 PA (DOWC ) DOW CHEM CO.  
 XX  
 PI Shukla V, Meade T, Larrinua I;  
 XX  
 DR WPI; 2003-290133/28.

PT New isolated nucleic acid having expression that results in an insect  
 PT resistant phenotype, useful for conferring insect resistance and for  
 PT producing insect-resistant plants.

PS Claim 1; SEQ ID NO 565; 396pp; English.

CC This invention relates to a novel isolated nucleic acid comprising, or  
 CC hybridizing under low stringent conditions to, any of the 1214 nucleic  
 CC acid sequences given in the specification, where the expression of the  
 CC nucleic acid in a plant results in an insect resistant phenotype. The  
 CC invention may be useful as a plant protectant or for gene therapy. The  
 CC genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza  
 CC sativa and Papaver rhoeas. The isolated nucleic acid and vector are  
 CC useful for conferring insect resistance and for producing insect-  
 CC resistant plants. The present sequence is that of a DNA sequence of the  
 CC invention which may confer insect resistance to plants.

SQ Sequence 619 BP; 163 A; 146 C; 146 G; 164 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.16e-23	Length:	619
Score:	236.50	Matches:	51
Percent Similarity:	96.5%	Conservative:	4
Best Local Similarity:	89.5%	Mismatches:	1
Query Match:	87.3%	Indels:	1
DB:	11	Gaps:	1

US-10-628-525A-33 (1-56) x ADM45158 (1-619)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20

Db 39 GTGGCTTCCTCAGTCTTTCTCTGACAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 98  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 Db 99 AACATGGTTGCACCTTTTCACTGGCCTTAAGTCAGTCGCTCATTCCTGTTTCAAGGAAG 158  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 159 CAAACCTTGACATCATCTTCCATTGCCAAGCGCGGAAGAGTGCAATGC 209

Search completed: April 1, 2006, 04:26:21  
 Job time : 136.845 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 15:18:57 ; Search time 903.068 Seconds  
(without alignments)  
2901.306 Million cell updates/sec

Title: US-10-628-525a-33

Perfect score: 271

Sequence: 1 MASSMLSSRAVATRTPAQA.....SRKQNLDTISAGGRVQC 56

Scoring table:

BLOSUM62 Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-Q=/abs/ABSSWEB spool-SUFFIX=p2n.rst -MINMATCH=0\_1 -LOOPECL=0 -MODE=LOCAL  
-DB=EST -OPMT=fastap -SUFFIX=p2n.rst -MINMATCH=0\_1 -LOOPECL=0 -MODE=LOCAL  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150  
-DOALIGN=200 -THR\_SCORE=pcpt -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=pc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs06h  
-USER=US10628525 @CGN 1.1 1109 @runat 31032006 095118 16742 -NCPUs=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:  
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2: gb\_est2.\*  
3: gb\_est3.\*  
4: gb\_hc1.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_est7.\*  
9: gb\_gest1.\*  
10: gb\_gest2.\*  
11: gb\_gest3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	246.5	91.0	347	7	CV017043 tbt_00452
2	244.5	90.2	244	7	CV019289 tbt_00055
3	244.5	90.2	256	7	CV016318 tbt_00421
4	244.5	90.2	265	5	BU673933 pSKD64 To
5	244.5	90.2	282	1	AB001554 AB001554
6	244.5	90.2	288	7	CV016732 tbt_00200
7	244.5	90.2	324	7	CV019439 tbt_00202

8	244.5	90.2	326	7	CV017891
9	244.5	90.2	331	7	CV016591
10	244.5	90.2	333	7	CV019882
11	244.5	90.2	341	7	CV019568
12	244.5	90.2	348	7	CV021773
13	244.5	90.2	362	7	CV016438
14	244.5	90.2	364	7	CV016988
15	244.5	90.2	369	7	CV017159
16	244.5	90.2	371	7	CV019231
17	244.5	90.2	386	7	CV021480
18	244.5	90.2	387	7	CV016216
19	244.5	90.2	404	7	CV016980
20	244.5	90.2	412	7	CV017309
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22	244.5	90.2	428	7	CV017696
23	244.5	90.2	431	7	CV018759
24	244.5	90.2	431	7	CV021294
25	244.5	90.2	440	7	CV020505
26	244.5	90.2	443	7	CV020326
27	244.5	90.2	443	7	CV021799
28	244.5	90.2	454	7	CV016694
29	244.5	90.2	459	7	CV020329
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31	244.5	90.2	462	7	CV020983
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33	244.5	90.2	470	7	CV019915
34	244.5	90.2	481	7	CV021008
35	244.5	90.2	484	7	CV017787
36	244.5	90.2	485	7	CV019762
37	244.5	90.2	489	7	CV018137
38	244.5	90.2	492	7	CV018376
39	244.5	90.2	493	7	CV019394
40	244.5	90.2	495	7	CV017271
41	244.5	90.2	496	7	CV018748
42	244.5	90.2	498	7	CV016349
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44	244.5	90.2	510	7	CV017397
45	244.5	90.2	511	7	CV019644
46	244.5	90.2	520	7	CV019831
47	244.5	90.2	520	7	CV020302
48	244.5	90.2	528	7	CV019398
49	244.5	90.2	533	7	CV018405
50	244.5	90.2	552	7	CV016524
51	244.5	90.2	554	7	CV016821
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53	244.5	90.2	561	7	CV019628
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55	244.5	90.2	567	7	CV019281
56	244.5	90.2	569	7	CV021484
57	244.5	90.2	572	7	CV016734
58	244.5	90.2	577	7	CV019916
59	244.5	90.2	585	7	CV017207
60	244.5	90.2	586	7	CV021286
61	244.5	90.2	587	7	CV019355
62	244.5	90.2	589	7	CV016194
63	244.5	90.2	589	7	CV021210
64	244.5	90.2	591	7	CV016565
65	244.5	90.2	606	7	CV017003
66	244.5	90.2	610	7	CV021592
67	244.5	90.2	616	7	CV017574
68	244.5	90.2	617	7	CV017362
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70	244.5	90.2	618	7	CV020759
71	244.5	90.2	623	7	CV019792
72	244.5	90.2	625	7	CV021007
73	244.5	90.2	633	7	CV016314
74	244.5	90.2	642	7	CV020007
75	244.5	90.2	647	7	CV018894
76	244.5	90.2	653	7	CV017348
77	243.5	89.9	410	7	CV017911
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CV747653 SAL\_US008  
CV742421 SAL\_US003  
CV744304 SAL\_US037  
CV747589 SAL\_US007  
CV655077 SAL\_US005  
CV744065 SAL\_US027

ALIGNMENTS

**ORGANISM** Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.

**REFERENCE**  
**AUTHORS** Li, W.Z., Shao, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q., Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q., Dong, H.T. and Li, D.B.

**TITLE** Large-scale identification of ESTs from Nicotiana tabacum by normalized cDNA library sequencing

**JOURNAL** Unpublished (2004)

**COMMENT** Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan Provincial Tobacco Group Dali Branch; Bioinformatics and Gene Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi 653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

**FEATURES**  
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**ORIGIN**

Alignment Scores:  
Pred. No.: 6e-23 Length: 244  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV019289 (1-244)

QY 1 MetAlaSerSerMetLeuSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20  
|||||:::|||||  
Db 8 ATGGCTTCCTGTTACTTTCCTCTGCAGCAGTAGCCACTGCACCAATGTAGCTCAAGCT 67  
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QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
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Db 68 AACATGGTTGCACCTTTCATCTGCTTAAAGTCAGCTGCCTCATCTCCCTGTATCAGGAAG 127  
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QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
|||||  
Db 128 CAAACCTTGCATCATCTTCCATTGCTAGCAATGGTGAAGAGTGCAATGC 178  
|||||

**RESULT 3**  
CV016318  
**LOCUS** tbt\_004219 Normalized Nicotiana tabacum cDNA library Nicotiana  
**DEFINITION** tabacum cDNA clone tbt\_004219 5', mRNA sequence.  
**ACCESSION** CV016318  
**VERSION** CV016318.1 GI:51454670  
**KEYWORDS** EST.  
**SOURCE** Nicotiana tabacum (common tobacco)  
**ORGANISM** Nicotiana tabacum

**REFERENCE**  
**AUTHORS** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 256)  
Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P., Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q., Dong, H.T. and Li, D.B.

**TITLE** Large-scale identification of ESTs from Nicotiana tabacum by normalized cDNA library sequencing

**JOURNAL** Unpublished (2004)

**COMMENT** Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan Provincial Tobacco Group Dali Branch; Bioinformatics and Gene Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi 653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

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**ORIGIN**

Alignment Scores:  
Pred. No.: 6.38e-23 Length: 256  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV016318 (1-256)

QY 1 MetAlaSerSerMetLeuSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20  
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QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
:::|||||  
Db 119 AACATGGTTGCACCTTTCATCTGCTTAAAGTCAGCTGCCTCATCTCCCTGTATCAGGAAG 178  
|||||  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
|||||  
Db 179 CAAACCTTGCATCATCTTCCATTGCTAGCAATGGTGAAGAGTGCAATGC 229  
|||||

**RESULT 4**  
BU673933  
**LOCUS** pSK064 Tobacco PCRscript cDNA library Nicotiana tabacum cDNA 5', 3'  
**DEFINITION** similar to RbcS, mRNA sequence.  
**ACCESSION** BU673933  
**VERSION** BU673933.1 GI:23515061  
**KEYWORDS** EST.  
**SOURCE** Nicotiana tabacum (common tobacco)  
**ORGANISM** Nicotiana tabacum

**REFERENCE**  
**AUTHORS** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 265)  
Tang, L., Bhat, S., Phillips, A., Guo, X., Krueger, A. and Petracek, M.  
**TITLE** Photosynthetic control of nuclear mRNA gene expression in tobacco  
**JOURNAL** Unpublished (2002)  
**COMMENT** Contact: Marie Petracek  
Department of Biochemistry and Molecular Biology  
Oklahoma State University  
360 Noble Research Center, Stillwater, OK 74078, USA  
Tel: (405) 744-6199  
Fax: (405) 744-7799  
Email: marie.petracek@biochem.okstate.edu  
95% identity at nucleotides 1067-1292 to Nicotiana plumbaginifolia rbc-8B gene for ribulose biphosphate carboxylase  
Seq primer: M13 forward and reverse  
High quality sequence stop: 265.

**FEATURES**  
**Location/Qualifiers**

## source

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1. .265
/organism="Nicotiana tabacum"
/mol_type="mRNA"
/cultivar="Petit Havana"
/db_xref="taxon:4097"
/tissue_type="leaf"
/dev_stage="3 week old"
/clone_lib="Tobacco PCRscript cDNA library"
/notes="Vector: PCR script; Site 1: SrfI site destroyed;
PCR amplified partial cDNAs generated using suppressive
subtractive hybridization enriching for mRNAs present in
the light but not when in the presence of photosynthetic
electron transport inhibitor DCMU, cloned by blunt end
cloning into PCR-script Amp SK(+) SrfI site, destroying
the SrfI site"

ORIGIN
Alignment Scores:
Pred. No.: 6,66e-23 Length: 265
Score: 244.50 Matches: 53
Percent Similarity: 96.5% Conservative: 2
Best Local Similarity: 93.0% Mismatches: 1
Query Match: 90.2% Indels: 1
DB: 5 Gaps: 1

US-10-628-525A-33 (1-56) x BU673933 (1-265)

QY 1 MetAlaSerSerMetLeuSerSerAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 52 ATGGCTTCCTCTGTTCTTTCTCTGAGCAGTTGCCACTCGCACCAATGTTCTCAAGCT 111
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 112 AACATGGTTGCACCTTTCTAGTCTGCTGCTCAATCCCTGTTTCAAGGAAG 171
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db 172 CAAAACCTTGACATCACTTCCTAGCTAGCAATGGTGAAGAGTGCAATGC 222

RESULT 5
AB001554 282 bp mRNA linear EST 27-MAY-1998
AB001554 Tobacco shoot (MTamaoki) Nicotiana tabacum cDNA clone
DEFINITION HRG331.1 mRNA sequence.
ACCESSION AB001554
VERSION AB001554.1 GI:1912039
KEYWORDS EST.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 282)
Tamaoki,M., Yamamoto,N. and Matsuoaka,M.
Isolation and characterization of cDNA clones with enhanced
expression in tobacco plants expressing the rice homeobox gene,
OSH1
JOURNAL Plant Cell Physiol. 38 (5), 638-642 (1997)
PUBMED 9210336
COMMENT Contact: Masanori Tamaoki
BioScience Cente
Nagoya University
Aichi 464-01, Japan
Tel: 052-789-5225
Fax: 052-789-5226
Email: 194d609d@sunspot.eds.ecip.nagoya-u.ac.jp.

FEATURES
source
1..282
/organism="Nicotiana tabacum"
/mol_type="mRNA"
/cultivar="Samun NN"
/db_xref="taxon:4097"
/clone="HRG331"

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/tissue_type="Shoot apex"
/clone_lib="Tobacco shoot (MTamaoki)"

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## ORIGIN

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Alignment Scores:
Pred. No.: 7.21e-23 Length: 282
Score: 244.50 Matches: 53
Percent Similarity: 96.5% Conservative: 2
Best Local Similarity: 93.0% Mismatches: 1
Query Match: 90.2% Indels: 1
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x AB001554 (1-282)

QY 1 MetAlaSerSerMetLeuSerSerAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 39 ATGGCTTCCTCTGTTCTTTCTCTGAGCAGTTGCCACTCGCACCAATGTTCTCAAGCT 98
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 99 AACATGGTTGCACCTTTCTAGTCTGCTGCTCAATCCCTGTTTCAAGGAAG 158
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db 159 CAAAACCTTGACATCACTTCCTAGCTAGCAATGGTGAAGAGTGCAATGC 209

RESULT 6
CV016732 288 bp mRNA linear EST 19-AUG-2004
tbt 002004 Normalized Nicotiana tabacum cDNA library Nicotiana
tabacum cDNA clone tbt_002004 5', mRNA sequence.
ACCESSION CV016732
VERSION CV016732.1 GI:51455084
KEYWORDS EST.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 288)
Li,W.Z., Jin,Q.C., Wang,S., Dai,C.E., Zeng,Z.L., Wang,Y.Q.,
Dong,Y., Shao,Y., Li,Y.P., Lu,X.P., Montero,D.C., Alvarez,S.P.,
Dong,H.T. and Li,D.B.
Large-scale identification of ESTs from Nicotiana tabacum by
normalized cDNA library sequencing
Contact: Wenzheng Li,Yan Shao,Yongping Li,Xiuping Lu,Limin
Song,Haitao Dong,Debao Li
The Tobacco Science Research Institute of Yunnan Province; Yunnan
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene
Network Research Group, Zhejiang University
The Tobacco Science Research Institute of Yunnan Province, Yuxi
653100, China
Email: webmaster@estarray.org, URL: http://www.estarray.org
Only the high quality region of sequence was submitted.
Seq primer: M13.
Location/Qualifiers
1..288
/organism="Nicotiana tabacum"
/mol_type="mRNA"
/db_xref="taxon:4097"
/clone="tbt_002004"
/tissue_type="Mixed"
/clone_lib="Normalized Nicotiana tabacum cDNA library"
/note="Vector: pBS-SK+"

ORIGIN
Alignment Scores:
Pred. No.: 7.4e-23 Length: 288
Score: 244.50 Matches: 53
Percent Similarity: 96.5% Conservative: 2
Best Local Similarity: 93.0% Mismatches: 1
Query Match: 90.2% Indels: 1

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DB: 7 Gaps: 1
US-10-628-525A-33 (1-56) x CV016732 (1-288)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
   |||
Db 2 ATGGCTTCCTCTGACTTCTCTGAGCAGTTGCCACTGACCAATGTTGCAAGCT 61

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
   ::|
Db 62 AACATGGTTGCACCTTTCACTGGTCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 121

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
   |||
Db 122 CAACACCTTGACATCACTTCATTCCTAGCAATGGTGAAGAGTGAATGC 172

RESULT 7
LOCUS CV019439
DEFINITION tbt_002022 Normalized Nicotiana tabacum cDNA library Nicotiana
ACCESSION CV019439
VERSION tbt_002022 5', mRNA sequence.
KEYWORDS EST.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum

REFERENCE 1 (bases 1 to 324)
AUTHORS Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,
Dong, H.T. and Li, D.B.
TITLE Large-scale identification of ESTs from Nicotiana tabacum by
normalized cDNA library sequencing
JOURNAL Unpublished (2004)
COMMENT Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin
Song, Haitao Dong, Debao Li
The Tobacco Science Research Institute of Yunnan Province; Yunnan
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene
Network Research Group, Zhejiang University
The Tobacco Science Research Institute of Yunnan Province, Yuxi
653100, China
Email: webmaster@estarray.org, URL: http://www.estarray.org
Only the high quality region of sequence was submitted.
Seq primer: M13.

FEATURES
source
1..324
/organism="Nicotiana tabacum"
/mol_type="mRNA"
/db_xref="taxon:4097"
/clone="tbt_002022"
/tissue_type="Mixed"
/clone_lib="Normalized Nicotiana tabacum cDNA library"
/note="Vector: pBS-SK+."

ORIGIN
Alignment Scores:
Pred. No.: 8.59e-23 Length: 324
Score: 244.50 Matches: 53
Percent Similarity: 96.5% Conservative: 2
Best Local Similarity: 93.0% Mismatches: 1
Query Match: 90.2% Indels: 1
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV019439 (1-324)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
   |||
Db 53 ATGGCTTCCTCTGACTTCTCTGAGCAGTTGCCACTGACCAATGTTGCTCAAGCT 112

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
   ::|

DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV017891 (1-326)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
   |||
Db 44 ATGGCTTCCTCTGACTTCTCTGAGCAGTTGCCACTGACCAATGTTGCTCAAGCT 103

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
   ::|
Db 104 AACATGGTTGCACCTTCATTCCTAGCTGCCTCATTCCTGTTTCAAGGAAG 163

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
   |||
Db 164 CAACACCTTGACATCACTTCATTCCTAGCAATGGTGAAGAGTGAATGC 214

RESULT 9
LOCUS CV017891
DEFINITION tbt_008734 Normalized Nicotiana tabacum cDNA library Nicotiana
ACCESSION CV017891
VERSION tbt_008734 5', mRNA sequence.
KEYWORDS EST.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum

REFERENCE 1 (bases 1 to 326)
AUTHORS Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,
Dong, H.T. and Li, D.B.
TITLE Large-scale identification of ESTs from Nicotiana tabacum by
normalized cDNA library sequencing
JOURNAL Unpublished (2004)
COMMENT Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin
Song, Haitao Dong, Debao Li
The Tobacco Science Research Institute of Yunnan Province; Yunnan
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene
Network Research Group, Zhejiang University
The Tobacco Science Research Institute of Yunnan Province, Yuxi
653100, China
Email: webmaster@estarray.org, URL: http://www.estarray.org
Only the high quality region of sequence was submitted.
Seq primer: M13.

FEATURES
source
1..326
/organism="Nicotiana tabacum"
/mol_type="mRNA"
/db_xref="taxon:4097"
/clone="tbt_008734"
/tissue_type="Mixed"
/clone_lib="Normalized Nicotiana tabacum cDNA library"
/note="Vector: pBS-SK+."

ORIGIN
Alignment Scores:
Pred. No.: 8.66e-23 Length: 326
Score: 244.50 Matches: 53
Percent Similarity: 96.5% Conservative: 2
Best Local Similarity: 93.0% Mismatches: 1
Query Match: 90.2% Indels: 1
DB: 7 Gaps: 1

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tabacum cDNA clone tbt\_011159 5', mRNA sequence.  
CV016591 GI:51454943  
EST.  
Nicotiana tabacum (common tobacco)  
Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 331)  
Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P., Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q., Dong, H.T. and Li, D.B.  
Large-scale identification of ESTs from Nicotiana tabacum by normalized cDNA library sequencing  
Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan Provincial Tobacco Group Dali Branch; Bioinformatics and Gene Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi 653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.  
Location/Qualifiers  
source  
1..331  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_011159"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+."  
ORIGIN  
Alignment Scores:  
Pred. No.: 8,83e-23 Length: 331  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservatives: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1  
US-10-628-525A-33 (1-56) x CV016591 (1-331)  
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 40 ATGGCTTCCTCTGTACTTTCTCTGAGCAGTTGCCACTCGCACTAATGTTGCTCAAGCT 99  
QY 21 SerMetValAlaProPheThrGlyLeuLySerAlaAla---PheProValSerArgLyS 39  
Db 100 AACATGGTTGCACCTTTCACTGCTTAAGTCAGCTGCCTCATCTTCCTGTTCAAGGAAG 159  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 160 CAAACCTTGACATCACTTCCTTCCATTGCTAGCAATGGTGAAGAGTGCAATGC 210  
RESULT 10  
CV019882  
LOCUS  
DEFINITION  
tbt\_006241 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum cDNA clone tbt\_006241 5', mRNA sequence.  
CV019882  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Nicotiana tabacum (common tobacco)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 333)  
CV019882  
tbt\_006241 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum cDNA clone tbt\_006241 5', mRNA sequence.  
CV019882  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Nicotiana tabacum (common tobacco)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 333)

AUTHORS  
Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P., Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q., Dong, H.T. and Li, D.B.  
Large-scale identification of ESTs from Nicotiana tabacum by normalized cDNA library sequencing  
Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan Provincial Tobacco Group Dali Branch; Bioinformatics and Gene Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi 653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.  
Location/Qualifiers  
source  
1..333  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_006241"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+."  
ORIGIN  
Alignment Scores:  
Pred. No.: 8,89e-23 Length: 333  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservatives: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1  
US-10-628-525A-33 (1-56) x CV019882 (1-333)  
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 47 ATGGCTTCCTCTGTCTTCTCTGAGCAGTTGCCACTCGCACTAATGTTGCTCAAGCT 106  
QY 21 SerMetValAlaProPheThrGlyLeuLySerAlaAla---PheProValSerArgLyS 39  
Db 107 AACATGGTTGCACCTTTCACTGCTTAAGTCAGCTGCCTCATCTTCCTGTTCAAGGAAG 166  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 167 CAAACCTTGACATCACTTCCTTCCATTGCTAGCAATGGTGAAGAGTGCAATGC 217  
RESULT 11  
CV019568  
LOCUS  
DEFINITION  
tbt\_006054 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum cDNA clone tbt\_006054 5', mRNA sequence.  
CV019568  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Nicotiana tabacum (common tobacco)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 341)  
Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P., Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q., Dong, H.T. and Li, D.B.  
Large-scale identification of ESTs from Nicotiana tabacum by normalized cDNA library sequencing  
Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan Provincial Tobacco Group Dali Branch; Bioinformatics and Gene

Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: <http://www.estarray.org>  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

#### FEATURES

source  
1. .341  
Location/Qualifiers  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clones="tbt\_006054"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

#### ORIGIN

Alignment Scores:  
Pred. No.: 9.16e-23 Length: 341  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV019558 (1-341)

QY 1 MetAlaSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
|||||:::|||||  
Db 40 ATGGCTTCCTCTGTTCTTCTCTGCAGCAGTTGCCACTCGCACCATTGTTCTCAAGCT 99  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
:::|||||  
Db 100 AACATGGTTGCACCTTTCACTGGTCTTAAGTCAGCTGCCTCAATTCCTGTTTCAAGGAAG 159  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
|||||  
Db 160 CAAACCTTGACATCACTTCATGCTAGCAATGGTGAAGAGTGCAATGC 210

#### RESULT 12

CV021773  
LOCUS  
DEFINITION  
tbt\_006135 Normalized Nicotiana tabacum cDNA library Nicotiana  
CV021773  
VERSION  
CV021773.1 GI:51463281  
EST.

SOURCE  
Nicotiana tabacum (common tobacco)

#### ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.

#### REFERENCE

AUTHORS  
Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.

TITLE  
Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing

#### JOURNAL

COMMENT  
Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin  
Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan  
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: <http://www.estarray.org>  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

#### FEATURES

source  
1. .348  
Location/Qualifiers  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"

/db\_xref="taxon:4097"  
/clones="tbt\_006135"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

#### ORIGIN

Alignment Scores:  
Pred. No.: 9.4e-23 Length: 348  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV021773 (1-348)

QY 1 MetAlaSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
|||||:::|||||  
Db 21 ATGGCTTCCTCTGTTCTTCTCTGCAGCAGTTGCCACTCGCACCATTGTTCTCAAGCT 80  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
:::|||||  
Db 81 AACATGGTTGCACCTTTCACTGGTCTTAAGTCAGCTGCCTCAATTCCTGTTTCAAGGAAG 140  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
|||||  
Db 141 CAAACCTTGACATCACTTCATGCTAGCAATGGTGAAGAGTGCAATGC 191

#### RESULT 13

#### LOCUS

DEFINITION  
tbt\_004103 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum cDNA clone tbt\_004103 5', mRNA sequence.

#### ACCESSION

CV016438

#### VERSION

CV016438.1 GI:51454790

#### KEYWORDS

EST.

#### SOURCE

Nicotiana tabacum (common tobacco)

#### ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.

#### REFERENCE

#### AUTHORS

Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.

#### TITLE

Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing

#### JOURNAL

#### COMMENT

Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin  
Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan  
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: <http://www.estarray.org>  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

#### FEATURES

#### source

1. .362  
Location/Qualifiers  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_004103"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

#### ORIGIN

Alignment Scores:  
Pred. No.: 9.88e-23 Length: 362  
Score: 244.50 Matches: 53

Percent Similarity: 96.5%  
 Best Local Similarity: 93.0%  
 Query Match: 90.2%  
 DB: 7

US-10-628-525A-33 (1-56) x CV016438 (1-362)

QY 1 MetAlaSerSerMetLeuSerAlaAlaValAlaThraArgThrAsnProAlaGlnAla 20  
 |||  
 Db 39 ATGGCTTCCTCTGTTCTTCCCTGAGAGTTGCCACTCGCACCAATGTTGCTCAAGCT 98  
 ::|  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 ::|  
 Db 99 AACATGGTTGCACCTTTCACCTGCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 158  
 |||  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 |||  
 Db 159 CAAACCTTGACATCACTTCCATTGCTAGCAATGGTGAAGAGTGCAATGC 209  
 |||

RESULT 14  
 CV016988  
 LOCUS  
 DEFINITION  
 tbt\_004320 Normalized Nicotiana tabacum cDNA library Nicotiana  
 tabacum cDNA clone tbt\_004320 5', mRNA sequence.  
 CV016988  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Nicotiana tabacum (common tobacco)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 asterids; lamids; Solanales; Solanaceae; Nicotiana.  
 REFERENCE  
 AUTHORS  
 Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
 Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
 Dong, H.T. and Li, D.B.  
 TITLE  
 Large-scale identification of ESTs from Nicotiana tabacum by  
 normalized cDNA library sequencing  
 JOURNAL  
 COMMENT  
 Unpublished (2004)  
 Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin  
 Song, Haitao Dong, Debao Li  
 The Tobacco Science Research Institute of Yunnan Province; Yunnan  
 Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
 Network Research Group, Zhejiang University  
 The Tobacco Science Research Institute of Yunnan Province, Yuxi  
 653100, China  
 Email: webmaster@estarray.org, URL: http://www.estarray.org  
 Only the high quality region of sequence was submitted.  
 Seq primer: M13.

FEATURES  
 source  
 1..364  
 /organism="Nicotiana tabacum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4097"  
 /clone="tbt\_004320"  
 /issue\_type="Mixed"  
 /clone\_lib="Normalized Nicotiana tabacum cDNA library"  
 /note="Vector: pBS-SK+."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 9,95E-23 Length: 364  
 Score: 244.50 Matches: 53  
 Percent Similarity: 96.5% Conservative: 2  
 Best Local Similarity: 93.0% Mismatches: 1  
 Query Match: 90.2% Indels: 1  
 DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV016988 (1-364)

QY 1 MetAlaSerSerMetLeuSerAlaAlaValAlaThraArgThrAsnProAlaGlnAla 20  
 |||  
 Db 41 ATGGCTTCCTCTGTTCTTCCCTGAGAGTTGCCACTCGCACCAATGTTGCTCAAGCT 100  
 |||

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 ::|  
 Db 101 AACATGGTTGCACCTTTCACCTGCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 160  
 |||  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 |||  
 Db 161 CAAACCTTGACATCACTTCCATTGCTAGCAATGGTGAAGAGTGCAATGC 211  
 |||

RESULT 15  
 CV017159  
 LOCUS  
 DEFINITION  
 tbt\_011057 Normalized Nicotiana tabacum cDNA library Nicotiana  
 tabacum cDNA clone tbt\_011057 5', mRNA sequence.  
 CV017159  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Nicotiana tabacum (common tobacco)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE  
 AUTHORS  
 Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
 Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
 Dong, H.T. and Li, D.B.  
 TITLE  
 Large-scale identification of ESTs from Nicotiana tabacum by  
 normalized cDNA library sequencing  
 JOURNAL  
 COMMENT  
 Unpublished (2004)  
 Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin  
 Song, Haitao Dong, Debao Li  
 The Tobacco Science Research Institute of Yunnan Province; Yunnan  
 Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
 Network Research Group, Zhejiang University  
 The Tobacco Science Research Institute of Yunnan Province, Yuxi  
 653100, China  
 Email: webmaster@estarray.org, URL: http://www.estarray.org  
 Only the high quality region of sequence was submitted.  
 Seq primer: M13.

FEATURES  
 source  
 1..369  
 /organism="Nicotiana tabacum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4097"  
 /clone="tbt\_011057"  
 /issue\_type="Mixed"  
 /clone\_lib="Normalized Nicotiana tabacum cDNA library"  
 /note="Vector: pBS-SK+."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.01E-22 Length: 369  
 Score: 244.50 Matches: 53  
 Percent Similarity: 96.5% Conservative: 2  
 Best Local Similarity: 93.0% Mismatches: 1  
 Query Match: 90.2% Indels: 1  
 DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV017159 (1-369)

QY 1 MetAlaSerSerMetLeuSerAlaAlaValAlaThraArgThrAsnProAlaGlnAla 20  
 |||  
 Db 34 ATGGCTTCCTCTGTTCTTCCCTGAGAGTTGCCACTCGCACCAATGTTGCTCAAGCT 93  
 ::|  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 ::|  
 Db 94 AACATGGTTGCACCTTTCACCTGCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 153  
 |||  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 |||  
 Db 154 CAAACCTTGACATCACTTCCATTGCTAGCAATGGTGAAGAGTGCAATGC 204  
 |||  
 RESULT 16

CV019231  
LOCUS  
DEFINITION tbt\_009718 Normalized Nicotiana tabacum cDNA library Nicotiana  
CV019231  
ACCESSION CV019231.1 GI:51457583  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Nicotiana tabacum (common tobacco)

REFERENCE  
AUTHORS Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, H.T., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.  
TITLE Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
JOURNAL  
COMMENT Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin  
Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan  
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

FEATURES  
source  
1..371  
/organism="Nicotiana tabacum"  
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/tissue type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

ORIGIN  
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Pred. No.: 1,02e-22 Length: 371  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV019231 (1-371)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 41 ATGGCTTCCTCTGTTCTTCTCTGAGCAGTTGGCCACTGCGACCAATGTTGCTCAAGCT 100

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 101 AACATGGTTGCACCTTTCATCGTCTTAAGTCAGCTGCCTCATCTGTTTCAAGGAAG 160

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 161 CAAACCTTGACATCACTTCCATGCTAGCAATGGTGAAGAGTGCAATGC 211

RESULT 17  
CV021480  
LOCUS  
DEFINITION tbt\_011140 Normalized Nicotiana tabacum cDNA library Nicotiana  
CV021480  
ACCESSION CV021480.1 GI:51462998  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Nicotiana tabacum (common tobacco)

REFERENCE  
AUTHORS Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, H.T., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.  
TITLE Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
JOURNAL  
COMMENT Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 386)  
Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, H.T., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.  
TITLE Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
JOURNAL  
COMMENT Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin  
Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan  
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

FEATURES  
source  
1..386  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_011140"  
/tissue type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.07e-22 Length: 386  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV021480 (1-386)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 42 ATGGCTTCCTCTGTTCTTCTCTGAGCAGTTGGCCACTGCGACCAATGTTGCTCAAGCT 101

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 102 AACATGGTTGCACCTTTCATCGTCTTAAGTCAGCTGCCTCATCTGTTTCAAGGAAG 161

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 162 CAAACCTTGACATCACTTCCATGCTAGCAATGGTGAAGAGTGCAATGC 212

RESULT 18  
CV016216  
LOCUS  
DEFINITION tbt\_011065 Normalized Nicotiana tabacum cDNA library Nicotiana  
CV016216  
ACCESSION CV016216.1 GI:51454568  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Nicotiana tabacum (common tobacco)

REFERENCE  
AUTHORS Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, H.T., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.  
TITLE Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
JOURNAL  
COMMENT Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin

REFERENCE  
AUTHORS Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, H.T., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.  
TITLE Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
JOURNAL  
COMMENT Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin

Song,Haitao Dong,Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan  
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

FEATURES  
source  
1. .387  
Location/Qualifiers  
/organism="Nicotiana tabacum"  
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/db\_xref="taxon:4097"  
/clone="tbt\_011065"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.08e-22 Length: 387  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV016216 (1-387)  
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
|||||:::|||||  
Db 47 ATGGCTTCCTCTGTTCTTCTCTGAGCAGTTGCCACTCGCACCATTGTCCTCAAGCT 106  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
:::|||||  
Db 107 AACATGGTTGCACCTTTCATCTGCTTAAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 166  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
|||||  
Db 167 CAAACCTTTGACATCATCTCCATTGCTAGCAATGGTGAAGAGTGCAATGC 217

RESULT 19  
CV016980  
LOCUS  
DEFINITION  
tabacum cDNA clone tbt\_011231 5', mRNA sequence.  
ACCESSION  
CV016980  
VERSION  
CV016980.1 GI:51455332  
KEYWORDS  
EST.  
SOURCE  
Nicotiana tabacum (common tobacco)

ORGANISM  
Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE  
AUTHORS  
Li,W.Z., Shao,Y., Li,Y.P., Lu,X.P., Montero,D.C., Alvarez,S.P.,  
Deng,Y., Jin,Q.C., Wang,S., Dai,C.E., Zeng,Z.L., Wang,Y.Q.,  
Dong,H.T. and Li,D.B.  
Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
Unpublished (2004)

JOURNAL  
COMMENT  
Contact: Wenzheng Li,Yan Shao,Yongping Li,Xiuping Lu,Limin  
Song,Haitao Dong,Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan  
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China

FEATURES  
source  
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/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_011065"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.08e-22 Length: 387  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

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/db\_xref="taxon:4097"  
/clone="tbt\_011231"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.14e-22 Length: 404  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV016980 (1-404)  
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
|||||:::|||||  
Db 57 ATGGCTTCCTCTGTTCTTCTCTGAGCAGTTGCCACTCGCACCATTGTCCTCAAGCT 116  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
:::|||||  
Db 117 AACATGGTTGCACCTTTCATCTGCTTAAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 176

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
|||||  
Db 177 CAAACCTTTGACATCATCTCCATTGCTAGCAATGGTGAAGAGTGCAATGC 227  
RESULT 20  
CV017309  
LOCUS  
DEFINITION  
tbt\_002756 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum cDNA clone tbt\_002756 5', mRNA sequence.  
ACCESSION  
CV017309  
VERSION  
CV017309.1 GI:51455661  
KEYWORDS  
EST.  
SOURCE  
Nicotiana tabacum (common tobacco)

ORGANISM  
Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE  
AUTHORS  
Li,W.Z., Shao,Y., Li,Y.P., Lu,X.P., Montero,D.C., Alvarez,S.P.,  
Deng,Y., Jin,Q.C., Wang,S., Dai,C.E., Zeng,Z.L., Wang,Y.Q.,  
Dong,H.T. and Li,D.B.  
Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
Unpublished (2004)

JOURNAL  
COMMENT  
Contact: Wenzheng Li,Yan Shao,Yongping Li,Xiuping Lu,Limin  
Song,Haitao Dong,Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan  
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China

FEATURES  
source  
1. .412  
Location/Qualifiers  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_002756"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.14e-22 Length: 404  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV016980 (1-404)  
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
|||||:::|||||  
Db 57 ATGGCTTCCTCTGTTCTTCTCTGAGCAGTTGCCACTCGCACCATTGTCCTCAAGCT 116  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
:::|||||  
Db 117 AACATGGTTGCACCTTTCATCTGCTTAAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 176



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Alignment Scores:
Pred. No.: 1.16e-22 Length: 412
Score: 244.50 Matches: 53
Percent Similarity: 96.5% Conservative: 2
Best Local Similarity: 93.0% Mismatches: 1
Query Match: 90.2% Indels: 1
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV017309 (1-412)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20
Db 70 ATGGCTTCCTCTGTTCTTTCTCTGAGCAGTTCGCCACTGCGACCAATGTTGCTCAAGCT 129

Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 130 AACATGTTGCACCTTTTCACTGGTCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 189

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 190 CAAACCTTGACATCACTTCCTATGCTAGCAATGTTGGAAGAGTGCAATGC 240

RESULT 21
CV021557 422 bp mRNA linear EST 19-AUG-2004
LOCUS tbt_007663 Normalized Nicotiana tabacum cDNA library Nicotiana
DEFINITION tbt_007663 Normalized Nicotiana tabacum cDNA library Nicotiana
ACCESSION CV021557
VERSION 1
KEYWORDS EST.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum

REFERENCE
AUTHORS Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 422)
Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,
Dong, H.T. and Li, D.B.
Large-scale identification of ESTs from Nicotiana tabacum by
normalized cDNA library sequencing
Unpublished (2004)
CONTACT: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin
Song, Haitao Dong, Debao Li
The Tobacco Science Research Institute of Yunnan Province; Yunnan
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene
Network Research Group, Zhejiang University
The Tobacco Science Research Institute of Yunnan Province, Yuxi
653100, China
Email: webmaster@estarray.org, URL: http://www.estarray.org
Only the high quality region of sequence was submitted.
Seq primer: M13.

FEATURES
source
1..422
/organism="Nicotiana tabacum"
/mol_type="mRNA"
/db_xref="taxon:4097"
/clone="tbt_007663"
/tissue_type="Mixed"
/clone_lib="Normalized Nicotiana tabacum cDNA library"
/note="Vector: pBS-SK+"

ORIGIN
Alignment Scores:
Pred. No.: 1.2e-22 Length: 422
Score: 244.50 Matches: 53
Percent Similarity: 96.5% Conservative: 2
Best Local Similarity: 93.0% Mismatches: 1
Query Match: 90.2% Indels: 1
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV021557 (1-422)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20
Db 60 ATGGCTTCCTCTGTTCTTTCTCTGAGCAGTTCGCCACTGCGACCAATGTTGCTCAAGCT 119

Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 120 AACATGTTGCACCTTTTCACTGGTCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 179

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 164 CAAACCTTGACATCACTTCCTATGCTAGCAATGTTGGAAGAGTGCAATGC 214

RESULT 22
CV017696 428 bp mRNA linear EST 19-AUG-2004
LOCUS tbt_004704 Normalized Nicotiana tabacum cDNA library Nicotiana
DEFINITION tbt_004704 Normalized Nicotiana tabacum cDNA library Nicotiana
ACCESSION CV017696
VERSION 1
KEYWORDS EST.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum

REFERENCE
AUTHORS Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 428)
Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,
Dong, H.T. and Li, D.B.
Large-scale identification of ESTs from Nicotiana tabacum by
normalized cDNA library sequencing
Unpublished (2004)
CONTACT: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin
Song, Haitao Dong, Debao Li
The Tobacco Science Research Institute of Yunnan Province; Yunnan
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene
Network Research Group, Zhejiang University
The Tobacco Science Research Institute of Yunnan Province, Yuxi
653100, China
Email: webmaster@estarray.org, URL: http://www.estarray.org
Only the high quality region of sequence was submitted.
Seq primer: M13.

FEATURES
source
1..428
/organism="Nicotiana tabacum"
/mol_type="mRNA"
/db_xref="taxon:4097"
/clone="tbt_004704"
/tissue_type="Mixed"
/clone_lib="Normalized Nicotiana tabacum cDNA library"
/note="Vector: pBS-SK+"

ORIGIN
Alignment Scores:
Pred. No.: 1.22e-22 Length: 428
Score: 244.50 Matches: 53
Percent Similarity: 96.5% Conservative: 2
Best Local Similarity: 93.0% Mismatches: 1
Query Match: 90.2% Indels: 1
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV017696 (1-428)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20
Db 60 ATGGCTTCCTCTGTTCTTTCTCTGAGCAGTTCGCCACTGCGACCAATGTTGCTCAAGCT 119

Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 120 AACATGTTGCACCTTTTCACTGGTCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 179

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 164 CAAACCTTGACATCACTTCCTATGCTAGCAATGTTGGAAGAGTGCAATGC 214

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Db 180 CAAAACCTTGACATCACTTCCATTGCTAGCAATGCTGGAAGAGTGCATGTC 230

RESULT 23  
CV018759  
LOCUS  
DEFINITION tbt\_001767 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum cDNA clone tbt\_001767 5', mRNA sequence.  
ACCESSION CV018759  
VERSION CV018759.1 GI:51457111  
KEYWORDS EST  
SOURCE Nicotiana tabacum (common tobacco)  
ORGANISM Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.  
REFERENCE 1 (bases 1 to 431)  
AUTHORS Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.  
TITLE Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
JOURNAL Unpublished (2004)  
COMMENT Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin  
Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan  
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

FEATURES  
Location/Qualifiers  
source 1..431  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_001767"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+."

ORIGIN  
Alignment Scores:  
Pred. No.: 1,23e-22 Length: 431  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV018759 (1-431)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 45 ATGGCTTCCTCTGTACTTTCCCTGAGCAGTTGCCACTCGCAATGTTGCTCAAGCT 104  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 105 AACATGGTTGGACCTTTTCACTGGTTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 164  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 165 CAAAACCTTGACATCACTTCCATTGCTAGCAATGCTGGAAGAGTGCATGTC 215

RESULT 24  
CV021294  
LOCUS  
DEFINITION tbt\_007662 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum cDNA clone tbt\_007662 5', mRNA sequence.  
ACCESSION CV021294  
VERSION CV021294.1 GI:51462802  
KEYWORDS EST

SOURCE Nicotiana tabacum (common tobacco)  
ORGANISM Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.  
REFERENCE 1 (bases 1 to 431)  
AUTHORS Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.  
TITLE Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
JOURNAL Unpublished (2004)  
COMMENT Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin  
Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan  
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

FEATURES  
Location/Qualifiers  
source 1..431  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_007662"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+."

ORIGIN  
Alignment Scores:  
Pred. No.: 1,23e-22 Length: 431  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV021294 (1-431)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 60 ATGGCTTCCTCTGTACTTTCCCTGAGCAGTTGCCACTCGCAATGTTGCTCAAGCT 119  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 120 AACATGGTTGGACCTTTTCACTGGTTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 179  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 180 CAAAACCTTGACATCACTTCCATTGCTAGCAATGCTGGAAGAGTGCATGTC 230

RESULT 25  
CV020505  
LOCUS  
DEFINITION tbt\_003364 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum cDNA clone tbt\_003364 5', mRNA sequence.  
ACCESSION CV020505  
VERSION CV020505.1 GI:51462013  
KEYWORDS EST  
SOURCE Nicotiana tabacum (common tobacco)  
ORGANISM Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.  
REFERENCE 1 (bases 1 to 440)  
AUTHORS Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.  
TITLE Large-scale identification of ESTs from Nicotiana tabacum by

normalized cDNA library sequencing  
Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan Provincial Tobacco Group Dali Branch; Bioinformatics and Gene Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi 653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

FEATURES  
source  
1. .440  
Location/Qualifiers  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_003364"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

## ORIGIN

Alignment Scores:  
Pred. No.: 1,27e-22 Length: 440  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV020505 (1-440)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db ATGGCTTCCTCTGTTCTTTCTCTGAGCAGTTGCCACTCGCACCATTGTTGCTCAAGCT 106  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAala---PheProValSerArgLys 39  
Db AACATGGTTGCACCTTTCATCTGCTTAAGTCAGCTGCCTCAATTCCTGTTTCAAGGAAG 166  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db CAAAACCTTGACATCATCTTCCATTGCTAGCAATGGTGAAGAGTGCATGC 217

RESULT 26  
CV020326  
LOCUS  
DEFINITION  
tbt\_002849 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum cDNA clone tbt\_002849 5', mRNA sequence.  
CV020326  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Nicotiana tabacum (common tobacco)

CV020326 443 bp mRNA linear EST 19-AUG-2004  
tbt\_002849 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum cDNA clone tbt\_002849 5', mRNA sequence.  
CV020326.1 GI:51461834  
EST.  
Nicotiana tabacum (common tobacco)

REFERENCE  
AUTHORS  
Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.  
Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
Unpublished (2004)

JOURNAL  
COMMENT  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan Provincial Tobacco Group Dali Branch; Bioinformatics and Gene Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi 653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org

Only the high quality region of sequence was submitted.  
Seq primer: M13.

FEATURES  
source  
1. .443  
Location/Qualifiers  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_002849"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

## ORIGIN

Alignment Scores:  
Pred. No.: 1,28e-22 Length: 443  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV020326 (1-443)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db ATGGCTTCCTCTGTTCTTTCTCTGAGCAGTTGCCACTCGCACCATTGTTGCTCAAGCT 107  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAala---PheProValSerArgLys 39  
Db AACATGGTTGCACCTTTCATCTGCTTAAGTCAGCTGCCTCAATTCCTGTTTCAAGGAAG 167  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db CAAAACCTTGACATCATCTTCCATTGCTAGCAATGGTGAAGAGTGCATGC 218

## RESULT 27

CV021799  
LOCUS  
DEFINITION  
tbt\_007702 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum cDNA clone tbt\_007702 5', mRNA sequence.  
CV021799  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Nicotiana tabacum (common tobacco)

CV021799 443 bp mRNA linear EST 19-AUG-2004  
tbt\_007702 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum cDNA clone tbt\_007702 5', mRNA sequence.  
CV021799.1 GI:51463307  
EST.  
Nicotiana tabacum (common tobacco)

REFERENCE  
AUTHORS  
Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.  
Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
Unpublished (2004)

JOURNAL  
COMMENT  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan Provincial Tobacco Group Dali Branch; Bioinformatics and Gene Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi 653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.

Seq primer: M13.

FEATURES  
source  
1. .443  
Location/Qualifiers

/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
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/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"



QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
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Db 164 CAAACCTTGACATTACCTGCTAGCAATGCTGGAAGAGTTCATATGC 214

RESULT 30  
CV019815  
LOCUS 460 bp mRNA linear EST 19-AUG-2004  
DEFINITION tbt\_004829 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum cDNA clone tbt\_004829 5', mRNA sequence.  
CV019815  
ACCESSION CV019815  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Nicotiana tabacum (common tobacco)  
Nicotiana tabacum  
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamiids; Solanales; Solanaceae; Nicotiana.  
REFERENCE 1 (bases 1 to 460)  
AUTHORS Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T., and Li, D.B.  
TITLE Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
JOURNAL Unpublished (2004)  
COMMENT Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin  
Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan  
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: <http://www.estarray.org>  
Only the high quality region of sequence was submitted.  
Seq primer: M13.  
FEATURES  
source  
1..460  
Location/Qualifiers  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_004829"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.34e-22 Length: 460  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV019815 (1-460)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
|||||  
Db 47 ATGGCTTCCTCTGTTCTTCTCTGAGCAGTGGCCACTGCCACCAATGTTGCTCAAGCT 106

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
:::|||||  
Db 107 AACATGGTTGCACCTTTCACCTGCTTAACTGCTCAAGTCGCTCATTCCTGTTTCAGGAAG 166

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
|||||  
Db 167 CAAACCTTGACATCACTTCCTGCTAGCAATGCTGGAAGAGTTCATATGC 217

Search completed: April 1, 2006, 19:23:02  
Job time : 904.068 secs

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 31, 2006, 22:47:42 ; Search time 74.8932 Seconds  
(without alignments)

1329.139 Million cell updates/sec  
(without alignments)

**Title:** US-10-628-525A-33

**Perfect score: 271**

Sequence: 1 MASSMLSSAAVATRTNPAQA.....SRKQNLDTSIASNGGRVQC 56

**Scoring table:**

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

robust processing: Minimum Match 0%  
Maximum Match 100%

Maximum Match 100%  
Listing first 150 summaries

**Command line parameters:**

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-QB/abseq/ABSSWB.spool-US10628525/runat.31032006.095123.16858/app_query.fasta.1
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blotsum62 -TRANS=human40.cdi
-LIST=150 -LOCALING=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=30
-MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abs802p -USER=US10628525 -OCGN_1_1_555_orunat.31032006.095123.16858
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCKS=100 -LONGLOG
-DEVTIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Database : Issued Patents NA:\*

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1: /csm2_6/pdata/1/ina/1 COMB.seq.*
2: /csm2_6/pdata/1/ina/5 COMB.seq.*
3: /csm2_6/pdata/1/ina/6A COMB.seq.*
4: /csm2_6/pdata/1/ina/6B COMB.seq.*
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6: /csm2_6/pdata/1/ina/7 COMB.seq.*
7: /csm2_6/pdata/1/ina/PP CRUS COMB.seq.*
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9: /csm2_6/pdata/1/ina/backfiles1.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query |        | DB | ID                | Description        |
|------------|-------|-------|--------|----|-------------------|--------------------|
|            |       | Match | Length |    |                   |                    |
| 1          | 240.5 | 88.7  | 177    | 2  | US-08-095-726-12  | Sequence 12, April |
| 2          | 240.5 | 88.7  | 177    | 2  | US-08-096-043-12  | Sequence 12, April |
| 3          | 240.5 | 88.7  | 177    | 2  | US-08-093-577-8   | Sequence 8, April  |
| 4          | 240.5 | 88.7  | 177    | 2  | US-08-331-004A-6  | Sequence 6, April  |
| 5          | 240.5 | 88.7  | 177    | 2  | US-08-096-622A-12 | Sequence 12, April |
| 6          | 240.5 | 88.7  | 177    | 6  | PCT-US95-13937A-6 | Sequence 6, April  |
| 7          | 240.5 | 88.7  | 204    | 3  | US-09-839-477-3   | Sequence 3, April  |
| 8          | 240.5 | 88.7  | 499    | 3  | US-09-495-797-41  | Sequence 41, April |
| 9          | 240.5 | 88.7  | 1442   | 2  | US-08-152-483B-8  | Sequence 8, April  |

Sequence 15, Appl  
Sequence 36, Appl  
Sequence 36, Appl  
Sequence 32, Appl  
Sequence 14, Appl  
Sequence 14, Appl  
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Sequence 33, Appl  
Sequence 29, Appl  
Sequence 41, Appl  
Sequence 42, Appl  
Sequence 8, Appl  
Sequence 8, Appl  
Sequence 8, Appl  
Sequence 1360, Ap  
Sequence 16642, A  
Sequence 12486, A  
Sequence 35, Appl  
Sequence 32, Appl  
Sequence 28, Appl  
Sequence 40, Appl  
Sequence 125, App  
Sequence 32, Appl  
Sequence 29, Appl  
Sequence 25, Appl  
Sequence 37, Appl  
Sequence 1, Appl  
Sequence 15109, A  
Sequence 15110, A  
Sequence 17409, A  
Sequence 17410, A  
Sequence 5683, Ap  
Sequence 1271, Ap  
Sequence 17524, A  
Sequence 1, Appl

3 US-09-471-573A-15  
2 US-08-095-726-39  
2 US-08-096-043-36  
2 US-08-093-577-32  
3 US-08-447-585-14  
3 US-08-852-340-14  
2 US-08-474-633A-9  
2 US-08-823-771-9  
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## ALIGNMENTS

RESULT 1

US-08-095-726-12  
; Sequence 12, Application US/08095726  
; Patent No. 5530188  
; GENERAL INFORMATION:  
; APPLICANT: Ausich, Rodney L  
; APPLICANT: Brinkhaus, Friedhelm L  
; APPLICANT: Mukharji, Indrani  
; APPLICANT: Proffitt, John H  
; APPLICANT: Yarger, James G  
; APPLICANT: Yen, Huel-Che B  
; TITLE OF INVENTION: Beta-Carotene Biosynthesis in  
; TITLE OF INVENTION: Genetically Engineered Hosts  
; NUMBER OF SEQUENCES: 79  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amoco Corp., Patents and Licensing Dept  
; STREET: 200 E Randolph St  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60680-0703  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/095,726  
; FILING DATE: 21-JUL-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/785,566  
; FILING DATE: 30-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Galloway, No. 5530188val B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 3128567180  
; TELEFAX: 3128564972  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-095-726-12  
Alignment Scores:  
Pred. No.: 4.23e-27 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 2 Gaps: 1  
US-10-628-525A-33 (1-56) x US-08-095-726-12 (1-177)  
Qy 1 MetalSerSerMetLeuSerSerAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 1 ATGGCTTCTCAGTCTTCTCTCTCAGCAGTTCACCCGAGCAATGTTCTCAAGCT 60  
Qy 21 SerMetValAlaProPheThrGlyLeuIysSerAlaAla---PheProValSerArgLys 39  
Db 61 AACATGGTGGCCCTTTCACTGGCCCTTAAGTCAGCTCATTCCCTGTTTCAAGGAAG 120  
Qy 40 GlnAsnLeuAapIleThrSerIleAlaSerAenGlyArgValGlnCys 56  
Db 121 CAAAACCTTGACATCATCTTCCATTGCCACGACGAGAGTGCATGTC 171  
RESULT 2  
US-08-096-043-12  
; Sequence 12, Application US/08096043  
; Patent No. 5530189  
; GENERAL INFORMATION:

APPLICANT: Ausich, Rodney L  
APPLICANT: Brinkhaus, Friedhelm L  
APPLICANT: Mukharji, Indrani  
APPLICANT: Proffitt, John H  
APPLICANT: Yarger, James G  
APPLICANT: Yen, Hwei-Che B  
TITLE OF INVENTION: Lycopen Biosynthesis in Genetically Engineered Hosts  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amoco Corp., Patents and Licensing Dept  
STREET: 200 E Randolph St  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60680-0703  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/096,043  
FILING DATE: 22-JUL-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/785,568  
FILING DATE: 30-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Galloway, No. 5530189val B  
TELEPHONE: 3128567180  
TELEFAX: 3128564972  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-096-043-12

Alignment Scores:  
Pred. No.: 4.23e-27 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 2 Gaps: 1

US-10-628-525A-33 (1-56) x US-08-096-043-12 (1-177)

QY 1 MetAlaSerMetLeuSerSerAlaAlaValAlaThraArgThrAenProAlaGlnAla 20  
Db 1 ATGGCTTCCTCAGTTCTTTCTGCGAGAGTGGCCACCGCAGCAATGTTGCTCAAGCT 60

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 61 AACATGGTGGCGCTTTCACTGCGCTTAAGTCAGCTGCCTCATTCCTCTGTTCAAGGAG 120

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56  
Db 121 CAAACCTTGACATCACTTCCATTGCGCAGCAGCGGGAAGAGTGCATGC 171

RESULT 3  
US-08-093-577-8  
Sequence 8, Application US/08093577  
Patent No. 5545816  
GENERAL INFORMATION:  
APPLICANT: Ausich, Rodney L  
APPLICANT: Brinkhaus, Friedhelm L  
APPLICANT: Mukharji, Indrani  
APPLICANT: Proffitt, John H

APPLICANT: Yarger, James G  
APPLICANT: Yen, Hwei-Che B  
TITLE OF INVENTION: Phytoene Biosynthesis in Genetically Engineered Hosts  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amoco Corp., Patents and Licensing Dept  
STREET: 200 E Randolph St  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60680-0703  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/093,577  
FILING DATE: 19-JUL-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/785,569  
FILING DATE: 30-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Galloway, No. 5545816val B  
TELEPHONE: 3128567180  
TELEFAX: 3128564972  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-093-577-8

Alignment Scores:  
Pred. No.: 4.23e-27 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 2 Gaps: 1

US-10-628-525A-33 (1-56) x US-08-093-577-8 (1-177)

QY 1 MetAlaSerMetLeuSerSerAlaAlaValAlaThraArgThrAenProAlaGlnAla 20  
Db 1 ATGGCTTCCTCAGTTCTTTCTGCGAGAGTGGCCACCGCAGCAATGTTGCTCAAGCT 60

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 61 AACATGGTGGCGCTTTCACTGCGCTTAAGTCAGCTGCCTCATTCCTCTGTTCAAGGAG 120

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56  
Db 121 CAAACCTTGACATCACTTCCATTGCGCAGCAGCGGGAAGAGTGCATGC 171

RESULT 4  
US-08-331-004A-6  
Sequence 6, Application US/08331004A  
Patent No. 5618988  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Randal  
APPLICANT: Eschenfeldt, William H  
APPLICANT: English, Jami  
APPLICANT: Brinkhaus, Friedhelm L  
TITLE OF INVENTION: Enhanced Carotenoid Accumulation  
TITLE OF INVENTION: in Storage Organs of Genetically Engineered Plants  
NUMBER OF SEQUENCES: 9

;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSES: Amoco Corporation, Law Dept  
;/ STREET: 55 Shuman Boulevard, Suite 600  
;/ CITY: Naperville  
;/ STATE: IL  
;/ COUNTRY: USA  
;/ ZIP: 60563-8437  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patent In Release #1.24  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/331,004A  
;/ FILING DATE:  
;/ CLASSIFICATION: 800  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Galloway, No. 5618988val B  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 7087172447  
;/ TELEFAX: 7087172430  
;/ INFORMATION FOR SEQ ID NO: 6:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 177 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: DNA (genomic)  
;/ US-08-331-004A-6

Alignment Scores:  
Pred. No.: 4,23e-27 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 2 Gaps: 1

US-10-628-525A-33 (1-56) x US-08-331-004A-6 (1-177)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 1 ATGGCTTCCTCAGTTCTTCTCTGAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAala---PheProValSerArgLys 39  
Db 61 AACATGGTGGCGCCTTTCACAGCTTAAGTCAGCTGCCTCATTCCTCTTTCAAGGAAG 120  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 121 CAAACCTTGACATCACTTCATTGCCACGACGGGGAAGAGTGCATATGC 171

RESULT 5  
US-08-096-623A-12  
; Sequence 12, Application US/08096623A  
; Patent No. 5684238  
; GENERAL INFORMATION:  
; APPLICANT: Ausich, Rodney L.  
; APPLICANT: Brinkhaus, Friedhelm L.  
; APPLICANT: Mukharji, Indrani  
; APPLICANT: Proffitt, John H.  
; APPLICANT: Yarger, James G.  
; APPLICANT: Yen, Huel-Che B.  
; TITLE OF INVENTION: Biosynthesis of Zeaxanthin and  
; TITLE OF INVENTION: Glycosylated Zeaxanthin in Genetically Engineered Hosts  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Wellah & Katz, Ltd.  
; STREET: 120 S. Riverside Plaza, 22nd Floor  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60606

;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patent In Release #1.0, Version #1.30  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/096,623A  
;/ FILING DATE: 22-JUL-1993  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 07/805,061  
;/ FILING DATE: 09-DEC-1991  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 07/662,921  
;/ FILING DATE: 28-FEB-1991  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 07/562,674  
;/ FILING DATE: 03-AUG-1990  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 07/525,551  
;/ FILING DATE: 18-MAY-1990  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 07/487,613  
;/ FILING DATE: 02-MAR-1990  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Gamson, Edward P.  
;/ REGISTRATION NUMBER: 29,381  
;/ REFERENCE/DOCKET NUMBER: AMO-006.1  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (312) 655-1500  
;/ TELEFAX: (312) 655-1501  
;/ INFORMATION FOR SEQ ID NO: 12:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 177 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: DNA (genomic)  
;/ POSITION IN GENOME:  
;/ UNITS: bp  
;/ MAP POSITION: 1 to 177  
;/ US-08-096-623A-12

Alignment Scores:  
Pred. No.: 4,23e-27 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 2 Gaps: 1

US-10-628-525A-33 (1-56) x US-08-096-623A-12 (1-177)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 1 ATGGCTTCCTCAGTTCTTCTCTGAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAala---PheProValSerArgLys 39  
Db 61 AACATGGTGGCGCCTTTCACAGCTTAAGTCAGCTGCCTCATTCCTCTTTCAAGGAAG 120  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 121 CAAACCTTGACATCACTTCATTGCCACGACGGGGAAGAGTGCATATGC 171

RESULT 6  
PCT-US95-13937A-6  
; Sequence 6, Application PC/TUS9513937A  
; GENERAL INFORMATION:  
; APPLICANT: Hauptmann, Randal  
; APPLICANT: Eschenfeldt, William H  
; APPLICANT: English, Jami  
; APPLICANT: Brinkhaus, Friedhelm L







;; TITLE OF INVENTION: HIGH LEVEL PRODUCTION OF P-HYDROXYBENZOIC ACID  
;; TITLE OF INVENTION: IN GREEN PLANTS  
;; FILE REFERENCE: BC1015 US NA  
;; CURRENT APPLICATION NUMBER: US/09/855,341  
;; CURRENT FILING DATE: 2001-05-15  
;; NUMBER OF SEQ ID NOS: 16  
;; SOFTWARE: MICROSOFT OFFICE 97  
;; SEQ ID NO 7  
;; LENGTH: 684  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence:synthetic CPL  
US-09-855-341-7

Alignment Scores:  
Pred. No.: 1.04e-23 Length: 684  
Score: 223.50 Matches: 47  
Percent Similarity: 93.0% Conservative: 6  
Best Local Similarity: 82.5% Mismatches: 3  
Query Match: 82.5% Indels: 1  
DB: 3 Gaps: 1

US-10-628-525A-33 (1-56) x US-09-855-341-7 (1-684)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20  
DB 1 ATGGCTTCCTCTGTCATTTCTTCAGCAGCTGTGGCCACACGCGCAATGTTACACAGCT 60  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
DB 61 AGCATGTTGCACCTTTCACCTGGTCTCAATCTTCAGCCACTTTCCTCTGTGTACAAAGAAG 120  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
DB 121 CAAACCTTCACATCACTTCTTCATGCTAGCATGCTGGTGGAGAGATTAGCTGC 171

RESULT 12

US-09-021-203-5

;; Sequence 5, Application US/09021203

;; Patent No. 6040504

;; GENERAL INFORMATION:

;; APPLICANT: De Framond, Annick

;; TITLE OF INVENTION: Cotton Promoter

;; FILE REFERENCE: CGC1313/CIP/CONT3

;; CURRENT APPLICATION NUMBER: US/09/021,203

;; CURRENT FILING DATE: 1998-02-10

;; NUMBER OF SEQ ID NOS: 6

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 5

;; LENGTH: 191

;; TYPE: DNA

;; ORGANISM: Gossypium hirsutum

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: (15)..(191)

US-09-021-203-5

Alignment Scores:

Pred. No.: 1.05e-21 Length: 191  
Score: 204.50 Matches: 45  
Percent Similarity: 88.1% Conservative: 7  
Best Local Similarity: 76.3% Mismatches: 4  
Query Match: 75.5% Indels: 3  
DB: 3 Gaps: 2

US-10-628-525A-33 (1-56) x US-09-021-203-5 (1-191)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18  
DB 15 ATGGCTTCCTCCATGATCTCATCGGCAACCATTCGCCACCGTGAAGTCTCTCCCGCGCA 74  
QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37

Db 75 CAGGCCAACATGCTGGCCCTTCACCGGCTCAAGTCTGCTCTCTCCAGTCACT 134  
QY 38 ArgGlyGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
DB 135 AGGAAGCCCAACCAACGACATCACTTCTTTCGAAGCAATGGTGGAGAGTGCATGC 191

RESULT 13

US-09-021-203-3

;; Sequence 3, Application US/09021203

;; Patent No. 6040504

;; GENERAL INFORMATION:

;; APPLICANT: De Framond, Annick

;; TITLE OF INVENTION: Cotton Promoter

;; FILE REFERENCE: CGC1313/CIP/CONT3

;; CURRENT APPLICATION NUMBER: US/09/021,203

;; CURRENT FILING DATE: 1998-02-10

;; NUMBER OF SEQ ID NOS: 6

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 3

;; LENGTH: 177

;; TYPE: DNA

;; ORGANISM: Gossypium hirsutum

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: (10)..(177)

US-09-021-203-3

Alignment Scores:

Pred. No.: 1.12e-21 Length: 177  
Score: 204.00 Matches: 45  
Percent Similarity: 87.7% Conservative: 5  
Best Local Similarity: 78.9% Mismatches: 5  
Query Match: 75.3% Indels: 2  
DB: 3 Gaps: 2

US-10-628-525A-33 (1-56) x US-09-021-203-3 (1-177)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20  
DB 10 ATGGCTTCCTCCATGATCTCATCGGCTACATTCGCACT---GCCTCTCCGCGCACAGGCT 66  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSerArgLys 39  
DB 67 AACATGCTGCTCTCTTCACCGGCTCAAGTCTGCTCTGCTTCCAGTCACTCAGGAAG 126  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
DB 127 GCCAACACGACATTAATTTCTTCGCAAGCAATGGCGGCGAGAGTGCATGC 177

RESULT 14

US-09-441-340-14

;; Sequence 14, Application US/09441340

;; Patent No. 6448476

;; GENERAL INFORMATION:

;; APPLICANT: Barry, Gerard F.

;; TITLE OF INVENTION: Phosphonate Metabolizing Plants

;; FILE REFERENCE: 38-21(15303)

;; CURRENT APPLICATION NUMBER: US/09/441,340

;; CURRENT FILING DATE: 1999-11-16

;; EARLIER APPLICATION NUMBER: 60/108,763

;; EARLIER FILING DATE: 1998-11-17

;; NUMBER OF SEQ ID NOS: 32

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 14

;; LENGTH: 174

;; TYPE: DNA

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Description of Artificial Sequence: chloroplast or  
;; OTHER INFORMATION: plastid transit peptide coding sequence and amino

;; OTHER INFORMATION: acid sequence translation

;; FEATURE:



Percent Similarity: 78.9% Conservatives: 4  
 Best Local Similarity: 71.9% Mismatches: 9  
 Query Match: 67.0% Indels: 3  
 DB: 3 Gaps: 2

US-10-628-525A-33 (1-56) x US-09-186-002-5 (1-268)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 Db 1 ATGGCTTCCTCTATGCTCTCTTCGGCTACTATGTT-----GCCTCTCGGCTCAGGCC 54  
 QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
 Db 55 ACTATGTCGCTCTTCAACGGACTTAAGTCCTCCGCTGCTTCCCGCCAGCCGCAAG 114  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 115 GCTAACACACGACATTACTTCATCACACGACGCGGAGAGATTAACTGC 165

## RESULT 18

US-08-391-339-9  
 ; Sequence 9, Application US/08391339  
 ; Patent No. 5463175  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kishore, Ganesh M.  
 ; APPLICANT: Barry, Gerard F.  
 ; TITLE OF INVENTION: Glyphosate Tolerant Plants  
 ; NUMBER OF SEQUENCES: 33  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dennis R. Hoerner, Jr.,  
 ; ADDRESSEE: Monsanto Co. B4P  
 ; STREET: 700 Chesterfield Village Parkway  
 ; CITY: St. Louis  
 ; STATE: Missouri  
 ; COUNTRY: USA  
 ; ZIP: 63198  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/391,339  
 ; FILING DATE:  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/156,968  
 ; FILING DATE:  
 ; APPLICATION NUMBER: US/07/717,370  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hoerner, Dennis R., Jr.  
 ; REGISTRATION NUMBER: 30,914  
 ; REFERENCE/DOCKET NUMBER: 38-21(10533)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (314)537-6099  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 279 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (recombinant)  
 ; US-08-391-339-9

Alignment Scores:  
 Pred. No.: 4.8e-18 Length: 279  
 Score: 181.50 Matches: 41  
 Percent Similarity: 78.9% Conservatives: 4  
 Best Local Similarity: 71.9% Mismatches: 9  
 Query Match: 67.0% Indels: 3  
 DB: 2 Gaps: 2

US-10-628-525A-33 (1-56) x US-08-391-339-9 (1-279)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 Db 12 ATGGCTTCCTCTATGCTCTCTTCGGCTACTATGTT-----GCCTCTCGGCTCAGGCC 65  
 QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
 Db 66 ACTATGTCGCTCTTCAACGGACTTAAGTCCTCCGCTGCTTCCCGCCAGCCGCAAG 125  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 126 GCTAACACACGACATTACTTCATCACACGACGCGGAGAGATTAACTGC 176

## RESULT 19

US-08-484-274A-9  
 ; Sequence 9, Application US/08484274A  
 ; Patent No. 5776760  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kishore, Ganesh M.  
 ; APPLICANT: Barry, Gerard F.  
 ; TITLE OF INVENTION: Glyphosate Tolerant Plants  
 ; NUMBER OF SEQUENCES: 33  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: P.O. Box 4433  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: USA  
 ; ZIP: 77210-4433  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/484,274A  
 ; FILING DATE: 07 June 1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Patterson, Melinda L.  
 ; REGISTRATION NUMBER: 33,062  
 ; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (713)789-2679  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 279 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (recombinant)  
 ; US-08-484-274A-9

Alignment Scores:  
 Pred. No.: 4.8e-18 Length: 279  
 Score: 181.50 Matches: 41  
 Percent Similarity: 78.9% Conservatives: 4  
 Best Local Similarity: 71.9% Mismatches: 9  
 Query Match: 67.0% Indels: 3  
 DB: 2 Gaps: 2

US-10-628-525A-33 (1-56) x US-08-484-274A-9 (1-279)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 Db 12 ATGGCTTCCTCTATGCTCTCTTCGGCTACTATGTT-----GCCTCTCGGCTCAGGCC 65  
 QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
 Db 66 ACTATGTCGCTCTTCAACGGACTTAAGTCCTCCGCTGCTTCCCGCCAGCCGCAAG 125  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

Db 126 GCTAACACGACATTACTTCCATCACAGCAGCGGGAAGATTAACTGC 176  
|||||  
RESULT 20  
US-09-612-404-9  
; Sequence 9, Application US/09612404  
; Patent No. RE38825  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Barry, Gerard F.  
; TITLE OF INVENTION: Glycosate Tolerant Plants  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; STREET: P. O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/612,404  
; FILING DATE: 07-Jul-2000  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,274A  
; FILING DATE: 07 June 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Patterson, Melinda L.  
; REGISTRATION NUMBER: 33,062  
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713)789-2679  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 279 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (recombinant)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-612-404-9

Alignment Scores:  
Pred. No.: 4,8e-18 Length: 279  
Score: 181.50 Matches: 41  
Percent Similarity: 78.9% Conservative: 4  
Best Local Similarity: 71.9% Mismatches: 9  
Query Match: 67.0% Indels: 3  
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-09-612-404-9 (1-279)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
|||||  
Db 12 ATGGCTTCCTCTATGCTCTCTTCGCGTACTATGGTT-----GCCTCTCCGGCTCAGGCC 65  
|||||  
QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
|||||  
Db 66 ACTATGGTCGCTCCCTTTCACGCGACTTAAGTCTCGCTGCCTTCCAGCCACCGCGAAG 125  
|||||  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAnGlyArgValGlnCys 56  
|||||  
Db 126 GCTAACACGACATTACTTCCATCACAGCAGCGGGAAGATTAACTGC 176  
|||||

RESULT 21  
US-08-090-523-5  
; Sequence 5, Application US/08090523  
; Patent No. 5498830

; GENERAL INFORMATION:  
; APPLICANT: Barry, Gerard F.  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Stark, David M.  
; TITLE OF INVENTION: Enhanced Starch Biosynthesis  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Grace L. Bonner, Monsanto Co. BB4F  
; STREET: 700 Chesterfield Parkway No. 5498830ch  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/090,523  
; FILING DATE: 19930712  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/709663  
; FILING DATE: 07-JUN-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/539763  
; FILING DATE: 18-JUN-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bonner, Grace L.  
; REGISTRATION NUMBER: 32,963  
; REFERENCE/DOCKET NUMBER: 38-21(10559)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 537-7286  
; TELEFAX: (314) 537-6047  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 355 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 88..354  
US-08-090-523-5

Alignment Scores:  
Pred. No.: 6,84e-18 Length: 355  
Score: 181.50 Matches: 41  
Percent Similarity: 78.9% Conservative: 4  
Best Local Similarity: 71.9% Mismatches: 9  
Query Match: 67.0% Indels: 3  
DB: 2 Gaps: 2

US-10-628-525A-33 (1-56) x US-08-090-523-5 (1-355)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
|||||  
Db 88 ATGGCTTCCTCTATGCTCTCTTCGCGTACTATGGTT-----GCCTCTCCGGCTCAGGCC 141  
|||||  
QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
|||||  
Db 142 ACTATGGTCGCTCCCTTTCACGCGACTTAAGTCTCGCTGCCTTCCAGCCACCGCGAAG 201  
|||||  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAnGlyArgValGlnCys 56  
|||||  
Db 202 GCTAACACGACATTACTTCCATCACAGCAGCGGGAAGATTAACTGC 252  
|||||

RESULT 22  
US-08-398-627-5  
; Sequence 5, Application US/08398627  
; Patent No. 5608149

;; GENERAL INFORMATION:  
;; APPLICANT: Barry, Gerard F.  
;; APPLICANT: Kishore, Ganesh M.  
;; APPLICANT: Stark, David M.  
;; TITLE OF INVENTION: Enhanced Starch Biosynthesis  
;; NUMBER OF SEQUENCES: 51  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Grace L. Bonner, Monsanto Co. BB4F  
;; STREET: 700 Chesterfield Parkway No. 5608149th  
;; CITY: St. Louis  
;; STATE: Missouri  
;; COUNTRY: USA  
;; ZIP: 63198  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/398,627  
;; FILING DATE: 03-MAR-1995  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/090,523  
;; FILING DATE: 12-JUL-1993  
;; APPLICATION NUMBER: US 07/709663  
;; FILING DATE: 07-JUN-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/539763  
;; FILING DATE: 18-JUN-1990  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Bonner, Grace L.  
;; REGISTRATION NUMBER: 32,963  
;; REFERENCE/DOCKET NUMBER: 38-21(10559)A  
;; TELEPHONE: (314) 537-7286  
;; TELEFAX: (314) 537-6047  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 355 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 88..354  
;; US-08-398-627-5

Alignment Scores:  
Pred. No.: 6,84e-18 Length: 355  
Score: 181.50 Matches: 41  
Percent Similarity: 78.9% Conservative: 4  
Best Local Similarity: 71.9% Mismatches: 9  
Query Match: 67.0% Indels: 3  
DB: 2 Gaps: 2

US-10-628-525A-33 (1-56) x US-08-398-627-5 (1-355)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
DB 88 ATGGCTTCCTCTATAGTCTCTTCCTCGCTACTATAGTT-----GCCTCTCGGCTCAGGCC 141  
QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
DB 142 ACTATGGTGGCTCTCTTCAACGACTTAAGTCTCGCTGCCTTCCAGCCACCCGCAAG 201  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
DB 202 GCTAACACGACATTACTTCCATCACAACGCGGGAAGAGTTAACTGC 252  
RESULT 23  
US-08-406-858-5

;; Sequence 5, Application US/08406858  
;; Patent No. 5648249  
;; GENERAL INFORMATION:  
;; APPLICANT: Barry, Gerard F.  
;; APPLICANT: Kishore, Ganesh M.  
;; APPLICANT: Stark, David M.  
;; APPLICANT: Zalewski, James C.  
;; TITLE OF INVENTION: Method of Improving the Quality of  
;; TITLE OF INVENTION: Stored Potatoes  
;; NUMBER OF SEQUENCES: 26  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Grace L. Bonner, Monsanto Company, BB4F  
;; STREET: 700 Chesterfield Parkway No. 5648249th  
;; CITY: St. Louis  
;; STATE: Missouri  
;; COUNTRY: USA  
;; ZIP: 63198  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/406,858  
;; FILING DATE:  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US94/05275  
;; FILING DATE: 18-MAY-1994  
;; APPLICATION NUMBER: US 08/070,155  
;; FILING DATE: 28-MAY-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Bonner, Grace L.  
;; REGISTRATION NUMBER: 32,963  
;; REFERENCE/DOCKET NUMBER: 38-21(10654)A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (314) 537-7286  
;; TELEFAX: (314) 537-6047  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 355 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 88..354  
;; US-08-406-858-5

Alignment Scores:  
Pred. No.: 6,84e-18 Length: 355  
Score: 181.50 Matches: 41  
Percent Similarity: 78.9% Conservative: 4  
Best Local Similarity: 71.9% Mismatches: 9  
Query Match: 67.0% Indels: 3  
DB: 2 Gaps: 2

US-10-628-525A-33 (1-56) x US-08-406-858-5 (1-355)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
DB 88 ATGGCTTCCTCTATAGTCTCTTCCTCGCTACTATAGTT-----GCCTCTCGGCTCAGGCC 141  
QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
DB 142 ACTATGGTGGCTCTCTTCAACGACTTAAGTCTCGCTGCCTTCCAGCCACCCGCAAG 201  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
DB 202 GCTAACACGACATTACTTCCATCACAACGCGGGAAGAGTTAACTGC 252

## RESULT 24

US-08-476-519-7  
; Sequence 7, Application US/08476519  
; Patent No. 5750876  
; GENERAL INFORMATION:  
; APPLICANT: Barry, Gerard F.  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Krohn, Bradley M.  
; TITLE OF INVENTION: No. 5750876el Isomylase Gene, Compositions  
; TITLE OF INVENTION: Containing It and Methods of Using Isomylases  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Grace L. Bonner, Monsanto Company, BB4F  
; STREET: 700 Chesterfield Parkway No. 5750876th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,519  
FILING DATE: 28-JUL-1994  
CLASSIFICATION: 800

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/281902  
FILING DATE: 28-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bonner, Grace L.  
REGISTRATION NUMBER: 32,963  
REFERENCE/DOCKET NUMBER: 38-21(13577)A

TELEPHONE: (314)537-7286  
TELEFAX: (314)537-6047  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

PUBLICATION INFORMATION:  
DOCUMENT NUMBER: WO 91/19806  
FILING DATE: 07-JUN-1991  
PUBLICATION DATE: 26-DEC-1991  
RELEVANT RESIDUES IN SEQ ID NO: 7: FROM 1 TO 355

US-08-476-519-7  
Alignment Scores:  
Pred. No.: 6.84e-18 Length: 355  
Score: 181.50 Matches: 41  
Percent Similarity: 78.9% Conservative: 4  
Best Local Similarity: 71.9% Mismatches: 9  
Query Match: 67.0% Indels: 3  
DB: 2 Gaps: 2

US-10-628-525A-33 (1-56) x US-08-476-519-7 (1-355)  
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
DB 88 ATGGCTTCTCTATGCTCTCTTCGCTACTAGTT-----GCCTCTCCGGCTCAGGCC 141

QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
DB 142 ACTATGGTTCGCTCTCTTCAACGGACTTAAGTCTCGCTGCTTCCAGCCACCCGCGAAG 201

QY 40 GlnAnLeuAspPileThrSerIleAlaSerAnGlyGlyArgValGlnCys 56  
DB 202 GCTAACACGACATTAATCTCCATCAACACGCGGAAGAGTTAACTGC 252

## RESULT 25

US-08-120-703A-5  
; Sequence 5, Application US/08120703A  
; Patent No. 6538178  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; TITLE OF INVENTION: Increased Starch Content in Plants  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Grace L. Bonner, Monsanto Co. BB4F  
; STREET: 700 Chesterfield Village Parkway No. 6538178th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/120,703A  
FILING DATE: 13-SEP-1993  
CLASSIFICATION: 800

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/709663  
FILING DATE: 07-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Bonner, Grace L.  
REGISTRATION NUMBER: 32,963  
REFERENCE/DOCKET NUMBER: 38-21(10639)A

TELEPHONE: (314) 537-7357  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

PUBLICATION INFORMATION:  
DOCUMENT NUMBER: WO 91/19806  
FILING DATE: 07-JUN-1991  
PUBLICATION DATE: 26-DEC-1991  
RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 355

US-08-120-703A-5  
Alignment Scores:  
Pred. No.: 6.84e-18 Length: 355  
Score: 181.50 Matches: 41  
Percent Similarity: 78.9% Conservative: 4  
Best Local Similarity: 71.9% Mismatches: 9  
Query Match: 67.0% Indels: 3  
DB: 2 Gaps: 2

US-10-628-525A-33 (1-56) x US-08-120-703A-5 (1-355)  
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
DB 88 ATGGCTTCTCTATGCTCTCTTCGCTACTAGTT-----GCCTCTCCGGCTCAGGCC 141

QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
DB 142 ACTATGGTTCGCTCTCTTCAACGGACTTAAGTCTCGCTGCTTCCAGCCACCCGCGAAG 201

QY 40 GlnAnLeuAspPileThrSerIleAlaSerAnGlyGlyArgValGlnCys 56  
DB 202 GCTAACACGACATTAATCTCCATCAACACGCGGAAGAGTTAACTGC 252

## RESULT 26

US-08-399-023-5  
; Sequence 5, Application US/08399023  
; Patent No. 6538179  
; GENERAL INFORMATION:

;; APPLICANT: Barry, Gerard P.  
;; APPLICANT: Kishore, Ganesh M.  
;; APPLICANT: Stark, David M.  
;; TITLE OF INVENTION: Enhanced Starch Biosynthesis  
;; NUMBER OF SEQUENCES: 51  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Grace L. Bonner, Monsanto Co. B84P  
;; STREET: 700 Chesterfield Parkway No. 6538179th  
;; CITY: St. Louis  
;; STATE: Missouri  
;; COUNTRY: USA  
;; ZIP: 63198  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/399,023  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/090,523  
;; FILING DATE:  
;; APPLICATION NUMBER: US 07/709663  
;; FILING DATE: 07-JUN-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/539763  
;; FILING DATE: 18-JUN-1990  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Bonner, Grace L.  
;; REGISTRATION NUMBER: 32,963  
;; REFERENCE/DOCKET NUMBER: 38-21(10559)A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (314) 537-7286  
;; TELEFAX: (314) 537-6047  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 355 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 88..354  
US-08-399-023-5

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Pred. No.: 6.84e-18 Length: 355  
Score: 181.50 Matches: 41  
Percent Similarity: 78.9% Conservative: 4  
Best Local Similarity: 71.9% Mismatches: 9  
Query Match: 67.0% Indels: 3  
DB: Gaps: 2  
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QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
Db 142 ACTATGGTCGCTCTTCAACGGACTTAAGTCTCCGCTCCCTTCCAGGCCACCCGCAAG 201  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 202 GCTAACACAGCAGATTACTTCCATCAACAGCAACGGCGGAAGAGTTAACTGC 252

RESULT 27  
PCT-US91-04036-5  
; Sequence 5, Application PC/TUS9104036

;; GENERAL INFORMATION:  
;; APPLICANT: Kishore, Ganesh M.  
;; TITLE OF INVENTION: Increased Starch Content in Plants  
;; NUMBER OF SEQUENCES: 23  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Monsanto Co.  
;; STREET: 700 Chesterfield Village Parkway  
;; CITY: St. Louis  
;; STATE: Missouri  
;; COUNTRY: USA  
;; ZIP: 63198  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US91/04036  
;; FILING DATE: 19910607  
;; CLASSIFICATION: 800  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: McBride, Thomas P.  
;; REGISTRATION NUMBER: 32706  
;; REFERENCE/DOCKET NUMBER: 38-21(10530)A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (314) 537-7357  
;; TELEFAX: (314) 537-6047  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 355 base pairs  
;; TYPE: NUCLEIC ACID  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 88..354  
PCT-US91-04036-5  
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Pred. No.: 6.84e-18 Length: 355  
Score: 181.50 Matches: 41  
Percent Similarity: 78.9% Conservative: 4  
Best Local Similarity: 71.9% Mismatches: 9  
Query Match: 67.0% Indels: 3  
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QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
Db 142 ACTATGGTCGCTCTTCAACGGACTTAAGTCTCCGCTCCCTTCCAGGCCACCCGCAAG 201  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 202 GCTAACACAGCAGATTACTTCCATCAACAGCAACGGCGGAAGAGTTAACTGC 252  
RESULT 28  
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; Sequence 5, Application PC/TUS9405275  
;; GENERAL INFORMATION:  
;; APPLICANT:  
;; TITLE OF INVENTION: Method of Improving the Quality of Stored  
;; NUMBER OF SEQUENCES: 26  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS



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/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
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/ APPLICATION NUMBER: PCT/US94/05275
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/070155
/ FILING DATE: 28-MAY-1993
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 355 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 88..354
PCT-US94-05275-5

Alignment Scores:
Pred. No.: 6.84e-18 Length: 355
Score: 181.50 Matches: 41
Percent Similarity: 78.9% Conservative: 4
Best Local Similarity: 71.9% Mismatches: 9
Query Match: 67.0% Indels: 3
DB: 6 Gaps: 2

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QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39
Db 142 ACTATGGTCGCTCTTCAACGGACTTAAGTCTCCGCTGCCTTCCAGCCACCCGCAAG 201
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56
Db 202 GCTAACACAGCATTAATCTCCATCACAACGCGGGAAGAGTTAACTGC 252

RESULT 29
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/ Sequence 7, Application PC/TUS9509323
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: Novel Isoamylase Gene, Compositions
/ TITLE OF INVENTION: Containing It and Methods of Using Isoamylases
/ NUMBER OF SEQUENCES: 11
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/09323
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/281902
/ FILING DATE: 28-JUL-1994
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 355 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ PUBLICATION INFORMATION:
/ DOCUMENT NUMBER: WO 91/19806
/ FILING DATE: 07-JUN-1991
/ PUBLICATION DATE: 26-DEC-1991
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PCT-US95-09323-7

Alignment Scores:
Pred. No.: 6.84e-18 Length: 355
Score: 181.50 Matches: 41
Percent Similarity: 78.9% Conservative: 4
Best Local Similarity: 71.9% Mismatches: 9
Query Match: 67.0% Indels: 3
DB: 6 Gaps: 2

US-10-628-525A-33 (1-56) x PCT-US95-09323-7 (1-355)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
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QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39
Db 142 ACTATGGTCGCTCTTCAACGGACTTAAGTCTCCGCTGCCTTCCAGCCACCCGCAAG 201
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56
Db 202 GCTAACACAGCATTAATCTCCATCACAACGCGGGAAGAGTTAACTGC 252

RESULT 30
US-09-011-151-1
/ Sequence 1, Application US/09011151
/ Patent No. 6380463
/ GENERAL INFORMATION:
/ APPLICANT: Jenson, Ian
/ TITLE OF INVENTION: DNA Constructs
/ FILE REFERENCE: PPD 50059/UST
/ CURRENT APPLICATION NUMBER: US/09/011,151
/ PRIOR FILING DATE: 1998-01-29
/ PRIOR APPLICATION NUMBER: PCT/GB96/01883
/ PRIOR FILING DATE: 1996-08-02
/ PRIOR APPLICATION NUMBER: GB 9515941.4
/ PRIOR FILING DATE: 1995-08-03
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1
/ LENGTH: 509
/ TYPE: DNA
/ ORGANISM: Arabidopsis sp.
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(507)
US-09-011-151-1

Alignment Scores:
Pred. No.: 1.16e-17 Length: 509
Score: 181.50 Matches: 41
Percent Similarity: 78.9% Conservative: 4
Best Local Similarity: 71.9% Mismatches: 9
Query Match: 67.0% Indels: 3
DB: 3 Gaps: 2

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QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
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QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39
Db 64 ACTATGGTCGCTCTTCAACGGACTTAAGTCTCCGCTGCCTTCCAGCCACCCGCAAG 123
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56
Db 124 GCTAACACAGCATTAATCTCCATCACAACGCGGGAAGAGTTAACTGT 174
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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

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Title: US-10-628-525A-33

Perfect score: 271

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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-YGAPO=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 2                 | 240.5 | 88.7        | 204    | 3  | US-09-839-477-3    |
| 3                 | 240.5 | 88.7        | 204    | 7  | US-10-758-064-3    |
| 4                 | 240.5 | 88.7        | 297    | 9  | US-10-487-901-7209 |
| 5                 | 240.5 | 88.7        | 377    | 9  | US-10-487-901-3504 |
| 6                 | 240.5 | 88.7        | 489    | 9  | US-10-487-901-3503 |
| 7                 | 240.5 | 88.7        | 504    | 9  | US-10-487-901-7207 |
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| Sequence 3, Appl  |       |             |        |    |                    |
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| Sequence 7209, Ap |       |             |        |    |                    |
| Sequence 3504, Ap |       |             |        |    |                    |
| Sequence 3503, Ap |       |             |        |    |                    |
| Sequence 7207, Ap |       |             |        |    |                    |

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| 8  | 240.5 | 88.7 | 718  | 9 | US-10-487-901-5765  | Sequence 5765, Ap  |
| 9  | 240.5 | 88.7 | 736  | 9 | US-10-487-901-1704  | Sequence 1704, Ap  |
| 10 | 240.5 | 88.7 | 736  | 9 | US-10-487-901-5043  | Sequence 5043, Ap  |
| 11 | 236.5 | 87.3 | 668  | 9 | US-10-487-901-7208  | Sequence 7208, Ap  |
| 12 | 236.5 | 83.6 | 169  | 5 | US-10-165-420-3     | Sequence 3, Appl   |
| 13 | 233.5 | 82.5 | 684  | 3 | US-09-855-341-7     | Sequence 7, Appl   |
| 14 | 233.5 | 82.5 | 684  | 3 | US-09-896-866B-16   | Sequence 16, Appl  |
| 15 | 233.5 | 82.5 | 684  | 6 | US-10-359-369-41    | Sequence 41, Appl  |
| 16 | 233.5 | 82.5 | 684  | 7 | US-10-699-050-16    | Sequence 16, Appl  |
| 17 | 233.5 | 82.5 | 684  | 7 | US-10-718-311-7     | Sequence 7, Appl   |
| 18 | 223.5 | 82.5 | 684  | 8 | US-10-462-162-33    | Sequence 33, Appl  |
| 19 | 221   | 81.5 | 714  | 9 | US-10-487-901-1703  | Sequence 1703, Ap  |
| 20 | 221   | 81.5 | 736  | 9 | US-10-487-901-5044  | Sequence 5044, Ap  |
| 21 | 218   | 80.4 | 683  | 9 | US-10-487-901-1713  | Sequence 1713, Ap  |
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| 23 | 218   | 80.4 | 737  | 9 | US-10-487-901-5766  | Sequence 5766, Ap  |
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| 25 | 215   | 79.3 | 753  | 9 | US-10-487-901-5764  | Sequence 5764, Ap  |
| 26 | 215   | 79.3 | 754  | 9 | US-10-487-901-5028  | Sequence 5028, Ap  |
| 27 | 209.5 | 77.3 | 385  | 3 | US-09-732-627A-1176 | Sequence 1176, Ap  |
| 28 | 207.5 | 76.6 | 724  | 3 | US-09-910-664-55    | Sequence 55, Appl  |
| 29 | 207.5 | 76.6 | 724  | 7 | US-10-333-184-54    | Sequence 54, Appl  |
| 30 | 207.5 | 76.6 | 726  | 7 | US-10-333-184-202   | Sequence 202, Appl |
| 31 | 207.5 | 76.6 | 771  | 3 | US-09-770-445-518   | Sequence 918, Appl |
| 32 | 207.5 | 76.6 | 1205 | 3 | US-09-770-445-41    | Sequence 41, Appl  |
| 33 | 206   | 76.0 | 654  | 9 | US-10-487-901-5042  | Sequence 5042, Ap  |
| 34 | 206   | 76.0 | 704  | 8 | US-10-425-115-85509 | Sequence 85509, A  |
| 35 | 205.5 | 75.8 | 151  | 6 | US-10-321-434-4     | Sequence 4, Appl   |
| 36 | 204.5 | 75.5 | 191  | 3 | US-09-756-643-5     | Sequence 5, Appl   |
| 37 | 204.5 | 75.5 | 1084 | 7 | US-10-343-810-5     | Sequence 3, Appl   |
| 38 | 204   | 75.3 | 177  | 3 | US-09-756-643-3     | Sequence 4, Appl   |
| 39 | 199.5 | 73.6 | 363  | 3 | US-09-770-791-468   | Sequence 468, Appl |
| 40 | 199.5 | 73.6 | 711  | 3 | US-09-910-664-32    | Sequence 32, Appl  |
| 41 | 199.5 | 73.6 | 711  | 7 | US-10-333-184-31    | Sequence 31, Appl  |
| 42 | 199.5 | 73.6 | 739  | 7 | US-10-333-184-182   | Sequence 182, Appl |
| 43 | 199.5 | 73.6 | 1036 | 8 | US-10-739-930-2595  | Sequence 2595, Ap  |
| 44 | 199.5 | 73.6 | 2581 | 8 | US-10-739-930-1173  | Sequence 1173, Ap  |
| 45 | 197   | 72.7 | 240  | 5 | US-10-062-727-306   | Sequence 306, Appl |
| 46 | 197   | 72.7 | 256  | 5 | US-10-062-727-366   | Sequence 366, Appl |
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| 48 | 197   | 72.7 | 341  | 5 | US-10-062-727-214   | Sequence 214, Appl |
| 49 | 197   | 72.7 | 344  | 5 | US-10-062-727-358   | Sequence 358, Appl |
| 50 | 197   | 72.7 | 351  | 5 | US-10-062-727-255   | Sequence 255, Appl |
| 51 | 197   | 72.7 | 363  | 5 | US-10-062-727-342   | Sequence 342, Appl |
| 52 | 197   | 72.7 | 367  | 5 | US-10-062-727-353   | Sequence 353, Appl |
| 53 | 197   | 72.7 | 381  | 5 | US-10-062-727-249   | Sequence 249, Appl |
| 54 | 197   | 72.7 | 383  | 5 | US-10-062-727-237   | Sequence 237, Appl |
| 55 | 197   | 72.7 | 401  | 5 | US-10-062-727-352   | Sequence 352, Appl |
| 56 | 197   | 72.7 | 407  | 5 | US-10-062-727-351   | Sequence 351, Appl |
| 57 | 197   | 72.7 | 410  | 5 | US-10-062-727-220   | Sequence 220, Appl |
| 58 | 197   | 72.7 | 412  | 5 | US-10-062-727-348   | Sequence 348, Appl |
| 59 | 197   | 72.7 | 413  | 5 | US-10-062-727-371   | Sequence 371, Appl |
| 60 | 197   | 72.7 | 423  | 5 | US-10-062-727-275   | Sequence 275, Appl |
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| 62 | 197   | 72.7 | 430  | 5 | US-10-062-727-297   | Sequence 297, Appl |
| 63 | 197   | 72.7 | 433  | 5 | US-10-062-727-245   | Sequence 245, Appl |
| 64 | 197   | 72.7 | 457  | 5 | US-10-062-727-230   | Sequence 230, Appl |
| 65 | 197   | 72.7 | 470  | 5 | US-10-062-727-252   | Sequence 252, Appl |
| 66 | 197   | 72.7 | 479  | 5 | US-10-062-727-1003  | Sequence 1003, Ap  |
| 67 | 197   | 72.7 | 484  | 5 | US-10-062-727-266   | Sequence 266, Appl |
| 68 | 197   | 72.7 | 502  | 5 | US-10-062-727-270   | Sequence 270, Appl |
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| 70 | 197   | 72.7 | 606  | 5 | US-10-062-727-1004  | Sequence 1004, Ap  |
| 71 | 195.5 | 72.1 | 767  | 3 | US-09-770-445-931   | Sequence 931, Appl |
| 72 | 195.5 | 72.1 | 780  | 3 | US-09-770-445-880   | Sequence 880, Appl |
| 73 | 194   | 71.6 | 934  | 8 | US-10-477-307-2     | Sequence 2, Appl   |
| 74 | 194   | 71.6 | 2034 | 8 | US-10-477-307-1     | Sequence 1, Appl   |
| 75 | 193.5 | 71.4 | 929  | 8 | US-10-739-930-1359  | Sequence 1359, Ap  |
| 76 | 193.5 | 71.4 | 1000 | 8 | US-10-739-930-1361  | Sequence 1361, Ap  |
| 77 | 193   | 71.2 | 341  | 5 | US-10-062-727-357   | Sequence 357, Appl |
| 78 | 192.5 | 71.0 | 363  | 3 | US-09-770-791-463   | Sequence 463, Appl |
| 79 | 192.5 | 71.0 | 392  | 3 | US-09-770-423-971   | Sequence 971, Appl |
| 80 | 191   | 70.5 | 231  | 5 | US-10-062-727-329   | Sequence 329, Appl |

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| 81    | 190   | 70.1 | 481   | 5 | US-10-062-727-267  | Sequence 267, App  |
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| 83    | 188   | 69.4 | 215   | 5 | US-10-062-727-302  | Sequence 302, App  |
| 84    | 188   | 69.4 | 424   | 9 | US-10-487-901-1710 | Sequence 1710, App |
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| 89    | 184.5 | 68.1 | 768   | 8 | US-10-739-930-1358 | Sequence 1358, App |
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| 94    | 181.5 | 67.0 | 178   | 6 | US-10-198-478-7    | Sequence 7, App    |
| 95    | 181.5 | 67.0 | 237   | 5 | US-10-214-932-31   | Sequence 31, App   |
| 96    | 181.5 | 67.0 | 264   | 5 | US-10-138-927-71   | Sequence 71, App   |
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| 100   | 181.5 | 67.0 | 264   | 6 | US-10-430-011-71   | Sequence 71, App   |
| 101   | 181.5 | 67.0 | 264   | 7 | US-10-602-395-27   | Sequence 27, App   |
| 102   | 181.5 | 67.0 | 268   | 6 | US-10-198-478-5    | Sequence 5, App    |
| 103   | 181.5 | 67.0 | 370   | 3 | US-09-770-791-365  | Sequence 365, App  |
| 104   | 181.5 | 67.0 | 696   | 5 | US-10-213-791-11   | Sequence 11, App   |
| 105   | 181.5 | 67.0 | 785   | 3 | US-09-770-445-862  | Sequence 862, App  |
| c 106 | 181.5 | 67.0 | 1630  | 5 | US-10-213-791-23   | Sequence 23, App   |
| c 107 | 181.5 | 67.0 | 5560  | 8 | US-10-849-939-5    | Sequence 5, App    |
| 108   | 181.5 | 67.0 | 10249 | 6 | US-10-198-478-14   | Sequence 14, App   |
| 109   | 181.5 | 67.0 | 10339 | 6 | US-10-198-478-13   | Sequence 13, App   |
| 110   | 181.5 | 67.0 | 10846 | 3 | US-09-923-109-5    | Sequence 5, App    |
| 111   | 181.5 | 67.0 | 10846 | 7 | US-10-164-204-5    | Sequence 5, App    |
| 112   | 181.5 | 67.0 | 10846 | 6 | US-10-705-430-5    | Sequence 5, App    |
| 113   | 181.5 | 67.0 | 20119 | 6 | US-10-148-907A-35  | Sequence 35, App   |
| 114   | 181   | 66.8 | 231   | 5 | US-10-062-727-260  | Sequence 260, App  |
| 115   | 181   | 66.8 | 244   | 5 | US-10-062-727-304  | Sequence 304, App  |
| 116   | 178.5 | 65.9 | 272   | 3 | US-09-987-899-661  | Sequence 661, App  |
| 117   | 178.5 | 65.9 | 295   | 3 | US-09-987-899-842  | Sequence 842, App  |
| 118   | 176.5 | 65.1 | 388   | 3 | US-09-987-899-814  | Sequence 814, App  |
| 119   | 175.5 | 64.8 | 236   | 3 | US-09-987-899-653  | Sequence 653, App  |
| 120   | 174.5 | 64.4 | 213   | 3 | US-09-987-899-643  | Sequence 643, App  |
| 121   | 174.5 | 64.4 | 217   | 3 | US-09-987-899-652  | Sequence 652, App  |
| 122   | 174.5 | 64.4 | 220   | 3 | US-09-987-899-606  | Sequence 606, App  |
| 123   | 174.5 | 64.4 | 220   | 3 | US-09-987-899-621  | Sequence 621, App  |
| 124   | 174.5 | 64.4 | 221   | 3 | US-09-987-899-658  | Sequence 658, App  |
| 125   | 174.5 | 64.4 | 223   | 3 | US-09-987-899-613  | Sequence 613, App  |
| 126   | 174.5 | 64.4 | 228   | 3 | US-09-987-899-604  | Sequence 604, App  |
| 127   | 174.5 | 64.4 | 228   | 3 | US-09-987-899-622  | Sequence 622, App  |
| 128   | 174.5 | 64.4 | 229   | 3 | US-09-987-899-599  | Sequence 599, App  |
| 129   | 174.5 | 64.4 | 230   | 3 | US-09-987-899-605  | Sequence 605, App  |
| 130   | 174.5 | 64.4 | 233   | 3 | US-09-987-899-584  | Sequence 584, App  |
| 131   | 174.5 | 64.4 | 235   | 3 | US-09-987-899-603  | Sequence 603, App  |
| 132   | 174.5 | 64.4 | 237   | 3 | US-09-987-899-642  | Sequence 642, App  |
| 133   | 174.5 | 64.4 | 238   | 3 | US-09-987-899-579  | Sequence 579, App  |
| 134   | 174.5 | 64.4 | 239   | 3 | US-09-987-899-526  | Sequence 526, App  |
| 135   | 174.5 | 64.4 | 239   | 3 | US-09-987-899-560  | Sequence 560, App  |
| 136   | 174.5 | 64.4 | 240   | 3 | US-09-987-899-497  | Sequence 497, App  |
| 137   | 174.5 | 64.4 | 240   | 3 | US-09-987-899-607  | Sequence 607, App  |
| 138   | 174.5 | 64.4 | 241   | 3 | US-09-987-899-522  | Sequence 522, App  |
| 139   | 174.5 | 64.4 | 241   | 3 | US-09-987-899-539  | Sequence 539, App  |
| 140   | 174.5 | 64.4 | 241   | 3 | US-09-987-899-551  | Sequence 551, App  |
| 141   | 174.5 | 64.4 | 242   | 3 | US-09-987-899-485  | Sequence 485, App  |
| 142   | 174.5 | 64.4 | 242   | 3 | US-09-987-899-500  | Sequence 500, App  |
| 143   | 174.5 | 64.4 | 243   | 3 | US-09-987-899-486  | Sequence 486, App  |
| 144   | 174.5 | 64.4 | 243   | 3 | US-09-987-899-499  | Sequence 499, App  |
| 145   | 174.5 | 64.4 | 244   | 3 | US-09-987-899-467  | Sequence 467, App  |
| 146   | 174.5 | 64.4 | 244   | 3 | US-09-987-899-530  | Sequence 530, App  |
| 147   | 174.5 | 64.4 | 245   | 3 | US-09-987-899-525  | Sequence 525, App  |
| 148   | 174.5 | 64.4 | 245   | 3 | US-09-987-899-573  | Sequence 573, App  |
| 149   | 174.5 | 64.4 | 245   | 3 | US-09-987-899-574  | Sequence 574, App  |
| 150   | 174.5 | 64.4 | 245   | 3 | US-09-987-899-647  | Sequence 647, App  |

RESULT 1

US-09-854-286-15

Sequence 15, Application US/09854286

Patent No. US20020178467A1

GENERAL INFORMATION:

APPLICANT: Monsanto Technology LLC

APPLICANT: Dehesh, Katayoon

TITLE OF INVENTION: Plastid Transit Peptide Sequences for Efficient Plastid Targeting

FILE REFERENCE: US 60/203,618 38-77(15378)

CURRENT APPLICATION NUMBER: US/09/854,286

CURRENT FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: US 60/203,618

PRIOR FILING DATE: 2000-05-12

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.0

SEQ ID NO 15

LENGTH: 174

TYPE: DNA

ORGANISM: Pisum sativum

FEATURE:

NAME/KEY: CDS

LOCATION: (1) .. (174)

US-09-854-286-15

Alignment Scores:

Pred. No.: 7,99e-28

Length: 174

Score: 240.50

Matches: 52

Percent Similarity: 96.5%

Conservative: 3

Best Local Similarity: 91.2%

Mismatches: 1

Query Match: 88.7%

Indels: 1

DB: 3

Gaps: 1

US-10-628-525A-33 (1-56) x US-09-854-286-15 (1-174)

QY 1 MetalaseSerMetLeuSerSerAlaAlaValAlaThraArgThrAsnProAlaGlnAla 20

|||||

Db 1 ATGGCTTCTCAGTCTTCTCTGAGCAGTGGCCACCGCAGCAATGTTGCTCAAGCT 60

|||||

QY 21 SerMetValAlaProPheThrGlyLeuIysSerAlaAla---PheProValSerArgLys 39

|||||

Db 61 AACATGGTTGCACCTTCACTGGCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 120

|||||

QY 40 GlnAnLeuApsIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56

|||||

Db 121 CAAAACCTTGACATCACCTTCATTGCCAGCAACGGCGGAAGAGTGCAATGC 171

|||||

RESULT 2

US-09-839-477-3

Sequence 3, Application US/09839477

Publication No. US20030167523A1

GENERAL INFORMATION:

APPLICANT: Shorosh, Basil S.

APPLICANT: DeBonte, Lorin R.

TITLE OF INVENTION: PLANTS CONTAINING A CYTOSOLIC ACETYL

TITLE OF INVENTION: COA-CARBOXYLASE

FILE REFERENCE: 07148-094001

CURRENT APPLICATION NUMBER: US/09/839,477

CURRENT FILING DATE: 2001-04-20

PRIOR APPLICATION NUMBER: US 60/198,794

PRIOR FILING DATE: 2000-04-20

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 204

TYPE: DNA

ORGANISM: Nicotiana tabacum

FEATURE:

NAME/KEY: CDS

LOCATION: (1) .... (204)

US-09-839-477-3

Alignment Scores:

```
Pred. No.: 9,87e-28 Length: 204
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 3 Gaps: 1

US-10-628-525A-33 (1-56) x US-09-839-477-3 (1-204)

Qy 1 MetAlaSerSerMetLeuSerSerAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 1 ATGGCTTCCTCAGTTCCTTCCTGACAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60

Qy 21 SerMetValAlaProPheThrGlyLeuYsSerAlaAla---PheProValSerArgLys 39
Db 61 AACATGGTTCACCTTTCACCTGGGCTTAAGTCAGCTGCCTCATTTCCCTGTTTCAAGGAAG 120

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 171

RESULT 3
US-10-758-064-3
; Sequence 3, Application US/10758064
; Publication No. US20040128718A1
; GENERAL INFORMATION:
; APPLICANT: Shorosh, Basil S.
; APPLICANT: DeBonte, Lorin R.
; TITLE OF INVENTION: PLANTS CONTAINING A CYTOSOLIC ACETYL
; FILE REFERENCE: 07148-094001
; CURRENT APPLICATION NUMBER: US/10758,064
; PRIOR FILING DATE: 2004-01-15
; PRIOR FILING DATE: US/09/839,477
; PRIOR FILING DATE: 2001-04-20
; PRIOR FILING DATE: US 60/198,794
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 204
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(204)
US-10-758-064-3

Alignment Scores:
Pred. No.: 9,87e-28 Length: 204
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-758-064-3 (1-204)

Qy 1 MetAlaSerSerMetLeuSerSerAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 1 ATGGCTTCCTCAGTTCCTTCCTGACAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60

Qy 21 SerMetValAlaProPheThrGlyLeuYsSerAlaAla---PheProValSerArgLys 39
Db 61 AACATGGTTCACCTTTCACCTGGGCTTAAGTCAGCTGCCTCATTTCCCTGTTTCAAGGAAG 120

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 171

RESULT 4
US-10-487-901-7209
; Sequence 7209, Application US/10487901
```

```
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7209
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-7209

Alignment Scores:
Pred. No.: 1.62e-27 Length: 297
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 9 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-7209 (1-297)

Qy 1 MetAlaSerSerMetLeuSerSerAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 97 ATGGCTTCCTCAGTTCCTTCCTGACAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 156

Qy 21 SerMetValAlaProPheThrGlyLeuYsSerAlaAla---PheProValSerArgLys 39
Db 157 AACATGGTTCACCTTTCACAGGCTTTAAGTCTGCTCATTTCCCTGTTTCAAGGAAG 216

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 217 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 267

RESULT 5
US-10-487-901-3504
; Sequence 3504, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3504
; LENGTH: 377
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; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-3504

Alignment Scores:
Pred. No.: 2,22e-27 Length: 377
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservatives: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-3504 (1-377)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 68 ATGGCTTCTCAGTTCTTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 127
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 128 AACATGGTTGCACCTTTCACAGGCTTAAAGTCGCTGCCTCAFTCCCTGTTCAAGAAAG 187
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 188 CAAAACCTTGACATCACTTCCATTGCCAGCAGCAGTTGCCACGACGCGGAGAGTGCAATGC 238

RESULT 6
US-10-487-901-3503
; Sequence 3503, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; FILE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; CURRENT APPLICATION NUMBER: US/10/487,901
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3503
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-3503

Alignment Scores:
Pred. No.: 3,14e-27 Length: 489
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservatives: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-3503 (1-489)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 79 ATGGCTTCTCAGTTCTTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 138
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
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Db 139 AACATGGTTGCACCTTTCACAGGCTTAAAGTCGCTGCCTCATTCCTCTGTTCAAGAAAG 198
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 199 CAAAACCTTGACATCACTTCCATTGCCAGCAGCAGTTGCCACGACGCGGAGAGTGCAATGC 249

RESULT 7
US-10-487-901-7207
; Sequence 7207, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; FILE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; CURRENT APPLICATION NUMBER: US/10/487,901
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7207
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-7207

Alignment Scores:
Pred. No.: 3,26e-27 Length: 504
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservatives: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-7207 (1-504)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 78 ATGGCTTCTCAGTTCTTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 137
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 138 AACATGGTTGCACCTTTCACAGGCTTAAAGTCGCTGCCTCATTCCTCTGTTCAAGAAAG 197
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 198 CAAAACCTTGACATCACTTCCATTGCCAGCAGCAGTTGCCACGCGGAGAGTGCAATGC 248

RESULT 8
US-10-487-901-5765
; Sequence 5765, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
```



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; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5765
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-5765

Alignment Scores:
Pred. No.: 5.21e-27 Length: 718
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-5765 (1-718)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 45 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 104
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 105 AACATGGTTGCACCTTTCCTGCTTAAAGTCAGTCGCTGCTCCCTGTTTCAAGGAAG 164
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 165 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 215

RESULT 9
US-10-487-901-1704
; Sequence 1704, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1704
; LENGTH: 736
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-1704

Alignment Scores:
Pred. No.: 5.38e-27 Length: 736
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-1704 (1-736)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 63 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 122
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 123 AACATGGTTGCACCTTTCCTGCTTAAAGTCAGTCGCTGCTCCCTGTTTCAAGGAAG 182
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 183 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 233

RESULT 11
US-10-487-901-7208
; Sequence 7208, Application US/10487901
; Publication No. US20050091708A1
```

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Query Match: 88.7% Indels: 1
DB: Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-1704 (1-736)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 63 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 122
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 123 AACATGGTTGCACCTTTCCTGCTTAAAGTCAGTCGCTGCTCCCTGTTTCAAGGAAG 182
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 183 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 233

RESULT 10
US-10-487-901-5043
; Sequence 5043, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5043
; LENGTH: 736
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-5043

Alignment Scores:
Pred. No.: 5.38e-27 Length: 736
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-5043 (1-736)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 63 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 122
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 123 AACATGGTTGCACCTTTCCTGCTTAAAGTCAGTCGCTGCTCCCTGTTTCAAGGAAG 182
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 183 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 233

RESULT 11
US-10-487-901-7208
; Sequence 7208, Application US/10487901
; Publication No. US20050091708A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Oreido, Jeremiah Vincent
/ APPLICANT: McCrery, David
/ APPLICANT: Pell, Randy
/ APPLICANT: Miller, Barbara
/ APPLICANT: Weglarz, Thaddeus
/ APPLICANT: Gachotte, Daniel
/ APPLICANT: Blakeslee, Beth
/ APPLICANT: Lartinus, Ignacio
/ APPLICANT: Reddy, Avutu
/ APPLICANT: Shukla, Vipula
/ APPLICANT: Crosley, Rodney
/ TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
/ FILE REFERENCE: DOM-08552
/ CURRENT APPLICATION NUMBER: US/10/487,901
/ CURRENT FILING DATE: 2004-02-26
/ NUMBER OF SEQ ID NOS: 7560
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 7208
/ LENGTH: 668
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic
/ US-10-487-901-7208

Alignment Scores:
Pred. No.: 1,97e-26 Length: 668
Score: 236.50 Matches: 51
Percent Similarity: 94.7% Conservative: 3
Best Local Similarity: 89.5% Mismatches: 2
Query Match: 87.3% Indels: 1
DB: 9 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-7208 (1-668)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 50 ATGGCGGGCTCAGTCTTCTCTCAGCAGCAGTGGCCACCGCAGCAATGTTGCTCAAGCT 109
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 110 AACATGGTGTGCACCTTTTCACAGGCTCTTAAGTCTGCTGCCTCATTCCTCTGTTTCAAGAAG 169
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56
Db 170 CAAAACCTTGACATCATTCCATTGCCAGCAACGGCGGAAGAGTGAATGC 220

RESULT 12
US-10-165-420-3
/ Sequence 3, Application US/10165420
/ Publication No. US20030084482A1
/ GENERAL INFORMATION:
/ APPLICANT: HALL, GERALD
/ APPLICANT: BASCOMB, NEWELL
/ APPLICANT: BOSSIE, MARK
/ TITLE OF INVENTION: PRODUCTION OF PROTEINS IN PLANTS
/ FILE REFERENCE: 57117 (71758)
/ CURRENT APPLICATION NUMBER: US/10/165,420
/ CURRENT FILING DATE: 2002-09-10
/ PRIOR APPLICATION NUMBER: 60/297,103
/ PRIOR FILING DATE: 2001-06-08
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 169
/ TYPE: DNA
/ ORGANISM: Nicotiana tabacum
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (3)..(167)
/ US-10-165-420-3
```

```
Alignment Scores:
Pred. No.: 1,14e-25 Length: 169
Score: 226.50 Matches: 50
Percent Similarity: 96.4% Conservative: 3
Best Local Similarity: 90.9% Mismatches: 1
Query Match: 83.1% Indels: 1
DB: 5 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-165-420-3 (1-169)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 3 ATGGGCTTCTCAGTCTTCTCTCAGCAGTGGCCACCGCAGCAATGTTGCTCAAGCT 62
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 63 AACATGGTGTGCACCTTTTCACAGGCTCTTAAGTCTGCTGCCTCATTCCTCTGTTTCAAGAAG 122
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAenGlyGlyArgVal 54
Db 123 CAAAACCTTGACATCATTCCATTGCCAGCAACGGCGGAAGAGTG 167

RESULT 13
US-09-855-341-7
/ Sequence 7, Application US/09855341
/ Patent No. US2002002715A1
/ GENERAL INFORMATION:
/ APPLICANT: VIITANEN, PAUL V.
/ APPLICANT: MEYER, KNUD
/ APPLICANT: VAN DYK, DREW
/ TITLE OF INVENTION: HIGH LEVEL PRODUCTION OF P-HYDROXYBENZOIC ACID
/ TITLE OF INVENTION: IN GREEN PLANTS
/ FILE REFERENCE: BC1015 US NA
/ CURRENT APPLICATION NUMBER: US/09/855,341
/ CURRENT FILING DATE: 2001-05-15
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: MICROSOFT OFFICE 97
/ SEQ ID NO 7
/ LENGTH: 684
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:synthetic CPL
/ US-09-855-341-7

Alignment Scores:
Pred. No.: 2,11e-24 Length: 684
Score: 223.50 Matches: 47
Percent Similarity: 93.0% Conservative: 6
Best Local Similarity: 82.5% Mismatches: 3
Query Match: 82.5% Indels: 1
DB: 3 Gaps: 1

US-10-628-525A-33 (1-56) x US-09-855-341-7 (1-684)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 1 ATGGGCTTCTCAGTCTTCTCTCAGCAGTGGCCACCGCAGCAATGTTTACACAAGCT 60
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 61 AGCATGGTGTGCACCTTTTCACAGGCTCTCAAAATCTTCAGCCACTTTCCTCTGTTTCAAGAAG 120
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56
Db 121 CAAAACCTTGACATCATTCCATTGCCAGCAACGGCGGAAGAGTGAATGC 171

RESULT 14
US-09-896-866B-16
/ Sequence 16, Application US/09896866B
/ Patent No. US20020151002A1
/ GENERAL INFORMATION:
/ APPLICANT: Flint, Dennis
```

```
; APPLICANT: Meyer, Knut
; APPLICANT: Viitanen, Paul
; TITLE OF INVENTION: Sinapoylglucose:Malate Sinapoyltransferase Form Malate Conjugates
; FILE REFERENCE: BC1034 US NA
; CURRENT APPLICATION NUMBER: US/09/896,866B
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/216,615
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: open reading frame of the chloroplast-targeted CPL fusion protein
US-09-896-866B-16

Alignment Scores:
Pred. No.: 2,11e-24 Length: 684
Score: 223.50 Matches: 47
Percent Similarity: 93.0% Conservative: 6
Best Local Similarity: 82.5% Mismatches: 3
Query Match: 82.5% Indels: 1
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x US-09-896-866B-16 (1-684)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgThrAsnProAlaGlnAla 20
Db 1 ATGGCTTCCTCTGCTCATTTCTTCAGCAGCTGTGGCCACAGCAGCAATGTTACACAAGCT 60
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 61 AGCATGGTTGCACCTTTCACCTGCTCTCAAAATCTTCAGCCACTTTCCTCTGTACAAAGAAG 120
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 121 CAAAACCTTGACATCATCTTCATTGCTAGCAATGGTGGGAAGAGTTAGCTGC 171

RESULT 15
US-10-359-369-41
; Sequence 41, Application US/10359369
; Publication No. US20030215927A1
; GENERAL INFORMATION:
; APPLICANT: E. I. duPont de Nemours and Company, Inc.
; APPLICANT: Viitanen, Paul
; APPLICANT: Meyer, Knut
; APPLICANT: Van Dyk, Drew
; TITLE OF INVENTION: UDP-Glucosyltransferases
; FILE REFERENCE: CL1821 US NA
; CURRENT APPLICATION NUMBER: US/10/359,369
; CURRENT FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: 60/355,511
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 41
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(684)
US-10-359-369-41

Alignment Scores:
Pred. No.: 2,11e-24 Length: 684
Score: 223.50 Matches: 47
Percent Similarity: 93.0% Conservative: 6
Best Local Similarity: 82.5% Mismatches: 3
```

```
Query Match: 82.5% Indels: 1
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-359-369-41 (1-684)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgThrAsnProAlaGlnAla 20
Db 1 ATGGCTTCCTCTGCTCATTTCTTCAGCAGCTGTGGCCACAGCAGCAATGTTACACAAGCT 60
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 61 AGCATGGTTGCACCTTTCACCTGCTCTCAAAATCTTCAGCCACTTTCCTCTGTACAAAGAAG 120
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 121 CAAAACCTTGACATCATCTTCATTGCTAGCAATGGTGGGAAGAGTTAGCTGC 171

RESULT 16
US-10-699-050-16
; Sequence 16, Application US/10699050
; Publication No. US20040142437A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Dennis
; APPLICANT: Meyer, Knut
; APPLICANT: Viitanen, Paul
; TITLE OF INVENTION: Sinapoylglucose:Malate Sinapoyltransferase Form Malate Conjugates
; FILE REFERENCE: BC1034 US NA
; CURRENT APPLICATION NUMBER: US/10/699,050
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: US/09/896,866B
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/216,615
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: open reading frame of the chloroplast-targeted CPL fusion protein
US-10-699-050-16

Alignment Scores:
Pred. No.: 2,11e-24 Length: 684
Score: 223.50 Matches: 47
Percent Similarity: 93.0% Conservative: 6
Best Local Similarity: 82.5% Mismatches: 3
Query Match: 82.5% Indels: 1
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-699-050-16 (1-684)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgThrAsnProAlaGlnAla 20
Db 1 ATGGCTTCCTCTGCTCATTTCTTCAGCAGCTGTGGCCACAGCAGCAATGTTACACAAGCT 60
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 61 AGCATGGTTGCACCTTTCACCTGCTCTCAAAATCTTCAGCCACTTTCCTCTGTACAAAGAAG 120
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 121 CAAAACCTTGACATCATCTTCATTGCTAGCAATGGTGGGAAGAGTTAGCTGC 171

RESULT 17
US-10-718-311-7
; Sequence 7, Application US/10718311
; Publication No. US2004014367A1
; GENERAL INFORMATION:
; APPLICANT: VIITANEN, PAUL V.
```

APPLICANT: MEYER, KNU  
APPLICANT: VAN DYK, DREW  
TITLE OF INVENTION: HIGH LEVEL PRODUCTION OF P-HYDROXYBENZOIC ACID  
FILE REFERENCE: BCI015 US NA  
CURRENT APPLICATION NUMBER: US/10/718,311  
PRIOR FILING DATE: 2003-11-20  
CURRENT APPLICATION NUMBER: US/09/855,341  
PRIOR FILING DATE: 2001-05-15  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: MICROSOFT OFFICE 97  
SEQ ID NO 7  
LENGTH: 684  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:synthetic CPL

US-10-718-311-7

Alignment Scores:

Pred. No.: 2,11e-24 Length: 684

Score: 223.50 Matches: 47

Percent Similarity: 93.0% Conservative: 6

Best Local Similarity: 82.5% Mismatches: 3

Query Match: 82.5% Indels: 1

DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-718-311-7 (1-684)

QY 1 MetaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20

DB 1 ATGGCTTCCTCTGTCATTTCTTCAGCAGCTGTTGCCACAGCAATGTTACACAAGCT 60

QY 21 SerMetValAlaProPheThrGlyLeuIysSerAlaAala---PheProValSerArgIys 39

DB 61 AGCATGGTTGCCACCTTTCTACTGGTCTCAAAATCTTCAGCCACTTTCCTCTTTACAAGAAG 120

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

DB 121 CAAACCTTGACATCACTTCATTGCTAGCAATGGTGGAGAAGATTAGCTGC 171

RESULT 18

US-10-462-162-33

Sequence 33, Application US/10462162

Publication No. US20040261147A1

GENERAL INFORMATION:

APPLICANT: E.I. duPont de Nemours and Company, Inc.

APPLICANT: Meyer, Knut

APPLICANT: Viitanen, Paul

APPLICANT: Flint, Dennis

TITLE OF INVENTION: High Level Production of Arbutin in Green Plants and Microbes

FILE REFERENCE: CL 2155 US NA

CURRENT APPLICATION NUMBER: US/10/462,162

CURRENT FILING DATE: 2003-06-16

NUMBER OF SEQ ID NOS: 54

SOFTWARE: Microsoft Office 97

SEQ ID NO 33

LENGTH: 684

TYPE: DNA

ORGANISM: Escherichia coli

US-10-462-162-33

Alignment Scores:

Pred. No.: 2,11e-24 Length: 684

Score: 223.50 Matches: 47

Percent Similarity: 93.0% Conservative: 6

Best Local Similarity: 82.5% Mismatches: 3

Query Match: 82.5% Indels: 1

DB: 8 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-462-162-33 (1-684)

QY 1 MetaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20

Db 1 ATGGCTTCCTCTGTCATTTCTTCAGCAGCTGTTGCCACAGCAATGTTACACAAGCT 60

QY 21 SerMetValAlaProPheThrGlyLeuIysSerAlaAala---PheProValSerArgIys 39

Db 61 AGCATGGTTGCCACCTTTCTACTGGTCTCAAAATCTTCAGCCACTTTCCTCTTTACAAGAAG 120

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

Db 121 CAAACCTTGACATCACTTCATTGCTAGCAATGGTGGAGAAGATTAGCTGC 171

RESULT 19

US-10-487-901-1703

Sequence 1703, Application US/10487901

Publication No. US20050091708A1

GENERAL INFORMATION:

APPLICANT: Oreido, Jeremiah Vincent

APPLICANT: McCrery, David

APPLICANT: Pell, Randy

APPLICANT: Miller, Barbara

APPLICANT: Weglarz, Thaddeus

APPLICANT: Gachotte, Daniel

APPLICANT: Blakeslee, Beth

APPLICANT: Larrinua, Ignacio

APPLICANT: Reddy, Avutu

APPLICANT: Shukla, Vipula

APPLICANT: Crosley, Rodney

TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteris

FILE REFERENCE: DOM-08552

CURRENT APPLICATION NUMBER: US/10/487,901

CURRENT FILING DATE: 2004-02-26

NUMBER OF SEQ ID NOS: 7560

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1703

LENGTH: 714

TYPE: DNA

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Synthetic

US-10-487-901-1703

Alignment Scores:

Pred. No.: 5,44e-24 Length: 714

Score: 221.00 Matches: 50

Percent Similarity: 91.4% Conservative: 3

Best Local Similarity: 86.2% Mismatches: 3

Query Match: 81.5% Indels: 2

DB: 9 Gaps: 2

US-10-628-525A-33 (1-56) x US-10-487-901-1703 (1-714)

QY 1 MetaSerSerMetLeuSerSer---AlaAlaValAlaThrArgThrAsnProAlaGln 19

Db 21 ATGGCTTCCTCAGTTATGTTCTCAGCTGCGCTGTTGCCACCGCGCCCAATGCTGCTCAA 80

QY 20 AlaSerMetValAlaProPheThrGlyLeuIysSerAla---AlaPheProValSerArg 38

Db 81 GCCAGTATGGTTGACCTTTCTACTGGCTCAAGTCGCAACCTCTCTCTCTTTCCAGA 140

QY 39 LysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

Db 141 AAACAAACCTTGACATTCTTCATTGCTAGCAACGGCGGAAGATTCAATGC 194

RESULT 20

US-10-487-901-5044

Sequence 5044, Application US/10487901

Publication No. US20050091708A1

GENERAL INFORMATION:

APPLICANT: Oreido, Jeremiah Vincent

APPLICANT: McCrery, David

APPLICANT: Pell, Randy

APPLICANT: Weglarz, Thaddeus

|                        |         |               |     |
|------------------------|---------|---------------|-----|
| Pred. No.:             | 1.5e-23 | Length:       | 693 |
| Score:                 | 218.00  | Matches:      | 49  |
| Percent Similarity:    | 91.4%   | Conservative: | 4   |
| Best Local Similarity: | 84.5%   | Mismatches:   | 3   |
| Query Match:           | 80.4%   | Indels:       | 2   |
| DB:                    | 9       | Gaps:         | 2   |

US-10-628-525A-33 (1-56) x US-10-487-901-1713 (1-683)

|    |     |                                                               |                                      |    |
|----|-----|---------------------------------------------------------------|--------------------------------------|----|
| Qy | 1   | MetAlaSerSerMetLeuSerSer                                      | ---AlaAlaValAlaThrArgThrAsnProAlaGln | 19 |
| Db | 40  | ATGGCTTCCTCTGTGATTTCTTCCTCAGCTGCTGCGGTTCACCGGGCTTAATGCTGCTCAA | 99                                   |    |
| Qy | 20  | AlaSerMetValAlaProPhrThrGlyLeuLysSerAla                       | ---AlaPheProValSerArg                | 38 |
| Db | 100 | GCACGACATGTTGCACCCCTTCACTGGCCCTCAAATCGCTTCCTTCCTTCCTGTTACCAGA | 15                                   |    |
| Qy | 39  | LysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys        | 56                                   |    |
| Db | 160 | AAACAAACCTTGACATTACATCCATTCCTAGCNAATGGTGGAGAGTCCATGC          | 213                                  |    |

RESULT 22

US-10-487-901-5045

; Sequence 5045, Application US/10487901

; Publication No. US20050091708A1

GENERAL INFORMATION:

; APPLICANT: Oreido, Jeremiah Vincent

; APPLICANT: McCrery, David

; APPLICANT: Pell, Randy

; APPLICANT: Miller, Barbara

; APPLICANT: Weglarz, Thaddeus

; APPLICANT: Gachotte, Daniel

; APPLICANT: Blakeslee, Beth

; APPLICANT: Larrinua, Ignacio

; APPLICANT: Reddy, Avutu

; APPLICANT: Shukla, Vipula

; APPLICANT: Crosley, Rodney

; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic

; FILE REFERENCE: DOW-08552

; CURRENT APPLICATION NUMBER: US/10/487,901

; CURRENT FILING DATE: 2004-02-26

; NUMBER OF SEQ ID NOS: 7560

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5045

; LENGTH: 737

; TYPE: DNA

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-487-901-5045

|                        |          |               |     |
|------------------------|----------|---------------|-----|
| Alignment Scores:      |          |               |     |
| Pred. No.:             | 1.66e-23 | Length:       | 737 |
| Score:                 | 218.00   | Matches:      | 49  |
| Percent Similarity:    | 91.4%    | Conservative: | 4   |
| Best Local Similarity: | 84.5%    | Mismatches:   | 3   |
| Query Match:           | 80.4%    | Indels:       | 2   |
| DB:                    | 9        | Gaps:         | 2   |

US-10-628-525A-33 (1-56) x US-10-487-901-5045 (1-737)

|    |     |                                                               |                                      |    |
|----|-----|---------------------------------------------------------------|--------------------------------------|----|
| Qy | 1   | MetAlaSerSerMetLeuSerSer                                      | ---AlaAlaValAlaThrArgThrAsnProAlaGln | 19 |
| Db | 40  | ATGGCTTCCTCTGTGATTTCTTCCTCAGCTGCTGCGGTTCACCGGGCTTAATGCTGCTCAA | 99                                   |    |
| Qy | 20  | AlaSerMetValAlaProPhrThrGlyLeuLysSerAla                       | ---AlaPheProValSerArg                | 38 |
| Db | 100 | GCACGACATGTTGCACCCCTTCACTGGCCCTCAAATCGCTTCCTTCCTTCCTGTTACCAGA | 15                                   |    |
| Qy | 39  | LysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys        | 56                                   |    |
| Db | 160 | AAACAAACCTTGACATTACATCCATTCCTAGCNAATGGTGGAGAGTCCATGC          | 213                                  |    |



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Db 62 ATGGCTTCTCAGTTATGTCTCAGCAGCTGCTGTTGGACGGCGCAATGCTGCTCAA 121
Qy 20 AlaSerMetValAlaProPheThrGlyLeuYsSerAla---AlaPheProValSerArg 38
Db 122 GCCAACATGGTTGCACCTTCACTGGGCTCAAGTCCGCTCTCTCTTCCCTGTACCAGG 181
Qy 39 LysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 182 AAACAAACCTTGACATTACCTCCATTGCTAGCAATGGTGGAGAGATTCAATGC 235

RESULT 26
US-10-487-901-5028
; Sequence 5028, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5028
; LENGTH: 754
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-5028

Alignment Scores:
Pred. No.: 4,98e-23 Length: 754
Score: 215.00 Matches: 48
Percent Similarity: 91.4% Conservative: 5
Best Local Similarity: 82.8% Mismatches: 3
Query Match: 79.3% Indels: 2
DB: 9 Gaps: 2

US-10-628-525A-33 (1-56) x US-10-487-901-5028 (1-754)
Qy 1 MetAlaSerSerMetLeuSerSer---AlaAlaValAlaThrArgThrAsnProAlaGln 19
Db 64 ATGGCTTCTCAGTTATGTCTCAGCAGCTGCTGTTGGACGGCGCAATGCTGCTCAA 123
Qy 20 AlaSerMetValAlaProPheThrGlyLeuYsSerAla---AlaPheProValSerArg 38
Db 124 GCCAACATGGTTGCACCTTCACTGGGCTCAAGTCCGCTCTCTCTTCCCTGTACCAGG 183
Qy 39 LysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 184 AAACAAACCTTGACATTACCTCCATTGCTAGCAATGGTGGAGAGATTCAATGC 237

RESULT 27
US-09-732-627A-1176
; Sequence 1176, Application US/09732627A
; Publication No. US20040123338A1
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: Plants
; FILE REFERENCE: 38-21(51770)B
; CURRENT APPLICATION NUMBER: US/09/732,627A
; CURRENT FILING DATE: 2000-12-08
```

```
; NUMBER OF SEQ ID NOS: 4930
; SEQ ID NO 1176
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3493-057-P1-M1-D1
US-09-732-627A-1176
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Alignment Scores:
Pred. No.: 1,46e-22 Length: 385
Score: 209.50 Matches: 45
Percent Similarity: 89.8% Conservative: 8
Best Local Similarity: 76.3% Mismatches: 3
Query Match: 77.3% Indels: 3
DB: 3 Gaps: 2
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US-10-628-525A-33 (1-56) x US-09-732-627A-1176 (1-385)

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Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 159 ATGGCTTCTCCTCCATGATCTCATCGGCAACCATTTGCCACCGTGAACCGCTCTCTCCCGGCA 218
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuYsSer---AlaAlaPheProValSer 37
Db 219 CAGGCCAACATGGTGGCCCCCTTTCACCGGCTCCTCAATCTGGCTCTGCTTTCCAGTCACC 278
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 279 AGGAGGCCAACCAACGACATCATCTTCTTTCGACGACACGCTGGGAGAGTGCATATGC 335
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#### RESULT 28

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US-09-910-664-55
; Sequence 55, Application US/09910664
; Publication No. US20020194646A1
; GENERAL INFORMATION:
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```
; APPLICANT: FOGUE, Greg P.
; APPLICANT: DELLA-CIOPPA, Guy R.
; APPLICANT: WOLFE, Gerson M.
; APPLICANT: ZHENG, Wenjin
; TITLE OF INVENTION: METHODS OF CREATING DWARP PHENOTYPES IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 008010189000U01
; CURRENT APPLICATION NUMBER: US/09/910,664
; CURRENT FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 724
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-910-664-55
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Alignment Scores:
Pred. No.: 6,86e-22 Length: 724
Score: 207.50 Matches: 47
Percent Similarity: 87.7% Conservative: 3
Best Local Similarity: 82.5% Mismatches: 4
Query Match: 76.6% Indels: 3
DB: 3 Gaps: 2
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US-10-628-525A-33 (1-56) x US-09-910-664-55 (1-724)

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Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 43 ATGGCTTCTCCTATGCTCTCTCCCGCGCTGTGGTT-----ACATCCCGGCTCAGGCC 96
Qy 21 SerMetValAlaProPheThrGlyLeuYs---SerAlaAlaPheProValSerArgLys 39
Db 97 ACCATGGTCGCTCCATTCACCGGCTTGAAGTCATCGCTGCATTCGCGGTCCACCGCAG 156
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
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Db 157 ACCAACAGGACATCATCTTCATCGCAAGCAACGGGGAAGAGTTAGCTGC 207

## RESULT 29

US-10-333-184-54

; Sequence 54, Application US/10333184

; Publication No. US20040088762A1

; GENERAL INFORMATION:

; APPLICANT: Reddy, Avutu

; APPLICANT: Larrinua, Ignacio

; APPLICANT: Skokut, Thomas

; APPLICANT: Smith, Doug

; APPLICANT: Hu, Zihua

; APPLICANT: Ruegger, Max

; APPLICANT: Shukla, Vipula

; APPLICANT: Bauer, Teresa

; APPLICANT: Weglarz, Ted

; APPLICANT: Blakslee, Beth

; APPLICANT: Oriedo, Jeremiah

; APPLICANT: Savickas, Philip

; APPLICANT: McCrery, David

; APPLICANT: Miller, Barbara

; APPLICANT: della-Cioppa, Gregory

; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Dwarfism Phenotype

; FILE REFERENCE: DOM-04681

; CURRENT APPLICATION NUMBER: US/10/333,184

; PRIOR FILING DATE: 2003-10-10

; PRIOR APPLICATION NUMBER: 60/219,809

; PRIOR FILING DATE: 2000-07-20

; NUMBER OF SEQ ID NOS: 571

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 54

; LENGTH: 724

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-10-333-184-54

## Alignment Scores:

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| Pred. No.:             | 6.86e-22 | Length:       | 724 |
| Score:                 | 207.50   | Matches:      | 47  |
| Percent Similarity:    | 87.7%    | Conservative: | 3   |
| Best Local Similarity: | 82.5%    | Mismatches:   | 4   |
| Query Match:           | 76.6%    | Indels:       | 3   |
| DB:                    | 7        | Gaps:         | 2   |

US-10-628-525A-33 (1-56) x US-10-333-184-54 (1-724)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20

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QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39

Db 97 ACCATGGTCGCTCCATTTCACCGGCTTGAAGTCATCCGCTGCATTCGCGTACCCGCGCAAG 156

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

Db 157 ACCAACAGGACATCATCTTCATCGCAAGCAACGGGGAAGAGTTAGCTGC 207

## RESULT 30

US-10-333-184-202

; Sequence 202, Application US/10333184

; Publication No. US20040088762A1

; GENERAL INFORMATION:

; APPLICANT: Reddy, Avutu

; APPLICANT: Larrinua, Ignacio

; APPLICANT: Skokut, Thomas

; APPLICANT: Smith, Doug

; APPLICANT: Hu, Zihua

; APPLICANT: Ruegger, Max

; APPLICANT: Shukla, Vipula

; APPLICANT: Bauer, Teresa

; APPLICANT: Weglarz, Ted

; APPLICANT: Blakslee, Beth

; APPLICANT: Oriedo, Jeremiah  
; APPLICANT: Savickas, Philip  
; APPLICANT: McCrery, David  
; APPLICANT: Miller, Barbara  
; APPLICANT: della-Cioppa, Gregory  
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Dwarfism Phenotype  
; FILE REFERENCE: DOM-04681  
; CURRENT APPLICATION NUMBER: US/10/333,184  
; CURRENT FILING DATE: 2003-10-10  
; PRIOR APPLICATION NUMBER: 60/219,809  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 571  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 202  
; LENGTH: 726  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-333-184-202

## Alignment Scores:

|                        |          |               |     |
|------------------------|----------|---------------|-----|
| Pred. No.:             | 6.89e-22 | Length:       | 726 |
| Score:                 | 207.50   | Matches:      | 47  |
| Percent Similarity:    | 87.7%    | Conservative: | 3   |
| Best Local Similarity: | 82.5%    | Mismatches:   | 4   |
| Query Match:           | 76.6%    | Indels:       | 3   |
| DB:                    | 7        | Gaps:         | 2   |

US-10-628-525A-33 (1-56) x US-10-333-184-202 (1-726)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20

Db 45 ATGGCTTCCTCTATGCTCTCTCCCGCGCTGTGGTT-----ACATCCCGGCTCAGGCC 98

QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39

Db 99 ACCATGGTCGCTCCATTTCACCGGCTTGAAGTCATCCGCTGCATTCGCGTACCCGCGCAAG 158

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

Db 159 ACCAACAGGACATCATCTTCATCGCAAGCAACGGGGAAGAGTTAGCTGC 209

Search completed: April 2, 2006, 02:04:07

Job time : 268.573 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 2, 2006, 01:09:48 ; Search time 174.864 Seconds  
(without alignments)  
1278.753 Million cell updates/sec

Title: us-10-628-525a-33

Perfect score: 271

Sequence: 1 MASSMLSSAAVATRTNPAQA.....SRQNLDITSIAHGGRVQC 56

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| Delop 6.0   |          |             | 7.0         |

Searched: 9263891 seqs, 1996499642 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Published Applications\_NA.New:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 1          | 181.5 | 67.0        | 264    | 8  | US-10-840-688-19 |
| 2          | 91    | 33.6        | 416    | 14 | US-11-192-801-25 |

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| 3  | 91   | 33.6 | 416     | 14 | US-11-192-801-30      | Sequence 30, Appl   |
| 4  | 91   | 33.6 | 3450    | 14 | US-11-192-801-17      | Sequence 17, Appl   |
| 5  | 91   | 33.6 | 3455    | 14 | US-11-192-801-36      | Sequence 16, Appl   |
| 6  | 91   | 33.6 | 4149    | 14 | US-11-192-801-13      | Sequence 13, Appl   |
| 7  | 65.5 | 24.2 | 484     | 9  | US-10-301-480-72126   | Sequence 72126, A   |
| 8  | 65.5 | 24.2 | 484     | 10 | US-10-301-480-685535  | Sequence 685535, A  |
| 9  | 64.5 | 23.8 | 201     | 8  | US-10-995-561-61428   | Sequence 61428, A   |
| 10 | 64.5 | 23.8 | 201     | 8  | US-10-995-561-69122   | Sequence 69122, A   |
| 11 | 64.5 | 23.8 | 23803   | 8  | US-10-995-561-13406   | Sequence 13406, A   |
| 12 | 64.5 | 23.8 | 26096   | 8  | US-10-995-561-13353   | Sequence 13353, A   |
| 13 | 63.5 | 23.4 | 2024    | 14 | US-11-079-122-9       | Sequence 9, Appl    |
| 14 | 63.5 | 23.4 | 2024    | 14 | US-11-079-122-10      | Sequence 10, Appl   |
| 15 | 63.5 | 23.4 | 2024    | 14 | US-11-079-122-14      | Sequence 14, Appl   |
| 16 | 63   | 23.2 | 1863    | 8  | US-10-750-185-46879   | Sequence 46879, A   |
| 17 | 63   | 23.2 | 1863    | 8  | US-10-750-623-66879   | Sequence 66879, A   |
| 18 | 62.5 | 23.1 | 573     | 6  | US-09-925-065A-427150 | Sequence 427150, A  |
| 19 | 62.5 | 23.1 | 589     | 10 | US-10-301-480-490520  | Sequence 490520, A  |
| 20 | 62.5 | 23.1 | 589     | 10 | US-10-301-480-1103929 | Sequence 1103929, A |
| 21 | 62.5 | 23.1 | 885     | 9  | US-10-932-182A-77417  | Sequence 77417, A   |
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| 23 | 61.5 | 22.7 | 557     | 6  | US-09-925-065A-461364 | Sequence 461364, A  |
| 24 | 61.5 | 22.7 | 557     | 6  | US-09-925-065A-933859 | Sequence 933859, A  |
| 25 | 61.5 | 22.7 | 692     | 6  | US-09-925-065A-933860 | Sequence 933860, A  |
| 26 | 61.5 | 22.7 | 692     | 6  | US-09-925-065A-921611 | Sequence 921611, A  |
| 27 | 61.5 | 22.7 | 787     | 6  | US-09-925-065A-921610 | Sequence 921610, A  |
| 28 | 61   | 22.5 | 562     | 6  | US-09-925-065A-483931 | Sequence 483931, A  |
| 29 | 61   | 22.5 | 4911    | 9  | US-10-932-182A-75783  | Sequence 75783, A   |
| 30 | 61   | 22.5 | 4911    | 9  | US-10-932-182A-75783  | Sequence 75783, A   |
| 31 | 60.5 | 22.3 | 879     | 10 | US-10-301-480-577229  | Sequence 577229, A  |
| 32 | 60.5 | 22.3 | 879     | 10 | US-10-301-480-1190638 | Sequence 1190638, A |
| 33 | 60.5 | 22.3 | 1993    | 14 | US-11-120-308-43      | Sequence 43, Appl   |
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| 35 | 60   | 22.1 | 537     | 9  | US-10-301-480-94718   | Sequence 94718, A   |
| 36 | 60   | 22.1 | 537     | 9  | US-10-301-480-94719   | Sequence 94719, A   |
| 37 | 60   | 22.1 | 537     | 10 | US-10-301-480-708126  | Sequence 708126, A  |
| 38 | 60   | 22.1 | 537     | 10 | US-10-301-480-708127  | Sequence 708127, A  |
| 39 | 60   | 22.1 | 537     | 10 | US-10-301-480-708128  | Sequence 708128, A  |
| 40 | 60   | 22.1 | 646     | 6  | US-09-925-065A-944984 | Sequence 944984, A  |
| 41 | 60   | 22.1 | 1817    | 11 | US-11-096-568A-34432  | Sequence 34432, A   |
| 42 | 60   | 22.1 | 116956  | 14 | US-11-143-980-1       | Sequence 1, Appl    |
| 43 | 59.5 | 22.0 | 525     | 6  | US-09-925-065A-800643 | Sequence 800643, A  |
| 44 | 59.5 | 22.0 | 528     | 10 | US-10-301-480-337736  | Sequence 337736, A  |
| 45 | 59.5 | 22.0 | 528     | 10 | US-10-301-480-337737  | Sequence 337737, A  |
| 46 | 59.5 | 22.0 | 528     | 10 | US-10-301-480-337738  | Sequence 337738, A  |
| 47 | 59.5 | 22.0 | 528     | 10 | US-10-301-480-337739  | Sequence 337739, A  |
| 48 | 59.5 | 22.0 | 528     | 10 | US-10-301-480-951145  | Sequence 951145, A  |
| 49 | 59.5 | 22.0 | 528     | 10 | US-10-301-480-951146  | Sequence 951146, A  |
| 50 | 59.5 | 22.0 | 528     | 10 | US-10-301-480-951147  | Sequence 951147, A  |
| 51 | 59.5 | 22.0 | 528     | 10 | US-10-301-480-951148  | Sequence 951148, A  |
| 52 | 59.5 | 22.0 | 531     | 6  | US-09-925-065A-259176 | Sequence 259176, A  |
| 53 | 59.5 | 22.0 | 531     | 6  | US-09-925-065A-259177 | Sequence 259177, A  |
| 54 | 59.5 | 22.0 | 531     | 6  | US-09-925-065A-259178 | Sequence 259178, A  |
| 55 | 59.5 | 22.0 | 531     | 6  | US-09-925-065A-259179 | Sequence 259179, A  |
| 56 | 59   | 21.8 | 1006    | 8  | US-10-750-185-45531   | Sequence 45531, A   |
| 57 | 59   | 21.8 | 1006    | 8  | US-10-750-623-45531   | Sequence 45531, A   |
| 58 | 59   | 21.8 | 1582    | 8  | US-10-750-185-42328   | Sequence 42328, A   |
| 59 | 59   | 21.8 | 1582    | 8  | US-10-750-623-42328   | Sequence 42328, A   |
| 60 | 59   | 21.8 | 2370    | 14 | US-11-128-061-442     | Sequence 442, A     |
| 61 | 59   | 21.8 | 2370    | 14 | US-11-128-049-442     | Sequence 442, A     |
| 62 | 58.5 | 21.6 | 201     | 8  | US-10-995-561-61429   | Sequence 61429, A   |
| 63 | 58.5 | 21.6 | 201     | 8  | US-10-995-561-69123   | Sequence 69123, A   |
| 64 | 58.5 | 21.6 | 151052  | 9  | US-10-330-773-503     | Sequence 503, A     |
| 65 | 58.5 | 21.6 | 295772  | 9  | US-10-330-773-503     | Sequence 503, A     |
| 66 | 58.5 | 21.6 | 1125000 | 8  | US-10-995-561-13286   | Sequence 13286, A   |
| 67 | 58   | 21.4 | 585     | 10 | US-10-301-480-302646  | Sequence 302646, A  |
| 68 | 58   | 21.4 | 585     | 10 | US-10-301-480-916055  | Sequence 916055, A  |
| 69 | 58   | 21.4 | 588     | 6  | US-09-925-065A-216134 | Sequence 216134, A  |
| 70 | 58   | 21.4 | 592     | 6  | US-09-925-065A-635611 | Sequence 635611, A  |
| 71 | 58   | 21.4 | 727     | 8  | US-10-821-234-354     | Sequence 354, A     |
| 72 | 58   | 21.4 | 971     | 10 | US-10-301-480-559838  | Sequence 559838, A  |
| 73 | 58   | 21.4 | 971     | 10 | US-10-301-480-1173247 | Sequence 1173247, A |
| 74 | 58   | 21.4 | 979     | 10 | US-10-301-480-582739  | Sequence 582739, A  |
| 75 | 58   | 21.4 | 979     | 10 | US-10-301-480-1196148 | Sequence 1196148, A |

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| 78    | 58   | 21.4 | 1495   | 14 | US-11-112-908-373     | Sequence 373, App |
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| C 81  | 58   | 21.4 | 2043   | 10 | US-10-301-480-707866  | Sequence 707866,  |
| C 82  | 58   | 21.4 | 49355  | 9  | US-10-330-773-787     | Sequence 787, App |
| C 83  | 58   | 21.4 | 94911  | 9  | US-10-330-773-823     | Sequence 823, App |
| C 84  | 58   | 21.4 | 161994 | 14 | US-11-112-908-57      | Sequence 57, Appl |
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| 86    | 57.5 | 21.2 | 588    | 6  | US-09-925-065A-70893  | Sequence 70893, A |
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| C 89  | 57.5 | 21.2 | 624    | 6  | US-09-925-065A-292502 | Sequence 292502,  |
| C 90  | 57.5 | 21.2 | 626    | 10 | US-10-301-480-369383  | Sequence 369383,  |
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| C 92  | 57.5 | 21.2 | 629    | 6  | US-09-925-065A-625003 | Sequence 625003,  |
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| C 100 | 57.5 | 21.2 | 1021   | 9  | US-10-301-480-127598  | Sequence 127598,  |
| C 101 | 57.5 | 21.2 | 1021   | 9  | US-10-301-480-127599  | Sequence 127599,  |
| C 102 | 57.5 | 21.2 | 1021   | 9  | US-10-301-480-131229  | Sequence 131229,  |
| C 103 | 57.5 | 21.2 | 1021   | 9  | US-10-301-480-131230  | Sequence 131230,  |
| C 104 | 57.5 | 21.2 | 1021   | 10 | US-10-301-480-741006  | Sequence 741006,  |
| C 105 | 57.5 | 21.2 | 1021   | 10 | US-10-301-480-741007  | Sequence 741007,  |
| C 106 | 57.5 | 21.2 | 1021   | 10 | US-10-301-480-741008  | Sequence 741008,  |
| C 107 | 57.5 | 21.2 | 1021   | 10 | US-10-301-480-744638  | Sequence 744638,  |
| C 108 | 57.5 | 21.2 | 1021   | 10 | US-10-301-480-744639  | Sequence 744639,  |
| C 109 | 57.5 | 21.2 | 1514   | 11 | US-11-096-568A-31322  | Sequence 31322, A |
| C 110 | 57.5 | 21.2 | 1556   | 8  | US-10-750-185-51095   | Sequence 51095, A |
| C 111 | 57.5 | 21.2 | 1556   | 8  | US-10-750-623-62676   | Sequence 62676, A |
| C 112 | 57   | 21.0 | 498    | 6  | US-09-925-065A-704720 | Sequence 704720,  |
| C 113 | 57   | 21.0 | 546    | 6  | US-09-925-065A-439013 | Sequence 439013,  |
| C 114 | 57   | 21.0 | 553    | 10 | US-10-301-480-500200  | Sequence 500200,  |
| C 115 | 57   | 21.0 | 553    | 10 | US-10-301-480-1113609 | Sequence 1113609, |
| C 116 | 57   | 21.0 | 554    | 6  | US-09-925-065A-887741 | Sequence 887741,  |
| C 117 | 57   | 21.0 | 554    | 6  | US-09-925-065A-887742 | Sequence 887742,  |
| C 118 | 57   | 21.0 | 554    | 6  | US-09-925-065A-912087 | Sequence 912087,  |
| C 119 | 57   | 21.0 | 555    | 6  | US-09-925-065A-141928 | Sequence 141928,  |
| C 120 | 57   | 21.0 | 595    | 6  | US-09-925-065A-141929 | Sequence 141929,  |
| C 121 | 57   | 21.0 | 599    | 6  | US-09-925-065A-856    | Sequence 856, App |
| C 122 | 57   | 21.0 | 599    | 9  | US-10-301-480-102093  | Sequence 102093,  |
| C 123 | 57   | 21.0 | 599    | 10 | US-10-301-480-715502  | Sequence 715502,  |
| C 124 | 57   | 21.0 | 624    | 6  | US-09-925-065A-686146 | Sequence 686146,  |
| C 125 | 57   | 21.0 | 1034   | 6  | US-09-925-065A-684054 | Sequence 684054,  |
| C 126 | 57   | 21.0 | 1585   | 7  | US-10-745-586-123     | Sequence 123, App |
| C 127 | 57   | 21.0 | 2172   | 8  | US-10-750-185-62676   | Sequence 62676, A |
| C 128 | 57   | 21.0 | 2172   | 8  | US-10-750-623-62676   | Sequence 62676, A |
| C 129 | 57   | 21.0 | 67858  | 8  | US-10-995-563-13484   | Sequence 13484, A |
| C 130 | 57   | 21.0 | 196200 | 14 | US-11-121-086-9       | Sequence 9, Appl  |
| C 131 | 57   | 21.0 | 246960 | 14 | US-11-121-086-8       | Sequence 8, Appl  |
| C 132 | 56.5 | 20.8 | 545    | 6  | US-09-925-065A-177982 | Sequence 177982,  |
| C 133 | 56.5 | 20.8 | 545    | 6  | US-09-925-065A-177983 | Sequence 177983,  |
| C 134 | 56.5 | 20.8 | 587    | 10 | US-10-301-480-381801  | Sequence 381801,  |
| C 135 | 56.5 | 20.8 | 587    | 10 | US-10-301-480-995210  | Sequence 995210,  |
| C 136 | 56.5 | 20.8 | 592    | 6  | US-09-925-065A-305818 | Sequence 305818,  |
| C 137 | 56.5 | 20.8 | 1305   | 9  | US-10-301-480-90172   | Sequence 90172, A |
| C 138 | 56.5 | 20.8 | 1305   | 10 | US-10-301-480-703581  | Sequence 703581,  |
| C 139 | 56.5 | 20.8 | 2015   | 14 | US-11-079-122-8       | Sequence 8, Appl  |
| C 140 | 56   | 20.7 | 426    | 9  | US-10-301-480-78716   | Sequence 78716, A |
| C 141 | 56   | 20.7 | 426    | 10 | US-10-301-480-692125  | Sequence 692125,  |
| C 142 | 56   | 20.7 | 494    | 6  | US-09-925-065A-558062 | Sequence 558062,  |
| C 143 | 56   | 20.7 | 494    | 6  | US-09-925-065A-558063 | Sequence 558063,  |
| C 144 | 56   | 20.7 | 528    | 6  | US-09-925-065A-573622 | Sequence 573622,  |
| C 145 | 56   | 20.7 | 641    | 10 | US-10-301-480-55964   | Sequence 55964,   |
| C 146 | 56   | 20.7 | 641    | 10 | US-10-301-480-1173373 | Sequence 1173373, |
| C 147 | 56   | 20.7 | 742    | 10 | US-10-301-480-544778  | Sequence 544778,  |
| C 148 | 56   | 20.7 | 742    | 10 | US-10-301-480-1158187 | Sequence 1158187, |

RESULT 1

US-10-840-688-19

Sequence 19, Application US/10840688

Publication NO. US2005028968A1

GENERAL INFORMATION:

APPLICANT: Weaver, Lisa M

APPLICANT: Mitsky, Timothy A

APPLICANT: Rapp, William D

APPLICANT: Gruys, Kenneth J

APPLICANT: Liang, Jihong

TITLE OF INVENTION: Plants with Increased Levels of One or More Amino Acids

FILE REFERENCE: REN-00-095

CURRENT APPLICATION NUMBER: US/10/840,688

CURRENT FILING DATE: 2004-05-06

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.2

SEQ ID NO 19

LENGTH: 264

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-10-840-688-19

Alignment Scores:

Pred. No.: 2,34e-12

Length: 264

Score: 181.50

Matches: 41

Percent Similarity: 78.9%

Conservative: 4

Best Local Similarity: 71.9%

Mismatches: 9

Query Match: 67.0%

Indels: 3

DB: 8

Gaps: 2

US-10-628-525A-33 (1-56) x US-10-840-688-19 (1-264)

Qy 1 MetalaserSerMetLeuSerSerAlaAlaValAlaAlaThrArgThrAsnProAlaGlnAla 20

Db 1 ATGGCTTCCTATGCTCTCTCCGCTACTATGGTT-----GCCTCTCCGGCTCAGGCC 54

Qy 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39

Db 55 ACTATGGTCCTCCCTTCAAGGACTTAAGTCTCGCTCGCTTCCAGCCACCCGCAAG 114

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

Db 115 GCTAACACGACATTACTTCCATCACAGCAACGCGGAAGAGTTAACTGC 165

RESULT 2

US-11-192-801-25

Sequence 25, Application US/11192801

Publication NO. US20050273882A1

GENERAL INFORMATION:

APPLICANT: Romano, Charles P.

TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants

FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn

CURRENT APPLICATION NUMBER: US/11/192,801

CURRENT FILING DATE: 2005-07-29

PRIOR APPLICATION NUMBER: US/10/232,665

PRIOR FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: US/09/377,466

PRIOR FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 25

LENGTH: 416

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: non-naturally occurring nucleotide sequence encoding Zea mays

OTHER INFORMATION: ribulose bis-phosphate carboxylase chloroplast  
OTHER INFORMATION: targeting peptide

FEATURE: CDS  
NAME/KEY: CDS  
LOCATION: (16)..(162)  
FEATURE: CDS  
NAME/KEY: CDS  
LOCATION: (326)..(415)  
FEATURE: intron  
NAME/KEY: intron  
LOCATION: (163)..(325)  
OTHER INFORMATION: I-Zm.rbcS

US-11-192-801-25

Alignment Scores:  
Pred. No.: 0.148 Length: 416  
Score: 91.00 Matches: 22  
Percent Similarity: 64.2% Conservative: 12  
Best Local Similarity: 41.5% Mismatches: 7  
Query Match: 33.6% Indels: 12  
DB: 14 Gaps: 3

US-10-628-525A-33 (1-56) x US-11-192-801-25 (1-416)

Qy 5 MetLeuSerSerAlaValAlaThrArgThrAsnProAlaGlnAlaSerMetValAla 24  
Db 31 ATGATGGCCTCGTGGCCACCGCC-----GTGCT 60  
Qy 25 ProPheThrGlyLeuLysSer---AlaAlaPheProValSerArgLysGlnAsnLeuAsp 43  
Db 61 CCGTTCTCTGGGGCTCAAGTCCACCGCAGCTCCCGTCCGCCCGCTCTCCAGAGC 120  
Qy 44 IleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56  
Db 121 CTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 156

#### RESULT 3

US-11-192-801-30  
Sequence 30, Application US/11192801  
Publication No. US20050273882A1  
GENERAL INFORMATION:  
APPLICANT: Romano, Charles P.  
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
CURRENT APPLICATION NUMBER: US/11/192,801  
CURRENT FILING DATE: 2005-07-29  
PRIOR APPLICATION NUMBER: US/10/232,665  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US/09/377,466  
PRIOR FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 30  
LENGTH: 416  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: modified  
OTHER INFORMATION: cauliflower mosaic virus promoter AS4

US-11-192-801-30

Alignment Scores:  
Pred. No.: 0.148 Length: 416  
Score: 91.00 Matches: 22  
Percent Similarity: 64.2% Conservative: 12  
Best Local Similarity: 41.5% Mismatches: 7  
Query Match: 33.6% Indels: 12  
DB: 14 Gaps: 3

US-10-628-525A-33 (1-56) x US-11-192-801-30 (1-416)

Qy 5 MetLeuSerSerAlaValAlaThrArgThrAsnProAlaGlnAlaSerMetValAla 24  
Db 31 ATGATGGCCTCGTGGCCACCGCC-----GTGCT 60

Db 31 ATGATGGCCTCGTGGCCACCGCC-----GTGCT 60  
Qy 25 ProPheThrGlyLeuLysSer---AlaAlaPheProValSerArgLysGlnAsnLeuAsp 43  
Db 61 CCGTTCTCTGGGGCTCAAGTCCACCGCAGCTCCCGTCCGCCCGCTCTCCAGAGC 120  
Qy 44 IleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56  
Db 121 CTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 156

#### RESULT 4

US-11-192-801-17  
Sequence 17, Application US/11192801  
Publication No. US20050273882A1  
GENERAL INFORMATION:  
APPLICANT: Romano, Charles P.  
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
CURRENT APPLICATION NUMBER: US/11/192,801  
CURRENT FILING DATE: 2005-07-29  
PRIOR APPLICATION NUMBER: US/10/232,665  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US/09/377,466  
PRIOR FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 17  
LENGTH: 3450  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: expression  
OTHER INFORMATION: cassette  
FEATURE:  
NAME/KEY: promoter  
LOCATION: (14)..(235)  
OTHER INFORMATION: P-CaMV.AS4  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: (240)..(304)  
OTHER INFORMATION: L-Ta.hcb1  
FEATURE:  
NAME/KEY: intron  
LOCATION: (318)..(805)  
OTHER INFORMATION: I-Ob.Act1  
FEATURE:  
NAME/KEY: transit peptide  
LOCATION: (825)..(971)  
OTHER INFORMATION: amino terminal TS-Zm.rbcS  
FEATURE:  
NAME/KEY: intron  
LOCATION: (972)..(1134)  
OTHER INFORMATION: I-Zm.rbcS  
FEATURE:  
NAME/KEY: transit peptide  
LOCATION: (1135)..(1221)  
OTHER INFORMATION: carboxy terminus TS-Zm.rbcS  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1222)..(3180)  
OTHER INFORMATION: Cry3Bb1 variant 11231mv1  
FEATURE:  
NAME/KEY: terminator  
LOCATION: (3198)..(3431)  
OTHER INFORMATION: T-Ta.hsp17

US-11-192-801-17

Alignment Scores:  
Pred. No.: 1.32 Length: 3450  
Score: 91.00 Matches: 22  
Percent Similarity: 64.2% Conservative: 12  
Best Local Similarity: 41.5% Mismatches: 7  
Query Match: 33.6% Indels: 12





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Pred. No.: 88.4 Length: 201
Score: 64.50 Matches: 21
Percent Similarity: 51.9% Conservatives: 6
Best Local Similarity: 40.4% Mismatches: 17
Query Match: 23.8% Indels: 8
DB: 2 Gaps: 2

US-10-628-525A-33 (1-56) x US-10-995-561-61428 (1-201)

QY 13 ThrArgThrAsnPro---AlaGlnAlaSerMetValAlaProPheThrGlyLeuLysSer 31
Db 46 ACCTCAGATGATCCACGCGCCTCATCTCCCAAAGTGTGGGATTCACAGGCATGARCCAC 105
QY 32 AlaAlaPheProValSerArgLysGlnAsnLeuAspIleThrSerIleAla-SerAsn-- 50
Db 106 TGTGCTGGCGCTGTTATTCTTAAACTGAACCTTTTCATTACTTCTTTAGCCAAAACACAG 165
QY 51 -----GlyGlyArgValGlnCys 56
Db 166 GCCTGCTGCATGTACAGGAGGAAGATAGCAATGT 199

RESULT 10
US-10-995-561-69122/c
; Sequence 69122, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69122
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-69122

Alignment Scores:
Pred. No.: 88.4 Length: 201
Score: 64.50 Matches: 21
Percent Similarity: 51.9% Conservatives: 6
Best Local Similarity: 40.4% Mismatches: 17
Query Match: 23.8% Indels: 8
DB: 2 Gaps: 2

US-10-628-525A-33 (1-56) x US-10-995-561-69122 (1-201)

QY 13 ThrArgThrAsnPro---AlaGlnAlaSerMetValAlaProPheThrGlyLeuLysSer 31
Db 156 ACCTCAGATGATCCACGCGCCTCATCTCCCAAAGTGTGGGATTCACAGGCATGARCCAC 97
QY 32 AlaAlaPheProValSerArgLysGlnAsnLeuAspIleThrSerIleAla-SerAsn-- 50
Db 96 TGTGCTGGCGCTGTTATTCTTAAACTGAACCTTTTCATTACTTCTTTAGCCAAAACACAG 37
QY 51 -----GlyGlyArgValGlnCys 56
Db 36 GCCTGCTGCATGTACAGGAGGAAGATAGCAATGT 3

RESULT 11
US-10-995-561-13406/c
; Sequence 13406, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559

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; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13406
; LENGTH: 23803
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13406

Alignment Scores:
Pred. No.: 1.23e+04 Length: 23803
Score: 64.50 Matches: 21
Percent Similarity: 51.9% Conservatives: 6
Best Local Similarity: 40.4% Mismatches: 17
Query Match: 23.8% Indels: 8
DB: 2 Gaps: 2

US-10-628-525A-33 (1-56) x US-10-995-561-13406 (1-23803)

QY 13 ThrArgThrAsnPro---AlaGlnAlaSerMetValAlaProPheThrGlyLeuLysSer 31
Db 20502 ACCTCAGATGATCCACGCGCCTCATCTCCCAAAGTGTGGGATTCACAGGCATGARCCAC 20443
QY 32 AlaAlaPheProValSerArgLysGlnAsnLeuAspIleThrSerIleAla-SerAsn-- 50
Db 20442 TGTGCTGGCGCTGTTATTCTTAAACTGAACCTTTTCATTACTTCTTTAGCCAAAACACAG 20383
QY 51 -----GlyGlyArgValGlnCys 56
Db 20382 GCCTGCTGCATGTACAGGAGGAAGATAGCAATGT 20349

RESULT 12
US-10-995-561-13353
; Sequence 13353, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13353
; LENGTH: 26096
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13353

Alignment Scores:
Pred. No.: 1.35e+04 Length: 26096
Score: 64.50 Matches: 21
Percent Similarity: 51.9% Conservatives: 6
Best Local Similarity: 40.4% Mismatches: 17
Query Match: 23.8% Indels: 8
DB: 2 Gaps: 2

US-10-628-525A-33 (1-56) x US-10-995-561-13353 (1-26096)

QY 13 ThrArgThrAsnPro---AlaGlnAlaSerMetValAlaProPheThrGlyLeuLysSer 31
Db 17808 ACCTCAGATGATCCACGCGCCTCATCTCCCAAAGTGTGGGATTCACAGGCATGARCCAC 17867
QY 32 AlaAlaPheProValSerArgLysGlnAsnLeuAspIleThrSerIleAla-SerAsn-- 50
Db 17868 TGTGCTGGCGCTGTTATTCTTAAACTGAACCTTTTCATTACTTCTTTAGCCAAAACACAG 17927
QY 51 -----GlyGlyArgValGlnCys 56
Db 17928 GCCTGCTGCATGTACAGGAGGAAGATAGCAATGT 17961

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Score: 63.50          Matches: 23
Percent Similarity: 44.4%      Conservative: 9
Best Local Similarity: 31.9%   Mismatches: 13
Query Match: 23.4%            Indels: 27
DB: 14                       Gaps: 3

US-10-628-525A-33 (1-56) x US-11-079-122-10 (1-2024)

Qy 4 SerMetLeuSerSerAlaAlaValAlaThrArgThr-----AsnProAlaGlnAlaSer 21
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1318 TCAAGCTTGAGCTCCTCGTCTCGGTGTTCTCAAGAACCTTGTTTCATCCCTTGCAAGCCAGC 1259
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 22 MetValAlaProPheThrGly----- 28
   ::: ::|::| |||
Db 1258 TTAACATCACCCACACACAGACACATGAGGCGTCTTGTTCTTCCCAATCTCAGCAGAAATCA 1199
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 29 -----LeuLysSerAlaAlaPheProValSerArg 38
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1198 ATGTCATATGGCACAATCTTAGCCCTGCTCGCAAAAGCCTCGAGCTTTCAGTGTGACACGG 1139
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 39 LysGlnAsnLeuAspIleThrSerIleAlaSerAsn 50
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1138 TCATCAAACTA-----ACACCAAACGCCAGCAAC 1109
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-11-079-122-14/c
; Sequence 14, Application US/11079122
; Publication No. US20050283858A1
; GENERAL INFORMATION:
; APPLICANT: Yao, Kening
; APPLICANT: Potts, Derek A
; APPLICANT: Leibell, Bradley D
; APPLICANT: Males, Daryl R
; TITLE OF INVENTION: Brassica AHAS Genes and Gene Alleles that Provide Resistance to
; TITLE OF INVENTION: Imidazolinone Herbicides
; FILE REFERENCE: 1478-001
; CURRENT APPLICATION NUMBER: US/11/079,122
; CURRENT FILING DATE: 2005-03-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 2024
; TYPE: DNA
; ORGANISM: Brassica juncea
US-11-079-122-14

Alignment Scores:
Pred. No.: 1.26e+03          Length: 2024
Score: 63.50                Matches: 23
Percent Similarity: 44.4%    Conservative: 9
Best Local Similarity: 31.9% Mismatches: 13
Query Match: 23.4%          Indels: 27
DB: 14                      Gaps: 3

US-10-628-525A-33 (1-56) x US-11-079-122-14 (1-2024)

Qy 4 SerMetLeuSerSerAlaAlaValAlaThrArgThr-----AsnProAlaGlnAlaSer 21
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1318 TCAAGCTTGAGCTCCTCGTCTCGGTGTTCTCAAGAACCTTGTTTCATCCCTTGCAAGCCAGC 1259
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 22 MetValAlaProPheThrGly----- 28
   ::: ::|::| |||
Db 1258 TTAACATCACCCACACACAGACACATGAGGCGTCTTGTTCTTCCCAATCTCAGCAGAAATCA 1199
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 29 -----LeuLysSerAlaAlaPheProValSerArg 38
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1198 ATGTCATATGGCACAATCTTAGCCCTGCTCGCAAAAGCCTCGAGCTTTCAGTGTGACACGG 1139
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 39 LysGlnAsnLeuAspIleThrSerIleAlaSerAsn 50
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1138 TCATCAAACTA-----ACACCAAACGCCAGCAAC 1109
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 16

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US-10-750-185-46879
; Sequence 46879, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46879
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Bovine 19866880966129
US-10-750-185-46879

Alignment Scores:
Pred. No.: 1.32e+03 Length: 1863
Score: 63.00 Matches: 17
Percent Similarity: 50.9% Conservatives: 11
Best Local Similarity: 30.9% Mismatches: 17
Query Match: 23.2% Indels: 10
DB: 8 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-750-185-46879 (1-1863)
QY 6 LeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAlaSerMetValAlaPro 25
   ::::::::::: :::::
Db 1315 ATCTATCCTCTGTCTGCTCCCTCTCTCTCTCTCAATATAGCACCTACTGTCATACC 1374
   ::::::::::: :::::-----LysSerAlaAlaPhePro 35
QY 26 PheThrGlyLeu-----
   ::::::::::: :::::
Db 1375 TTCACCTGGCCTAGGGGATTTGTGACAGCTGAGTCCAGATTCAGTCGGGGAGGCCACCG 1434
   ::::::::::: :::::
QY 36 ValSerArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsn 50
   ::::::::::: :::::
Db 1435 TCCAGCAGAGAGACGACACTGCCCTTACTAGTGTGCGTCGCAT 1479
   ::::::::::: :::::

RESULT 17
US-10-750-623-46879
; Sequence 46879, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46879
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Bovine 19866880966129
US-10-750-623-46879

Alignment Scores:
Pred. No.: 1.32e+03 Length: 1863
Score: 63.00 Matches: 17
Percent Similarity: 50.9% Conservatives: 11
Best Local Similarity: 30.9% Mismatches: 17
Query Match: 23.2% Indels: 10
DB: 8 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-750-185-46879 (1-1863)
QY 6 LeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAlaSerMetValAlaPro 25
   ::::::::::: :::::
Db 1315 ATCTATCCTCTGTCTGCTCCCTCTCTCTCTCTCAATATAGCACCTACTGTCATACC 1374
   ::::::::::: :::::-----LysSerAlaAlaPhePro 35
QY 26 PheThrGlyLeu-----
   ::::::::::: :::::
Db 1375 TTCACCTGGCCTAGGGGATTTGTGACAGCTGAGTCCAGATTCAGTCGGGGAGGCCACCG 1434
   ::::::::::: :::::
QY 36 ValSerArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsn 50
   ::::::::::: :::::
Db 1435 TCCAGCAGAGAGACGACACTGCCCTTACTAGTGTGCGTCGCAT 1479
   ::::::::::: :::::

RESULT 18
US-09-925-065A-427150/c
; Sequence 427150, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 427150
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-427150

Alignment Scores:
Pred. No.: 447 Length: 573
Score: 62.50 Matches: 19
Percent Similarity: 36.2% Conservatives: 10
Best Local Similarity: 23.8% Mismatches: 24
Query Match: 23.1% Indels: 27
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x US-09-925-065A-427150 (1-573)
QY 1 MetaLaserSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
   ::::::::::: :::::
Db 337 ATGATCTCAGCTTGTGGAACTCTGCTCTCTGCTTCAAGAGACTCTCTGCTCAGCC 278
   ::::::::::: :::::
QY 21 SerMetValAlaProPheThrGly-----
   ::::::::::: :::::
Db 277 TCYCAAGTAGCTGGGATTACAGGCACCCACCACCATCACGCTGCTAGTTTGTATTATTTA 218
   ::::::::::: :::::
QY 29 -----LeuLysSerAlaAla 33
   ::::::::::: :::::
Db 217 GTAGAGATGGAGTTTGGCACATTGGCCAGGCTGGTGTGAACTGCTGCTACCTCAAGTGAT 158
   ::::::::::: :::::

```

QY 34 PheProValSerArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArg 53  
Db 157 CTGCCAGCCTCAGCCTCCCAAGGCTGGGATTACAGATGTGAGCCACCAAGCGGCCAA 98

## RESULT 19

US-10-301-480-490520  
; Sequence 490520, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 490520  
; LENGTH: 589  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-490520

Alignment Scores:  
Pred. No.: 460 Length: 589  
Score: 62.50 Matches: 19  
Percent Similarity: 36.2% Conservative: 10  
Best Local Similarity: 23.8% Mismatches: 24  
Query Match: 23.1% Indels: 27  
DB: 10 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-301-480-490520 (1-589)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 253 ATGATCTCAGCTTGTCTGGAACCTCTGCCTCTGGTTCAAGAGACTCTCTCGCTCAGCC 312  
QY 21 SerMetValAlaProPheThrGly----- 28  
Db 313 TCYCAAGTAGCTGGGATTACAGGACCCACCACCATCAGCCTGGCTAAGTTTGTATTTTAA 372  
QY 29 -----LeuLysSerAlaAla 33  
Db 373 GTAGAGATGGAGTTTGGCCACATTGGCCAGGCTGGTCTTGAACCTGCTGACCTCAAGTGAT 432  
QY 34 PheProValSerArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArg 53  
Db 433 CTGCCAGCCTCAGCCTCCCAAGGCTGGGATTACAGATGTGAGCCACCAAGCGGCCAA 492

## RESULT 20

US-10-301-480-1103929  
; Sequence 1103929, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1103929  
; LENGTH: 589  
; TYPE: DNA

; ORGANISM: Homo sapien  
US-10-301-480-1103929  
Alignment Scores:  
Pred. No.: 460 Length: 589  
Score: 62.50 Matches: 19  
Percent Similarity: 36.2% Conservative: 10  
Best Local Similarity: 23.8% Mismatches: 24  
Query Match: 23.1% Indels: 27  
DB: 10 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-301-480-1103929 (1-589)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 253 ATGATCTCAGCTTGTCTGGAACCTCTGCCTCTGGTTCAAGAGACTCTCTCGCTCAGCC 312  
QY 21 SerMetValAlaProPheThrGly----- 28  
Db 313 TCYCAAGTAGCTGGGATTACAGGACCCACCACCATCAGCCTGGCTAAGTTTGTATTTTAA 372  
QY 29 -----LeuLysSerAlaAla 33  
Db 373 GTAGAGATGGAGTTTGGCCACATTGGCCAGGCTGGTCTTGAACCTGCTGACCTCAAGTGAT 432  
QY 34 PheProValSerArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArg 53  
Db 433 CTGCCAGCCTCAGCCTCCCAAGGCTGGGATTACAGATGTGAGCCACCAAGCGGCCAA 492

## RESULT 21

US-10-932-182A-77417  
; Sequence 77417, Application US/10932182A  
; Publication No. US20060046253A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 77417  
; LENGTH: 885  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-10-932-182A-77417

Alignment Scores:  
Pred. No.: 701 Length: 885  
Score: 62.50 Matches: 16  
Percent Similarity: 52.1% Conservative: 9  
Best Local Similarity: 33.3% Mismatches: 20  
Query Match: 23.1% Indels: 3  
DB: 9 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-932-182A-77417 (1-885)

QY 7 SerSerAlaAlaValAlaThrArgThrAsnProAlaGln-----AlaSerMetVal 23  
Db 502 TCTAGCTCTGCTGTAAGCACCATTGCAAGTTCTGCTGAAGTTCTGTCGACGCTCTGTT 561  
QY 24 AlaProPheThrGlyLeuLysSerAlaAlaPheProValSerArgLysGlnAsnLeuAsp 43  
Db 562 GCAAGCTCTGCTAGTTTTCGCAATACCAGCTCCAGGTTCTTCTACATCTTCTATCTCA 621  
QY 44 IleThrSerIleAlaSerAsnGly 51  
Db 622 GTCACTCTCAGTGGTCCAAATGGT 645

RESULT 22  
US-10-932-182A-77417  
; Sequence 77417, Application US/10932182A  
; Publication No. US20060046253A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 77417  
; LENGTH: 885  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-10-932-182A-77417

Alignment Scores:  
Pred. No.: 701 Length: 885  
Score: 62.50 Matches: 16  
Percent Similarity: 52.1% Conservative: 9  
Best Local Similarity: 33.3% Mismatches: 20  
Query Match: 23.1% Indels: 3  
DB: 9 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-932-182A-77417 (1-885)  
QY 7 SerSerAlaAlaValAlaThrArgThrAsnProAlaGln-----AlaSerMetVal 23  
Db 502 TCTAGCTCGTGTGAAGCACCATTGCGAAGTCTGTTGCAAGCTCTGTT 561  
QY 24 AlaProPheThrGlyLeuLysSerAlaAlaPheProValSerArgLysGlnAsnLeuAsp 43  
Db 562 GCAAGCTCGTAGTTTCCCAATACCACAGCTCCAGTTCTTCTACATCTTCTATCTCA 621  
QY 44 IleThrSerIleAlaSerAengly 51  
Db 622 GTCACTCCAGTGTGCCAAATGTT 645

RESULT 23  
US-09-925-065A-461364/C  
; Sequence 461364, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 461364  
; LENGTH: 557  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-461364

Alignment Scores:  
Pred. No.: 569 Length: 557  
Score: 61.50 Matches: 19  
Percent Similarity: 50.0% Conservative: 6  
Best Local Similarity: 38.0% Mismatches: 21  
Query Match: 22.7% Indels: 4  
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x US-09-925-065A-461364 (1-557)  
QY 6 LeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAlaSerMetValAlaPr 25  
Db 264 CTGCCTAGTGAGCTGTGAAAAAGAGCCACCATCTCCAGATGCCAAAATGGTAGCTCC 205  
QY 25 oPheThrGlyLeuLysSerAlaAlaPheProValSerArgLysGlnAsnLeuAspIleth 45  
Db 204 ACTGACA-----GCTTGCCACCATGCCCTCGAAAAGCCACACACACTCAATACCAG 154  
QY 45 rSerIleAlaSerAsnGlyGlyArgVal 54  
Db 153 CCCATGGAAACAGCTGGGAGGGGGGTG 126

RESULT 24  
US-09-925-065A-933859/C  
; Sequence 933859, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 933859  
; LENGTH: 692  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-933859

Alignment Scores:  
Pred. No.: 712 Length: 692  
Score: 61.50 Matches: 18  
Percent Similarity: 52.4% Conservative: 4  
Best Local Similarity: 42.9% Mismatches: 19  
Query Match: 22.7% Indels: 1  
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x US-09-925-065A-933859 (1-692)  
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 294 ATGGCTTCCCAACAATTTCCAGTGCCTTAATTCATCTCTGCAATTAACCAAGTCCAAG 235  
QY 21 SerMetValAlaProPheThr---GlyLeuLysSerAlaAlaPheProValSerArgLys 39  
Db 234 TCCAAAGTCTCACCTGCACACACAGGCAAGTCCCTCTCTGCTGTGAGCCTGTATAAACCAAAA 175  
QY 40 GlnAsn 41  
Db 174 GCAAAAT 169

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RESULT 25
US-09-925-065A-933860/c
; Sequence 933860, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 933860
; LENGTH: 692
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-933860

Alignment Scores:
Pred. No.: 712          Length: 692
Score: 61.50           Matches: 18
Percent Similarity: 52.4% Conservatives: 4
Best Local Similarity: 42.9% Mismatches: 19
Query Match: 22.7%      Indels: 1
DB: 6                  Gaps: 1

US-10-628-525A-33 (1-56) x US-09-925-065A-933860 (1-692)
QY 1 MetAlaSerMetLeuSerSerAlaAlaValAlaThrArgThrAnProAlaGlnAla 20
Db 294 ATGGCTTCCCAACAATTCCTCAGTGCCTTAATTCATTCCTGCATTACCCCAAGTCCAAG 235
QY 21 SerMetValAlaProPheThr---GlyLeuLysSerAlaAlaPheProValSerArgLys 39
Db 234 TCCAAAGTCTCACCTGACACAGGCAAGTCCCTTCTGCTGTGAGCCTGTAAACCAAAA 175
QY 40 GlnAsn 41
Db 174 GCAAAAT 169

RESULT 26
US-09-925-065A-921611
; Sequence 921611, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 921610
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-921610

Alignment Scores:
Pred. No.: 813          Length: 787
Score: 61.50           Matches: 18
Percent Similarity: 52.4% Conservatives: 4
Best Local Similarity: 42.9% Mismatches: 19
Query Match: 22.7%      Indels: 1
DB: 6                  Gaps: 1

US-10-628-525A-33 (1-56) x US-09-925-065A-921610 (1-787)
QY 1 MetAlaSerMetLeuSerSerAlaAlaValAlaThrArgThrAnProAlaGlnAla 20
Db 400 ATGGCTTCCCAACAATTCCTCAGTGCCTTAATTCATTCCTGCATTACCCCAAGTCCAAG 459
QY 21 SerMetValAlaProPheThr---GlyLeuLysSerAlaAlaPheProValSerArgLys 39
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Job time : 182.864 Secs



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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 20:18:18 ; Search time 1530.93 Seconds  
(without alignments)  
2022.653 Million cell updates/sec

Title: US-10-628-525A-33  
Perfect score: 271  
Sequence: 1 MASSMLSSAAVATETPAQA.....SRQNLDTISASNGRVC 56

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

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-Q=/abss/ABSSWEB.spool/US10628525/runat\_31032006\_095128\_16978/app\_query.fasta\_1  
-DB=Pending Patents NA.Main -QPMT=fastap -SUFFIX=p2n.tnmp -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=150 -DOCLALIGN=200 -THR SCORE=ext -THR MAX=100  
-THR MIN=0 -ALIGN=30 -MODES=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abss06h  
-USER=US10628525 @CGN 1.1.19447 @runat\_31032006\_095128\_16978 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA.Main:  
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2: /cgn2\_6/ptodata/1/pna/PCTUSB COMB.seq:  
3: /cgn2\_6/ptodata/1/pna/PCTUSC COMB.seq:  
4: /cgn2\_6/ptodata/1/pna/US06 COMB.seq:  
5: /cgn2\_6/ptodata/1/pna/US075 COMB.seq:  
6: /cgn2\_6/ptodata/1/pna/US076 COMB.seq:  
7: /cgn2\_6/ptodata/1/pna/US077 COMB.seq:  
8: /cgn2\_6/ptodata/1/pna/US078 COMB.seq:  
9: /cgn2\_6/ptodata/1/pna/US079 COMB.seq:  
10: /cgn2\_6/ptodata/1/pna/US080 COMB.seq:  
11: /cgn2\_6/ptodata/1/pna/US081 COMB.seq:  
12: /cgn2\_6/ptodata/1/pna/US082 COMB.seq:  
13: /cgn2\_6/ptodata/1/pna/US083 COMB.seq:  
14: /cgn2\_6/ptodata/1/pna/US084 COMB.seq:  
15: /cgn2\_6/ptodata/1/pna/US085 COMB.seq:  
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19: /cgn2\_6/ptodata/1/pna/US089 COMB.seq:  
20: /cgn2\_6/ptodata/1/pna/US090 COMB.seq:  
21: /cgn2\_6/ptodata/1/pna/US091 COMB.seq:  
22: /cgn2\_6/ptodata/1/pna/US092 COMB.seq:  
23: /cgn2\_6/ptodata/1/pna/US093 COMB.seq:  
24: /cgn2\_6/ptodata/1/pna/US094 COMB.seq:  
25: /cgn2\_6/ptodata/1/pna/US095A COMB.seq:  
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27: /cgn2\_6/ptodata/1/pna/US095C COMB.seq:

| Result No. | Score                                  | Query Match | Length | DB ID | Description       |
|------------|----------------------------------------|-------------|--------|-------|-------------------|
| 1          | 240.5                                  | 88.7        | 171    | 15    | US-08-543-608-4   |
| 2          | 240.5                                  | 88.7        | 174    | 33    | US-09-854-286-15  |
| 3          | 240.5                                  | 88.7        | 177    | 6     | US-07-662-921C-10 |
| 4          | 240.5                                  | 88.7        | 177    | 7     | US-07-785-566B-12 |
| 5          | 240.5                                  | 88.7        | 177    | 7     | US-07-785-568B-12 |
| 6          | 240.5                                  | 88.7        | 177    | 7     | US-07-785-569A-8  |
| 7          | 240.5                                  | 88.7        | 177    | 8     | US-07-805-061B-12 |
| 28:        | /cgn2_6/ptodata/1/pna/US096A COMB.seq: |             |        |       |                   |
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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|            |       |             |        |       | Sequence 12, Appl |

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| 57 | 223.5 | 82.5 | 684 | 51 | US-10-462-162-33    | Sequence 33, Appl  |  |  |  |  |  |  | US-09-637-086A-36843 | Sequence 36843, A  |
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| 66 | 221   | 81.5 | 725 | 1  | PCT-US02-27882-228  | Sequence 228, App  |  |  |  |  |  |  | US-09-654-617-221037 | Sequence 221037, A |
| 67 | 221   | 81.5 | 736 | 1  | PCT-US02-27884-5044 | Sequence 5044, Ap  |  |  |  |  |  |  | US-09-684-016-221037 | Sequence 221037, A |
| 68 | 221   | 81.5 | 736 | 51 | US-10-487-901-5044  | Sequence 5044, Ap  |  |  |  |  |  |  | US-09-637-086A-38154 | Sequence 38154, A  |
| 69 | 221   | 81.5 | 741 | 1  | PCT-US02-27882-857  | Sequence 857, App  |  |  |  |  |  |  | US-09-637-086D-38762 | Sequence 38762, A  |
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| 73 | 218   | 80.4 | 698 | 3  | PCT-US04-33379-128  | Sequence 128, App  |  |  |  |  |  |  | US-09-654-617-222640 | Sequence 222640, A |
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| 78 | 218   | 80.4 | 737 | 51 | US-10-487-901-5045  | Sequence 5045, Ap  |  |  |  |  |  |  | US-09-637-086D-36603 | Sequence 36603, A  |
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ALIGNMENTS

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RESULT 1
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; GENERAL INFORMATION:
; APPLICANT: Trulson, Anna J.
; TITLE OF INVENTION: A Method for Visually Selecting
; TITLE OF INVENTION: Transformed Plants Cells or Tissues by Carotenoid
; TITLE OF INVENTION: Pigmentation
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greer, Burns & Crain, Ltd.
; STREET: 233 South Wacker Drive, Suite 8660, Sears
; STREET: Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/543,608
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V.
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: PET02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-993-0080
; TELEFAX: 312-993-0633
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
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; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..171
US-08-543-608-4
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Score: 240.50 Matches: 52
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Query Match: 88.7% Indels: 1
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US-10-628-525A-33 (1-56) x US-08-543-608-4 (1-171)
QY 1 MetAlaSerSerMetLeuSerAlaAlaValAlaThrArgThrAenProAlaGlnAla 20
Db 1 ATGGCTTCCTCACTTCTTCTCTGCGAGCATGTCACCGCGAGCAATGTTGCTCAAGCT 60
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 61 AACATGGTGGCGCTTTCATCTGCGCTTAAGTCAGCTGCCTCATCTCCCTGTTTCAAGGAAG 120
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCACCGCGAAGAGTGCAATGC 171
RESULT 2
US-09-854-286-15
; Sequence 15, Application US/09854286
; GENERAL INFORMATION:
```

```
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Deheah, Katayoon
; TITLE OF INVENTION: Plastid Transit Peptide Sequences for Efficient Plastid Targeting
; FILE REFERENCE: US 60/203,618 38-77(15378)
; CURRENT APPLICATION NUMBER: US/09/854,286
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/203,618
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 174
; TYPE: DNA
; ORGANISM: Pisum sativum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(174)
US-09-854-286-15
Alignment Scores:
Pred. No.: 9,69e-29 Length: 174
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 33 Gaps: 1
US-10-628-525A-33 (1-56) x US-09-854-286-15 (1-174)
QY 1 MetAlaSerSerMetLeuSerAlaAlaValAlaThrArgThrAenProAlaGlnAla 20
Db 1 ATGGCTTCCTCACTTCTTCTCTGCGAGCATGTCACCGCGAGCAATGTTGCTCAAGCT 60
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 61 AACATGGTGGCGCTTTCATCTGCGCTTAAGTCAGCTGCCTCATCTCCCTGTTTCAAGGAAG 120
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCACCGCGAAGAGTGCAATGC 171
RESULT 3
US-07-662-921C-10
; Sequence 10, Application US/07662921C
; GENERAL INFORMATION:
; APPLICANT: Ausich, Rodney L
; APPLICANT: Brinkhaus, Friedhelm L
; APPLICANT: Mukharji, Indrani
; APPLICANT: Proffitt, John H
; APPLICANT: Yarger, James G
; APPLICANT: Yen, Huel-Che B
; TITLE OF INVENTION: Biosynthesis of Zeaxanthin and Glycosylated
; TITLE OF INVENTION: Zeaxanthin in Genetically Engineered Hosts
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corp., Patents and Licensing Dept
; STREET: 200 E Randolph St
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60680-0703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/662,921C
; FILING DATE: 19910228
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, Norval B
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: 3128567180  
TELEFAX: 3128564972  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-662-921C-10

Alignment Scores:  
Pred. No.: 9,96e-29 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x US-07-662-921C-10 (1-177)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThraAsnProAlaGlnAla 20  
Db 1 ATGGCTTCCTCAGTTCTTCTCTGCGAGTGGCCACCGCAGCAATGTTGCTCAAGCT 60

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 61 AACATGGTGGCGCTTTCATCTGAGCTTAAGTCAAGCTCCTCATTCCTCTTTCAAGGAAG 120

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAAGAGTGCAATGC 171

## RESULT 4

US-07-785-566B-12  
Sequence 12, Application US/07785566B  
GENERAL INFORMATION:  
APPLICANT: Ausich, Rodney L  
APPLICANT: Brinkhaus, Friedhelm L  
APPLICANT: Mukharji, Indrani  
APPLICANT: Proffitt, John H  
APPLICANT: Yarger, James G  
APPLICANT: Yen, Huel-Che B  
TITLE OF INVENTION: Beta-Carotene Biosynthesis in  
TITLE OF INVENTION: Genetically Engineered Hosts  
NUMBER OF SEQUENCES: 79  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amoco Corp., Patents and Licensing Dept  
STREET: 200 E Randolph St  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60680-0703  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/785,566B  
FILING DATE: 19911030  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Galloway, Norval B  
TELEPHONE: 3128567180  
TELEFAX: 3128564972  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
US-07-785-566B-12

Alignment Scores:  
Pred. No.: 9,96e-29 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x US-07-785-566B-12 (1-177)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThraAsnProAlaGlnAla 20  
Db 1 ATGGCTTCCTCAGTTCTTCTCTGCGAGTGGCCACCGCAGCAATGTTGCTCAAGCT 60

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 61 AACATGGTGGCGCTTTCATCTGAGCTTAAGTCAAGCTCCTCATTCCTCTTTCAAGGAAG 120

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAAGAGTGCAATGC 171

## RESULT 5

US-07-785-566B-12  
Sequence 12, Application US/07785566B  
GENERAL INFORMATION:  
APPLICANT: Ausich, Rodney L  
APPLICANT: Brinkhaus, Friedhelm L  
APPLICANT: Mukharji, Indrani  
APPLICANT: Proffitt, John H  
APPLICANT: Yarger, James G  
APPLICANT: Yen, Huel-Che B  
TITLE OF INVENTION: Lycopene Biosynthesis in  
TITLE OF INVENTION: Genetically Engineered Hosts  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amoco Corp., Patents and Licensing Dept  
STREET: 200 E Randolph St  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60680-0703  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/785,566B  
FILING DATE: 19921030  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Galloway, Norval B  
TELEPHONE: 3128567180  
TELEFAX: 3128564972  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-785-566B-12

Alignment Scores:  
Pred. No.: 9,96e-29 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1

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Query Match:      88.7%      Indels:      1
DB:              7          Gaps:         1

US-10-628-525A-33 (1-56) x US-07-785-568B-12 (1-177)

Qy  1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAenProAlaGlnAla 20
Db  1 ATGGCTTCCTCAGTCTTTCCCTCTGCAGCAGTTCACCCGACGCAATGTTGCTCAAGCT 60

Qy  21 SerMetValAlaProPheThrGlyLeuLySerAlaAla---PheProValSerArgLys 39
Db  61 AACATGGTGGCGCTTTCCTGGCTTAAGTCAGCTGCCTCATTTCCCTGTTTCAGGNAG 120

Qy  40 GlnAsnLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56
Db  121 CAAACACTTGACATCACTTCCATTGCGACGACGCGGAGAGTGCATATGC 171

RESULT 6
US-07-785-569A-8
; Sequence 8, Application US/07785569A
; GENERAL INFORMATION:
; APPLICANT: Ausich, Rodney L
; APPLICANT: Brinkhaus, Friedhelm L
; APPLICANT: Mukharji, Indrani
; APPLICANT: Proffitt, John H
; APPLICANT: Yarger, James G
; APPLICANT: Yen, Hwei-Che B
; TITLE OF INVENTION: Phytoene Biosynthesis in
; TITLE OF INVENTION: Genetically Engineered Hosts
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corp., Patents and Licensing Dept
; STREET: 200 E Randolph St
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60680-0703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/785,569A
; FILING DATE: 19911030
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, Norval B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3128567180
; TELEFAX: 3128564972
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-785-569A-8

Alignment Scores:
Pred. No.:      9,96e-29      Length:      177
Score:          240.50       Matches:      52
Percent Similarity: 96.5%    Conservative: 3
Best Local Similarity: 91.2% Mismatches:      1
Query Match:    88.7%      Indels:      1
DB:            7          Gaps:         1

US-10-628-525A-33 (1-56) x US-07-785-569A-8 (1-177)

Qy  1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAenProAlaGlnAla 20
Db  1 ATGGCTTCCTCAGTCTTTCCCTCTGCAGCAGTTCACCCGACGCAATGTTGCTCAAGCT 60

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Db 128 AACATGGTTGCACCTTTTCACAGGCTTAAAGTCTGCTGCCTCAATTCCTCTTCAAGAAAG 187
QY 40 GlnAsnLeuAspIleThrSerIleAlaValAlaThrArgThrAsnProAlaGlnAla 56
Db 188 CAAACCTTGACATCACTTCCATTGCGACGCGGGAAGAGTGCAATGC 238

RESULT 14
US-10-487-901-3504
; Sequence 3504, Application US/10487901
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3504
; LENGTH: 377
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-3504

Alignment Scores:
Pred. No.: 3,46e-28 Length: 377
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 51 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-3504 (1-377)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 68 ATGGCTTCTCAGTTCTTCTCCAGCAGAGTTGCCACCGGAGCAATGTTGCTCAAGCT 127
QY 21 SerMetValAlaProPheThrGlyLeuIysSerAlaAla---PheProValSerArgLys 39
Db 128 AACATGGTTGCACCTTTTCACAGGCTTAAAGTCTGCTGCCTCAATTCCTCTTCAAGAAAG 187
QY 40 GlnAsnLeuAspIleThrSerIleAlaValAlaThrArgThrAsnProAlaGlnAla 56
Db 188 CAAACCTTGACATCACTTCCATTGCGACGCGGGAAGAGTGCAATGC 238

RESULT 15
PCT-US02-27884-3503
; Sequence 3503, Application PC/TUS0227884
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; APPLICANT: Dow Agro Sciences, LLC
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOW-07611
; CURRENT APPLICATION NUMBER: PCT/US02/27884
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3503
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27884-3503

Alignment Scores:
Pred. No.: 5,31e-28 Length: 489
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 51 Gaps: 1

US-10-628-525A-33 (1-56) x PCT-US02-27884-3503 (1-489)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 79 ATGGCTTCTCAGTTCTTCTCCAGCAGAGTTGCCACCGGAGCAATGTTGCTCAAGCT 138
QY 21 SerMetValAlaProPheThrGlyLeuIysSerAlaAla---PheProValSerArgLys 39
Db 139 AACATGGTTGCACCTTTTCACAGGCTTAAAGTCTGCTGCCTCAATTCCTCTTCAAGAAAG 198
QY 40 GlnAsnLeuAspIleThrSerIleAlaValAlaThrArgThrAsnProAlaGlnAla 56
Db 199 CAAACCTTGACATCACTTCCATTGCGACGCGGGAAGAGTGCAATGC 249

RESULT 16
US-10-487-901-3503
; Sequence 3503, Application US/10487901
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3503
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-3503

Alignment Scores:
Pred. No.: 5,31e-28 Length: 489
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 51 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-3503 (1-489)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 79 ATGGCTTCTCAGTTCTTCTCCAGCAGAGTTGCCACCGGAGCAATGTTGCTCAAGCT 138
QY 21 SerMetValAlaProPheThrGlyLeuIysSerAlaAla---PheProValSerArgLys 39
Db 139 AACATGGTTGCACCTTTTCACAGGCTTAAAGTCTGCTGCCTCAATTCCTCTTCAAGAAAG 198
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Oy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 199 CAAACCTTGACATCACTTCCATTGCCAGCAACGCGGAGAGTGAATGC 249

RESULT 17
PCT-US02-27883-1433
; Sequence 1433, Application PC/TUS0227883
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; APPLICANT: Dow Agro Sciences, LLC
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Disease Resistance
; FILE REFERENCE: DOW-07613
; CURRENT APPLICATION NUMBER: PCT/US02/27883
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 2324
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1433
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27883-1433

Alignment Scores:
Pred. No.: 5,37e-28 Length: 492
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x PCT-US02-27883-1433 (1-492)

Oy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 66 ATGGCTTCCTCAGTCTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 125

Oy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 126 AACATGGTTGCACCTTTCACCTGGTCTTAAGTCTGCTGCCTCAATTCCTGTTTCAAGGAAG 185

Oy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 186 CAAACCTTGACATCACTTCCATTGCCAGCAACGCGGAGAGTGAATGC 236

RESULT 18
PCT-US02-27884-7207
; Sequence 7207, Application PC/TUS0227884
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; APPLICANT: Dow Agro Sciences, LLC
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOW-07611
; CURRENT APPLICATION NUMBER: PCT/US02/27884
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7207
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27884-7207

Alignment Scores:
Pred. No.: 5,58e-28 Length: 504
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1
```

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US-10-628-525A-33 (1-56) x PCT-US02-27884-7207 (1-504)

Oy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 78 ATGGCTTCCTCAGTCTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 137

Oy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 138 AACATGGTTGCACCTTTCACAGGTCTTAAGTCTGCTGCCTCAATTCCTGTTTCAAGGAAG 197

Oy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 198 CAAACCTTGACATCACTTCCATTGCCAGCAACGCGGAGAGTGAATGC 248

RESULT 19
US-10-487-901-7207
; Sequence 7207, Application US/10487901
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakelee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7207
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-7207

Alignment Scores:
Pred. No.: 5,58e-28 Length: 504
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-7207 (1-504)

Oy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 78 ATGGCTTCCTCAGTCTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 137

Oy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 138 AACATGGTTGCACCTTTCACAGGTCTTAAGTCTGCTGCCTCAATTCCTGTTTCAAGGAAG 197

Oy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 198 CAAACCTTGACATCACTTCCATTGCCAGCAACGCGGAGAGTGAATGC 248

RESULT 20
PCT-US02-27883-13
; Sequence 13, Application PC/TUS0227883
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; APPLICANT: Dow Agro Sciences, LLC
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Disease Resistance
```

```

; FILE REFERENCE: DOW-07613
; CURRENT APPLICATION NUMBER: PCT/US02/27883
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 2324
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Nicotiana benthamiana
PCT-US02-27883-13

Alignment Scores:
Pred. No.: 7,06e-28 Length: 581
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x PCT-US02-27883-13 (1-581)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 63 ATGGCTTCCTCAGTTCTTTCTCAGCAGCAGTTGCCACCCGAGCAATGTTGCTCAAGCT 122
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 123 AACATGGTTGCACCTTTCACCTGGTCTTAAGTCAGCTGCTCGTTCCTCTGTTTCAAGGAAG 182
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 183 CAAAACCTTGACATCACTTCCATTGCCAGCAGCGGCGGAAGAGTGCAATGC 233

RESULT 21
PCT-US02-27883-1213
; Sequence 1213, Application PC/TUS0227883
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Disease Resistance
; FILE REFERENCE: DOW-07613
; CURRENT APPLICATION NUMBER: PCT/US02/27883
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 2324
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1213
; LENGTH: 608
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27883-1213

Alignment Scores:
Pred. No.: 7.6e-28 Length: 608
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x PCT-US02-27883-1213 (1-608)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 38 ATGGCTTCCTCAGTTCTTTCTCAGCAGCAGTTGCCACCCGAGCAATGTTGCTCAAGCT 97
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 98 AACATGGTTGCACCTTTCACAGGCTTAAGTCTGCTGCTCATTCCTCTGTTTCAAGGAAG 157
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 183 CAAAACCTTGACATCACTTCCATTGCCAGCAGCGGCGGAAGAGTGCAATGC 233
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Db 158 CAAAACCTTGACATCACTTCCATTGCCAGCAGCGGCGGAAGAGTGCAATGC 208

RESULT 22
PCT-US02-27883-1225
; Sequence 1225, Application PC/TUS0227883
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Disease Resistance
; FILE REFERENCE: DOW-07613
; CURRENT APPLICATION NUMBER: PCT/US02/27883
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 2324
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1225
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27883-1225

Alignment Scores:
Pred. No.: 7.73e-28 Length: 614
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x PCT-US02-27883-1225 (1-614)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 46 ATGGCTTCCTCAGTTCTTTCTCAGCAGCAGTTGCCACCCGAGCAATGTTGCTCAAGCT 105
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 106 AACATGGTTGCACCTTTCACCTGGTCTTAAGTCAGCTGCTCGTTCCTCTGTTTCAAGGAAG 165
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 166 CAAAACCTTGACATCACTTCCATTGCCAGCAGCGGCGGAAGAGTGCAATGC 216

RESULT 23
PCT-US02-27883-1218
; Sequence 1218, Application PC/TUS0227883
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Disease Resistance
; FILE REFERENCE: DOW-07613
; CURRENT APPLICATION NUMBER: PCT/US02/27883
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 2324
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1218
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc feature
; LOCATION: (490)..(490)
; OTHER INFORMATION: The residue at this position can be any nucleotide.
PCT-US02-27883-1218

Alignment Scores:
Pred. No.: 7.75e-28 Length: 615
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
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```

Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x PCT-US02-27883-1218 (1-615)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
DB 47 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 106

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAala---PheProValSerArgLys 39
DB 107 AACATGGTTGCACCTTTTCACAGGCTTTAAGTCTGCTGCTCCTCATCTCTGTTTCAGGAAG 166

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB 167 CAAACCTTGACATCACTTCATTGCCAGCAACGGCGGAAGAGTGCAATGC 217

RESULT 24
PCT-US02-27883-1222
; Sequence 1222, Application PC/TUS0227883
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; APPLICANT: Dow Agro Sciences, LLC
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Disease Resistance
; FILE REFERENCE: DOW-07613
; CURRENT APPLICATION NUMBER: PCT/US02/27883
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 2324
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1222
; LENGTH: 632
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27883-1222

Alignment Scores:
Pred. No.: 8, 1e-28 Length: 632
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservativeness: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x PCT-US02-27883-1222 (1-632)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
DB 52 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 111

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAala---PheProValSerArgLys 39
DB 112 AACATGGTTGCACCTTTTCACAGGCTTTAAGTCTGCTGCTCCTCATCTCTGTTTCAGGAAG 171

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB 172 CAAACCTTGACATCACTTCATTGCCAGCAACGGCGGAAGAGTGCAATGC 222

RESULT 25
PCT-US02-27883-1217
; Sequence 1217, Application PC/TUS0227883
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; APPLICANT: Dow Agro Sciences, LLC
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Disease Resistance
; FILE REFERENCE: DOW-07613
; CURRENT APPLICATION NUMBER: PCT/US02/27883
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 2324
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1217
; LENGTH: 684

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27883-1217

Alignment Scores:
Pred. No.: 9, 23e-28 Length: 684
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservativeness: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x PCT-US02-27883-1217 (1-684)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
DB 47 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 106

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAala---PheProValSerArgLys 39
DB 107 AACATGGTTGCACCTTTTCACAGGCTTTAAGTCTGCTGCTCCTCATCTCTGTTTCAGGAAG 166

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB 167 CAAACCTTGACATCACTTCATTGCCAGCAACGGCGGAAGAGTGCAATGC 217

RESULT 26
PCT-US02-27884-5765
; Sequence 5765, Application PC/TUS0227884
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; APPLICANT: Dow Agro Sciences, LLC
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteristics
; FILE REFERENCE: DOW-07611
; CURRENT APPLICATION NUMBER: PCT/US02/27884
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5765
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27884-5765

Alignment Scores:
Pred. No.: 1e-27 Length: 718
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservativeness: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x PCT-US02-27884-5765 (1-718)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
DB 45 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 104

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAala---PheProValSerArgLys 39
DB 105 AACATGGTTGCACCTTTTCACAGGCTTTAAGTCTGCTGCTCCTCATCTCTGTTTCAGGAAG 164

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB 165 CAAACCTTGACATCACTTCATTGCCAGCAACGGCGGAAGAGTGCAATGC 215

RESULT 27
US-10-487-901-5765
; Sequence 5765, Application US/10487901

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; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crowsley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5765
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-5765

Alignment Scores:
Pred. No.: 1e-27 Length: 718
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 51 Gaps: 1

US-10-628-525a-33 (1-56) x US-10-487-901-5765 (1-718)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
DB 45 ATGGCTTCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 104
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
DB 105 AACATGGTTGCACCTTTTCACTGCTCTTAAGTCAGCTGCCTCGTTCCTGTTTCAAGGAAG 164
QY 40 GlnAenLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56
DB 165 CAAAACCTTGACATCATTCCATTGCCAACGCGGAAGAGTGCATATGC 215

RESULT 28
PCT-US02-27884-1704
; Sequence 1704, Application PC/TUS0227884
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; APPLICANT: Dow Agro Sciences, LLC
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-07611
; CURRENT APPLICATION NUMBER: PCT/US02/27884
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1704
; LENGTH: 736
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27884-1704

Alignment Scores:
Pred. No.: 1.04e-27 Length: 736
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1

US-10-628-525a-33 (1-56) x PCT-US02-27884-1704 (1-736)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
DB 63 ATGGCTTCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 122
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
DB 123 AACATGGTTGCACCTTTTCACTGCTCTTAAGTCAGCTGCCTCGTTCCTGTTTCAAGGAAG 182
QY 40 GlnAenLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56
DB 183 CAAAACCTTGACATCATTCCATTGCCAACGCGGAAGAGTGCATATGC 233

RESULT 30
US-10-487-901-1704
; Sequence 1704, Application US/10487901
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula

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Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1

US-10-628-525a-33 (1-56) x PCT-US02-27884-1704 (1-736)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
DB 63 ATGGCTTCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 122
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
DB 123 AACATGGTTGCACCTTTTCACTGCTCTTAAGTCAGCTGCCTCGTTCCTGTTTCAAGGAAG 182
QY 40 GlnAenLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56
DB 183 CAAAACCTTGACATCATTCCATTGCCAACGCGGAAGAGTGCATATGC 233

RESULT 29
PCT-US02-27884-5043
; Sequence 5043, Application PC/TUS0227884
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; APPLICANT: Dow Agro Sciences, LLC
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-07611
; CURRENT APPLICATION NUMBER: PCT/US02/27884
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5043
; LENGTH: 736
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27884-5043

Alignment Scores:
Pred. No.: 1.04e-27 Length: 736
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1

US-10-628-525a-33 (1-56) x PCT-US02-27884-5043 (1-736)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
DB 63 ATGGCTTCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 122
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
DB 123 AACATGGTTGCACCTTTTCACTGCTCTTAAGTCAGCTGCCTCGTTCCTGTTTCAAGGAAG 182
QY 40 GlnAenLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56
DB 183 CAAAACCTTGACATCATTCCATTGCCAACGCGGAAGAGTGCATATGC 233

RESULT 30
US-10-487-901-1704
; Sequence 1704, Application US/10487901
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula

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; APPLICANT: Crosley, Rodney  
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri  
; FILE REFERENCE: DOM-08552  
; CURRENT APPLICATION NUMBER: US/10/487,901  
; CURRENT FILING DATE: 2004-02-26  
; NUMBER OF SEQ ID NOS: 7560  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1704  
; LENGTH: 736  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-487-901-1704

Alignment Scores:  
Pred. NO.: 1.04e-27 Length: 736  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 51 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-1704 (1-736)

|    |     |                                                               |     |
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| Qy | 1   | MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla  | 20  |
| Db | 63  | ATGGCTTCCTCAGTTCTTCTCCTCAGCAGCAGTTCGCCACCGCAGCAATGTTGCTCAAGCT | 122 |
| Qy | 21  | SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys  | 39  |
| Db | 123 | AACATGTTTGACCTTTTCACTGGTCTTAAGTCAGTCGCTCCCTGTTTCAAGGAAG       | 182 |
| Qy | 40  | GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys           | 56  |
| Db | 183 | CAAAACCTTGACATCACTTCATTGCCAGCAACGCGGAGAGTGCAATGC              | 233 |

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Job time : 1533.83 secs



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 21:21:57 ; Search time 104.728 Seconds  
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1603.719 Million cell updates/sec

Title: US-10-628-525A-33

Perfect score: 271

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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6698573 seqs, 1499593917 residues

Total number of hits satisfying chosen parameters: 13397146

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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-TRANS=human40.cdi -LIST=150 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100  
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-USER=US10628525 @CGN 1 1 1552 @runat\_31032006\_095132\_17106 -NCPU=6 -ICPU=3  
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7: /SID55/ptodata/2/pna/US11 NEW COMB.seq.\*  
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10: /SID55/ptodata/2/pna/US14 NEW COMB.seq.\*  
11: /SID55/ptodata/2/pna/US15 NEW COMB.seq.\*  
12: /SID55/ptodata/2/pna/US16 NEW COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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| 1          | 223.5 | 82.5        | 684    | 8  | US-11-336-680-33    |
| 2          | 212.5 | 78.4        | 323    | 8  | US-11-331-019-8290  |
| 3          | 212.5 | 78.4        | 350    | 8  | US-11-331-019-38696 |
| 4          | 212.5 | 78.4        | 359    | 8  | US-11-331-019-7156  |
| 5          | 212.5 | 78.4        | 369    | 8  | US-11-331-019-37546 |

|      |    |                       |                    |
|------|----|-----------------------|--------------------|
| 375  | 8  | US-11-331-032-18420   | Sequence 18420, A  |
| 379  | 8  | US-11-331-019-36580   | Sequence 36580, A  |
| 381  | 8  | US-11-331-019-38462   | Sequence 38462, A  |
| 381  | 8  | US-11-331-019-38951   | Sequence 38951, A  |
| 381  | 8  | US-11-331-019-19877   | Sequence 19877, A  |
| 391  | 8  | US-11-331-019-36843   | Sequence 36843, A  |
| 399  | 8  | US-11-331-019-36471   | Sequence 36471, A  |
| 405  | 8  | US-11-331-019-38154   | Sequence 38154, A  |
| 405  | 8  | US-11-331-019-38762   | Sequence 38762, A  |
| 411  | 8  | US-11-331-019-36603   | Sequence 36603, A  |
| 414  | 8  | US-11-331-019-7434    | Sequence 7434, Ap  |
| 415  | 8  | US-11-331-019-8439    | Sequence 8439, Ap  |
| 415  | 8  | US-11-331-019-37318   | Sequence 37318, A  |
| 419  | 8  | US-11-331-019-39124   | Sequence 39124, A  |
| 420  | 8  | US-11-331-019-37373   | Sequence 37373, A  |
| 422  | 8  | US-11-331-019-39412   | Sequence 39412, A  |
| 433  | 8  | US-11-331-019-8542    | Sequence 8542, Ap  |
| 434  | 8  | US-11-331-019-39634   | Sequence 39634, A  |
| 435  | 8  | US-11-331-019-37716   | Sequence 37716, A  |
| 436  | 8  | US-11-331-019-38865   | Sequence 38865, A  |
| 437  | 8  | US-11-331-019-39767   | Sequence 39767, A  |
| 440  | 8  | US-11-331-019-39351   | Sequence 39351, A  |
| 456  | 8  | US-11-331-019-38846   | Sequence 38846, A  |
| 461  | 8  | US-11-331-019-8383    | Sequence 8383, Ap  |
| 463  | 8  | US-11-331-019-8391    | Sequence 8391, Ap  |
| 553  | 8  | US-11-331-019-36740   | Sequence 36740, A  |
| 562  | 8  | US-11-331-019-36830   | Sequence 36830, A  |
| 582  | 8  | US-11-331-019-36677   | Sequence 36677, A  |
| 594  | 8  | US-11-331-019-36853   | Sequence 36853, A  |
| 622  | 8  | US-11-331-019-36754   | Sequence 36754, A  |
| 632  | 8  | US-11-331-019-36808   | Sequence 36808, A  |
| 647  | 8  | US-11-331-019-7368    | Sequence 7368, Ap  |
| 249  | 8  | US-11-331-019-9010    | Sequence 9010, Ap  |
| 385  | 10 | US-11-314-834-1176    | Sequence 1176, Ap  |
| 300  | 8  | US-11-331-019-7840    | Sequence 7840, Ap  |
| 342  | 8  | US-11-331-019-6832    | Sequence 6832, Ap  |
| 359  | 8  | US-11-331-019-8560    | Sequence 8560, Ap  |
| 396  | 8  | US-11-331-019-39018   | Sequence 39018, A  |
| 421  | 8  | US-11-331-019-37526   | Sequence 37526, A  |
| 449  | 8  | US-11-331-019-9356    | Sequence 9356, Ap  |
| 466  | 8  | US-11-331-019-8425    | Sequence 8425, Ap  |
| 413  | 8  | US-11-331-019-9351    | Sequence 9351, Ap  |
| 438  | 8  | US-11-331-019-40040   | Sequence 40040, A  |
| 382  | 8  | US-11-331-019-38933   | Sequence 38933, A  |
| 389  | 8  | US-11-331-019-38514   | Sequence 38514, A  |
| 392  | 8  | US-11-331-019-39037   | Sequence 39037, A  |
| 407  | 8  | US-11-331-019-38139   | Sequence 38139, A  |
| 408  | 8  | US-11-331-019-39105   | Sequence 39105, A  |
| 417  | 8  | US-11-331-019-37795   | Sequence 37795, A  |
| 423  | 8  | US-11-331-019-9359    | Sequence 9359, Ap  |
| 424  | 8  | US-11-331-019-39347   | Sequence 39347, A  |
| 472  | 8  | US-11-330-364-6351    | Sequence 6351, Ap  |
| 730  | 8  | US-11-056-3558-49339  | Sequence 49339, A  |
| 743  | 7  | US-10-953-349-8894    | Sequence 8894, Ap  |
| 743  | 8  | US-11-056-3558-36037  | Sequence 36037, A  |
| 743  | 8  | US-11-056-3558-47209  | Sequence 47209, A  |
| 762  | 8  | US-11-056-3558-97594  | Sequence 97594, A  |
| 762  | 8  | US-11-056-3558-108833 | Sequence 108833, A |
| 772  | 8  | US-11-056-3558-107434 | Sequence 107434, A |
| 772  | 8  | US-11-056-3558-118673 | Sequence 118673, A |
| 1597 | 12 | US-60-752-355-716     | Sequence 716, App  |
| 1761 | 8  | US-11-056-3558-108015 | Sequence 108015, A |
| 1761 | 8  | US-11-056-3558-119254 | Sequence 119254, A |
| 231  | 8  | US-11-331-019-8716    | Sequence 8716, Ap  |
| 281  | 8  | US-11-331-019-38707   | Sequence 38707, A  |
| 282  | 8  | US-11-331-019-40760   | Sequence 40760, A  |
| 284  | 8  | US-11-331-019-36524   | Sequence 36524, A  |
| 285  | 8  | US-11-331-019-36633   | Sequence 36633, A  |
| 292  | 8  | US-11-331-019-8985    | Sequence 8985, Ap  |
| 294  | 8  | US-11-331-019-9070    | Sequence 9070, Ap  |
| 312  | 8  | US-11-331-019-40770   | Sequence 40770, A  |
| 316  | 8  | US-11-331-019-9053    | Sequence 9053, Ap  |

|     |       |      |     |   |                     |                   |
|-----|-------|------|-----|---|---------------------|-------------------|
| 79  | 207   | 76.4 | 317 | 8 | US-11-331-019-39605 | Sequence 39605, A |
| 80  | 207   | 76.4 | 339 | 8 | US-11-331-019-38787 | Sequence 38787, A |
| 81  | 207   | 76.4 | 342 | 8 | US-11-331-019-39585 | Sequence 39585, A |
| 82  | 207   | 76.4 | 343 | 8 | US-11-331-019-6978  | Sequence 6978, Ap |
| 83  | 207   | 76.4 | 346 | 8 | US-11-331-019-7826  | Sequence 7826, Ap |
| 84  | 207   | 76.4 | 352 | 8 | US-11-331-019-40716 | Sequence 40716, A |
| 85  | 207   | 76.4 | 354 | 8 | US-11-331-019-40514 | Sequence 40514, A |
| 86  | 207   | 76.4 | 356 | 8 | US-11-331-019-36496 | Sequence 36496, A |
| 87  | 207   | 76.4 | 359 | 8 | US-11-331-019-38246 | Sequence 38246, A |
| 88  | 207   | 76.4 | 359 | 8 | US-11-331-019-38704 | Sequence 38704, A |
| 89  | 207   | 76.4 | 359 | 8 | US-11-331-019-39045 | Sequence 39045, A |
| 90  | 207   | 76.4 | 378 | 8 | US-11-331-019-40754 | Sequence 40754, A |
| 91  | 207   | 76.4 | 381 | 8 | US-11-331-019-6546  | Sequence 6546, Ap |
| 92  | 207   | 76.4 | 381 | 8 | US-11-331-019-38959 | Sequence 38959, A |
| 93  | 207   | 76.4 | 386 | 8 | US-11-331-019-36583 | Sequence 36583, A |
| 94  | 207   | 76.4 | 390 | 8 | US-11-331-019-38573 | Sequence 38573, A |
| 95  | 207   | 76.4 | 392 | 8 | US-11-331-019-36467 | Sequence 36467, A |
| 96  | 207   | 76.4 | 392 | 8 | US-11-331-019-38962 | Sequence 38962, A |
| 97  | 207   | 76.4 | 392 | 8 | US-11-331-019-39903 | Sequence 39903, A |
| 98  | 207   | 76.4 | 398 | 8 | US-11-331-019-36470 | Sequence 36470, A |
| 99  | 207   | 76.4 | 401 | 8 | US-11-331-019-38281 | Sequence 38281, A |
| 100 | 207   | 76.4 | 401 | 8 | US-11-331-019-6840  | Sequence 6840, Ap |
| 101 | 207   | 76.4 | 403 | 8 | US-11-331-019-6581  | Sequence 6581, Ap |
| 102 | 207   | 76.4 | 403 | 8 | US-11-331-019-38620 | Sequence 38620, A |
| 103 | 207   | 76.4 | 405 | 8 | US-11-331-019-36272 | Sequence 36272, A |
| 104 | 207   | 76.4 | 409 | 8 | US-11-331-019-37634 | Sequence 37634, A |
| 105 | 207   | 76.4 | 411 | 8 | US-11-331-019-9160  | Sequence 9160, Ap |
| 106 | 207   | 76.4 | 411 | 8 | US-11-331-019-39962 | Sequence 39962, A |
| 107 | 207   | 76.4 | 415 | 8 | US-11-331-019-8421  | Sequence 8421, Ap |
| 108 | 207   | 76.4 | 416 | 8 | US-11-331-019-40013 | Sequence 40013, A |
| 109 | 207   | 76.4 | 417 | 8 | US-11-331-019-38032 | Sequence 38032, A |
| 110 | 207   | 76.4 | 417 | 8 | US-11-331-019-39806 | Sequence 39806, A |
| 111 | 207   | 76.4 | 419 | 8 | US-11-331-019-37232 | Sequence 37232, A |
| 112 | 207   | 76.4 | 421 | 8 | US-11-331-019-6568  | Sequence 6568, Ap |
| 113 | 207   | 76.4 | 422 | 8 | US-11-331-019-40171 | Sequence 40171, A |
| 114 | 207   | 76.4 | 423 | 8 | US-11-331-019-37817 | Sequence 37817, A |
| 115 | 207   | 76.4 | 423 | 8 | US-11-331-019-39410 | Sequence 39410, A |
| 116 | 207   | 76.4 | 424 | 8 | US-11-331-019-39419 | Sequence 39419, A |
| 117 | 207   | 76.4 | 425 | 8 | US-11-331-019-8186  | Sequence 8186, Ap |
| 118 | 207   | 76.4 | 427 | 8 | US-11-331-019-37120 | Sequence 37120, A |
| 119 | 207   | 76.4 | 427 | 8 | US-11-331-019-40372 | Sequence 40372, A |
| 120 | 207   | 76.4 | 429 | 8 | US-11-331-019-39780 | Sequence 39780, A |
| 121 | 207   | 76.4 | 431 | 8 | US-11-331-019-39555 | Sequence 39555, A |
| 122 | 207   | 76.4 | 431 | 8 | US-11-331-019-39717 | Sequence 39717, A |
| 123 | 207   | 76.4 | 433 | 8 | US-11-331-019-8008  | Sequence 8008, Ap |
| 124 | 207   | 76.4 | 433 | 8 | US-11-331-019-37680 | Sequence 37680, A |
| 125 | 207   | 76.4 | 435 | 8 | US-11-331-019-39700 | Sequence 39700, A |
| 126 | 207   | 76.4 | 435 | 8 | US-11-331-019-39738 | Sequence 39738, A |
| 127 | 207   | 76.4 | 437 | 8 | US-11-331-019-40244 | Sequence 40244, A |
| 128 | 207   | 76.4 | 439 | 8 | US-11-331-019-39637 | Sequence 39637, A |
| 129 | 207   | 76.4 | 439 | 8 | US-11-331-019-40219 | Sequence 40219, A |
| 130 | 207   | 76.4 | 441 | 8 | US-11-331-019-40464 | Sequence 40464, A |
| 131 | 207   | 76.4 | 442 | 8 | US-11-331-019-39613 | Sequence 39613, A |
| 132 | 207   | 76.4 | 442 | 8 | US-11-331-019-39979 | Sequence 39979, A |
| 133 | 207   | 76.4 | 446 | 8 | US-11-331-019-36213 | Sequence 36213, A |
| 134 | 207   | 76.4 | 448 | 8 | US-11-331-019-39873 | Sequence 39873, A |
| 135 | 207   | 76.4 | 451 | 8 | US-11-331-019-6116  | Sequence 6116, Ap |
| 136 | 207   | 76.4 | 456 | 8 | US-11-331-019-8531  | Sequence 8531, Ap |
| 137 | 207   | 76.4 | 601 | 8 | US-11-331-019-36811 | Sequence 36811, A |
| 138 | 207   | 76.4 | 604 | 8 | US-11-331-019-36656 | Sequence 36656, A |
| 139 | 207   | 76.4 | 665 | 8 | US-11-331-019-36735 | Sequence 36735, A |
| 140 | 205.5 | 75.8 | 666 | 8 | US-11-331-019-36709 | Sequence 36709, A |
| 141 | 205.5 | 75.8 | 404 | 8 | US-11-331-019-38120 | Sequence 38120, A |
| 142 | 205.5 | 75.8 | 424 | 8 | US-11-331-019-39430 | Sequence 39430, A |
| 143 | 205   | 75.6 | 386 | 8 | US-11-331-019-39972 | Sequence 39972, A |
| 144 | 205   | 75.6 | 397 | 8 | US-11-331-019-34443 | Sequence 34443, A |
| 145 | 205   | 75.6 | 451 | 8 | US-11-331-019-38790 | Sequence 38790, A |
| 146 | 204.5 | 75.5 | 285 | 8 | US-11-331-019-36325 | Sequence 36325, A |
| 147 | 204.5 | 75.5 | 294 | 8 | US-11-331-019-40747 | Sequence 40747, A |
| 148 | 204.5 | 75.5 | 358 | 8 | US-11-331-019-8984  | Sequence 8984, Ap |
| 149 | 204.5 | 75.5 | 362 | 8 | US-11-331-019-38912 | Sequence 38912, A |
| 150 | 204.5 | 75.5 | 363 | 8 | US-11-331-019-38252 | Sequence 38252, A |

ALIGNMENTS

RESULT 1

US-11-336-680-33

Sequence 33, Application US/11336680

GENERAL INFORMATION:

APPLICANT: E.I. duPont de Nemours and Company, Inc.

APPLICANT: Meyer, Knut

APPLICANT: Viitanen, Paul

APPLICANT: Flint, Dennis

TITLE OF INVENTION: High Level Production of Arbutin in Green Plants and Microbes

FILE REFERENCE: CL 2155 US NA

CURRENT APPLICATION NUMBER: US/11/336,680

CURRENT FILING DATE: 2006-01-20

NUMBER OF SEQ ID NOS: 54

SOFTWARE: PatentIn version 3.2

SEQ ID NO 33

LENGTH: 684

TYPE: DNA

ORGANISM: Escherichia coli

US-11-336-680-33

Alignment Scores:

Pred. No.: 1,74e-23 Length: 684

Score: 223.50 Matches: 47

Percent Similarity: 93.0% Conservative: 6

Best Local Similarity: 82.5% Mismatches: 3

Query Match: 8 Indels: 1

DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x US-11-336-680-33 (1-684)

QY 1 MetaLaserSerMetLeuSerSerAlaValAlaThrArgThrAsnProAlaGlnAla 20

Db 1 ATGGTCTCTCTGTCATTTCTTCAGCAGCTGTTCACACGACGCAATGTTACACAAGCT 60

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39

Db 61 AGCATGGTTGACCTTCTCAGTGTCTCAATCTTCAGCCACTTCCCTGTTACAAAGAAG 120

QY 40 GlnAnLeuAapPileThrSerIleAlaSerAnGlyGlyArgValGlnCys 56

Db 121 CAAAACCTTGACATCATCTTCATCTAGCAATGCTGGAAGAGTTAGCTGC 171

RESULT 2

US-11-331-019-8290

Sequence 8290, Application US/11331019

GENERAL INFORMATION:

APPLICANT: Fincher, Karen L.

APPLICANT: La Rosa, Thomas J.

APPLICANT: McCarter, David W.

APPLICANT: Pear, Julie R.

TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

FILE REFERENCE: 16517.359 - 38-21(51375)C/US

CURRENT APPLICATION NUMBER: US/11/331,019

CURRENT FILING DATE: 2006-01-13

PRIOR APPLICATION NUMBER: US 09/637,086

PRIOR FILING DATE: 2000-08-11

PRIOR APPLICATION NUMBER: US 60/149,881

PRIOR FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 52949

SEQ ID NO 8290

LENGTH: 323

TYPE: DNA

ORGANISM: Gossypium hirsutum

FEATURE:

OTHER INFORMATION: Clone ID: LIB3120-031-Q1-K1-D12

US-11-331-019-8290

Alignment Scores:

Pred. No.: 2.62e-22 Length: 323

Score: 212.50 Matches: 46  
Percent Similarity: 89.8% Conservative: 7  
Best Local Similarity: 78.0% Mismatches: 3  
Query Match: 78.4% Indels: 3  
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-8290 (1-323)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18  
Db 66 ATGGCCTCTCCATGATCTCATCGCAACCATTCGCCACCGTGAACCGCTCTCCCGGCA 125  
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37  
Db 126 CAGGCCAACATGTGGGCCCCCTTCACCGGCCTCAAAATCTGCCTCTGCTTTCCCAATGCC 185  
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 186 AGGAGGCCAACACGACATCACTTCTTGCAGCAACCGTGGGAGAGTGCAATGC 242

## RESULT 3

US-11-331-019-38696  
; Sequence 38696, Application US/11331019

; GENERAL INFORMATION:

; APPLICANT: Fincher, Karen L.

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: McCarter, David W.

; APPLICANT: Pear, Julie R.

; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

; FILE OF INVENTION: Plants

; FILE REFERENCE: 16517.359 - 38-21(51375)C/US

; CURRENT APPLICATION NUMBER: US/11/331.019

; PRIOR FILING DATE: 2006-01-13

; PRIOR APPLICATION NUMBER: US 09/637,086

; PRIOR FILING DATE: 2000-08-11

; PRIOR APPLICATION NUMBER: US 60/149,881

; PRIOR FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 52949

; SEQ ID NO 38696

; TYPE: DNA

; ORGANISM: Gossypium hirsutum

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3165-034-P1-K1-H11

US-11-331-019-38696

Alignment Scores:  
Pred. No.: 2,95e-22 Length: 350  
Score: 212.50 Matches: 46  
Percent Similarity: 89.8% Conservative: 7  
Best Local Similarity: 78.0% Mismatches: 3  
Query Match: 78.4% Indels: 3  
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-38696 (1-350)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18  
Db 66 ATGGCCTCTCCATGATCTCATCGCAACCATTCGCCACCGTGAACCGCTCTCCCGGCA 125  
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37  
Db 126 CAGGCCAACATGTGGGCCCCCTTCACCGGCCTCAAAATCTGCCTCTGCTTTCCCAATGCC 185  
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 186 AGGAGGCCAACACGACATCACTTCTTGCAGCAACCGTGGGAGAGTGCAATGC 242

## RESULT 4

US-11-331-019-7156

; Sequence 7156, Application US/11331019

; GENERAL INFORMATION:

; APPLICANT: Fincher, Karen L.

Alignment Scores:  
Pred. No.: 3.19e-22 Length: 369  
Score: 212.50 Matches: 46  
Percent Similarity: 89.8% Conservative: 7

; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: McCarter, David W.  
; APPLICANT: Pear, Julie R.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US  
; CURRENT APPLICATION NUMBER: US/11/331.019  
; PRIOR FILING DATE: 2006-01-13  
; PRIOR APPLICATION NUMBER: US 09/637,086  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: US 60/149,881  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 52949  
; SEQ ID NO 7156  
; LENGTH: 359  
; TYPE: DNA  
; ORGANISM: Gossypium hirsutum  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3120-017-Q1-K1-E2  
US-11-331-019-7156

Alignment Scores:  
Pred. No.: 3.07e-22 Length: 359  
Score: 212.50 Matches: 46  
Percent Similarity: 89.8% Conservative: 7  
Best Local Similarity: 78.0% Mismatches: 3  
Query Match: 78.4% Indels: 3  
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-7156 (1-359)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18  
Db 66 ATGGCCTCTCCATGATCTCATCGCAACCATTCGCCACCGTGAACCGCTCTCCCGGCA 125  
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37  
Db 126 CAGGCCAACATGTGGGCCCCCTTCACCGGCCTCAAAATCTGCCTCTGCTTTCCCAATGCC 185  
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 186 AGGAGGCCAACACGACATCACTTCTTGCAGCAACCGTGGGAGAGTGCAATGC 242

## RESULT 5

US-11-331-019-37546

; Sequence 37546, Application US/11331019

; GENERAL INFORMATION:

; APPLICANT: Fincher, Karen L.

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: McCarter, David W.

; APPLICANT: Pear, Julie R.

; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

; FILE OF INVENTION: Plants

; FILE REFERENCE: 16517.359 - 38-21(51375)C/US

; CURRENT APPLICATION NUMBER: US/11/331.019

; PRIOR FILING DATE: 2006-01-13

; PRIOR APPLICATION NUMBER: US 09/637,086

; PRIOR FILING DATE: 2000-08-11

; PRIOR APPLICATION NUMBER: US 60/149,881

; PRIOR FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 52949

; SEQ ID NO 37546

; LENGTH: 369

; TYPE: DNA

; ORGANISM: Gossypium hirsutum

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3165-018-P1-K1-B9

US-11-331-019-37546

|                        |       |             |   |
|------------------------|-------|-------------|---|
| Best Local Similarity: | 78.0% | Mismatches: | 3 |
| Query Match:           | 78.4% | Indels:     | 3 |
| DB:                    | 8     | Gaps:       | 2 |

US-10-628-525A-33 (1-56) x US-11-331-019-37546 (1-369)

|    |     |                                                                |
|----|-----|----------------------------------------------------------------|
| Qy | 1   | MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla18  |
| Db | 118 | ATGGCTCTCTCCATGATCTCATCGGACCACTTGCACCGTGAACCGCTCTCTCCCGGCA177  |
| Qy | 19  | GlnAlaSerMetValAlaProPhoThrGlyLeuIysSerAla---AlaPheProValSer37 |
| Db | 178 | CAGGCCAACTGGTGGCCCCCTTCACGGGCTCAAAATCGCTCTGCTTTTCCCAAGTCACC237 |
| Qy | 38  | ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys56    |
| Db | 238 | AGGAAGGCCAACCAACAGACATCACTTCTCTTGCAGACACGCTGGGAGAGTGCATATGC294 |

## RESULT 6

```

US-11-331-032-18420
; Sequence 18420, Application US/11331032
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Xiao, Jinhua
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 1517.361 - 38-21(51462)C/US
; CURRENT APPLICATION NUMBER: US/11/331,032
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/666,355
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US 60/155,005
; PRIOR FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 25978

```

OTHER INFORMATION: Clone ID: uC-gsflnu33B002b03b1  
US-11-331-032-18420

|                        |          |     |
|------------------------|----------|-----|
| Alignment Scores:      |          |     |
| Pred. No.:             | 3,278-22 | 375 |
| Score:                 | 212.50   | 46  |
| Percent Similarity:    | 89.8%    | 7   |
| Best Local Similarity: | 78.0%    | 3   |
| Query Match:           | 78.4%    | 3   |
| DB:                    | 8        | 2   |
| Length:                |          |     |
| Matches:               |          |     |
| Conservative:          |          |     |
| Mismatches:            |          |     |
| Indels:                |          |     |
| Gaps:                  |          |     |

US-10-628-525A-33 (1-56) x US-11-331-032-18420 (1-375)

|    |     |                                                              |     |
|----|-----|--------------------------------------------------------------|-----|
| Qy | 1   | MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla  | 18  |
| Db | 48  | ATGGCTCTCTCATGATCTCATCGCAACCATTTGCCACCGTGAACGCTCTCTCCCGGCA   | 107 |
| Qy | 19  | GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer | 37  |
| Db | 108 | CAGGCCAACATGTTGGCCCCCTTCACGGGCTCAAATCTGCCTCTGCTTTTCCCACTCAC  | 167 |
| Qy | 38  | ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys       | 56  |
| Db | 168 | AGGAAGGCCCAACACGACATCACTCTCTTCAAGCAACGGTGGGAGTGCAATGC        | 224 |

## RESULT 7

US-11-331-019-36580  
; Sequence 36580, Application US/11331019  
; GENERAL INFORMATION:  
; APPLICANT: Fincher, Karen L.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: McCarter, David W.  
; APPLICANT: Pear, Julie R.

```

? TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
?
? TITLE OF INVENTION: Plants
?
? FILE REFERENCE: 16517.359 - 38-21(51375)C/US
?
? CURRENT APPLICATION NUMBER: US/11/331,019
?
? CURRENT FILING DATE: 2006-01-13
?
? PRIOR APPLICATION NUMBER: US 09/637,086
?
? PRIOR FILING DATE: 2000-08-11
?
? PRIOR APPLICATION NUMBER: US 60/149,881
?
? PRIOR FILING DATE: 1999-08-19
?
? NUMBER OF SEQ ID NOS: 52949
?
? SEQ ID NO 36580
?
? LENGTH: 379
?
? TYPE: DNA
?
? ORGANISM: Gossypium hirsutum
?
? FEATURE:
?
? OTHER INFORMATION: Clone ID: LIB3165-006-P1-K1-P12
?
? US-11-331-019-36580

```

| Alignment Scores:      |          |
|------------------------|----------|
| Pred. No.:             | 3,329-22 |
| Score:                 | 212.50   |
| Percent Similarity:    | 89.8%    |
| Best Local Similarity: | 78.0%    |
| Query Match:           | 78.4%    |
| DB:                    | 8        |
| Length:                | 379      |
| Matches:               | 46       |
| Conservative:          | 7        |
| Mismatches:            | 3        |
| Indels:                | 3        |
| Gaps:                  | 2        |

US-10-628-525A-33 (1-56) x US-11-331-019-36580 (1-379)

[illegible]

## RESULT 8

```

US-11-331-019-38462
;
; Sequence 38462, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 38462
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-031-P1-K1-H7
US-11-331-019-38462

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|                        |          |                 |
|------------------------|----------|-----------------|
| Alignment Scores:      |          |                 |
| Pred. No.:             | 3,35e-22 | 381             |
| Score:                 | 212.50   | 46              |
| Percent Similarity:    | 89.8%    | Conservative: 7 |
| Best Local Similarity: | 78.0%    | Mismatches: 3   |
| Query Match:           | 78.4%    | Indels: 2       |
| DB:                    | 8        | Gaps: 2         |

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US-10-628-525A-33 (1-56) x US-11-331-019-38462 (1-381)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 66 ATGGCCTCTCTCCATGATCTCATCGGCAACCATTCGACCGTGACCGCTCTCTCCCGGCA 125
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 126 CAGGCCAACATGTTGGCCCCCTTACCGGCTTCAAAATCTGCCTCTGCTTTCCAGTCACC 185
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 186 AGGAAGGCCAACACGACATCACTTCTTTCAGCAACGGTGGGAGAGTGCAATGC 242

RESULT 9
US-11-331-019-38951
; Sequence 38951, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517,359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 38951
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-034-Pl-K4-H11
US-11-331-019-38951

Alignment Scores:
Pred. No.: 3,35e-22 Length: 381
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-38951 (1-381)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 66 ATGGCCTCTCTCCATGATCTCATCGGCAACCATTCGACCGTGACCGCTCTCTCCCGGCA 125
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 126 CAGGCCAACATGTTGGCCCCCTTACCGGCTTCAAAATCTGCCTCTGCTTTCCAGTCACC 185
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 186 AGGAAGGCCAACACGACATCACTTCTTTCAGCAACGGTGGGAGAGTGCAATGC 242

RESULT 10
US-11-331-019-19877
; Sequence 19877, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

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Db 48 ATGGCTCTCCATGATCTATCGCAACCAATTCACCGTGAACCGTCTCTCCCGGCA 107
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 108 CAGGCCAACATGCTGTGGCCCTTCACCGGCTCAATCTGCCTCTGCTTTCCCAATCACC 167
Qy 38 ArgLysGlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 56
Db 168 AGGAAGGCCAACACGACATCACTTCTTGTGCAAGCAACCGTGGGAGAGTGCAATGC 224

RESULT 15
US-11-331-019-36603
; Sequence 36603, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 36603
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-006-P1-K1-H5
US-11-331-019-36603

Alignment Scores:
Pred. No.: 3.74e-22 Length: 411
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-36603 (1-411)
Qy 1 MetAlaSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 95 ATGGCTCTCCATGATCTATCGCAACCAATTCACCGTGAACCGTCTCTCCCGGCA 154
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 155 CAGGCCAACATGCTGTGGCCCTTCACCGGCTCAATCTGCCTCTGCTTTCCCAATCACC 214
Qy 38 ArgLysGlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 56
Db 215 AGGAAGGCCAACACGACATCACTTCTTGTGCAAGCAACCGTGGGAGAGTGCAATGC 271

RESULT 16
US-11-331-019-7434
; Sequence 7434, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
```

```
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 7434
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3120-019-Q1-K1-H9
US-11-331-019-7434

Alignment Scores:
Pred. No.: 3.78e-22 Length: 414
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-7434 (1-414)
Qy 1 MetAlaSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 39 ATGGCTCTCCATGATCTATCGCAACCAATTCACCGTGAACCGTCTCTCCCGGCA 98
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 99 CAGGCCAACATGCTGTGGCCCTTCACCGGCTCAATCTGCCTCTGCTTTCCCAATCACC 158
Qy 38 ArgLysGlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 56
Db 159 AGGAAGGCCAACACGACATCACTTCTTGTGCAAGCAACCGTGGGAGAGTGCAATGC 215

RESULT 17
US-11-331-019-8439
; Sequence 8439, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 8439
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3120-034-Q1-K1-B12
US-11-331-019-8439

Alignment Scores:
Pred. No.: 3.8e-22 Length: 415
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-8439 (1-415)
Qy 1 MetAlaSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 54 ATGGCTCTCCATGATCTATCGCAACCAATTCACCGTGAACCGTCTCTCCCGGCA 113
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Db 108 CAGGCCAACATGGTGGCCCCCTTACCGGCTCAAAATCGCTCTGCTTTCCCGAGTCACC 167
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db 168 AGGAAGGCCAACACGACATCACTTCTTGTCAAGCAACGCTGGGAGAGTGCAATGC 224

RESULT 21
US-11-331-019-37373
; Sequence 37373, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517,359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 37373
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-016-P1-K1-B1
US-11-331-019-37373

Alignment Scores:
Pred. No.: 3.86e-22 Length: 420
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservatives: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-37373 (1-420)
Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 78 ATGGCTCTCTCCATGATCTCATCGCAACCATTTGCCACCGCTCTCTCCCGGCA 137
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 138 CAGGCCAACATGGTGGCCCCCTTACCGGCTCAAAATCTGCCTCTGCTTTCCCGAGTCACC 197
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db 198 AGGAAGGCCAACACGACATCACTTCTTGTCAAGCAACGCTGGGAGAGTGCAATGC 254

RESULT 22
US-11-331-019-39412
; Sequence 39412, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517,359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 39412
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-039-Q1-K1-F8
US-11-331-019-39412

Alignment Scores:
Pred. No.: 3.89e-22 Length: 422
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservatives: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-39412 (1-422)
Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 71 ATGGCTCTCTCCATGATCTCATCGCAACCATTTGCCACCGCTCTCTCCCGGCA 130
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 131 CAGGCCAACATGGTGGCCCCCTTACCGGCTCAAAATCTGCCTCTGCTTTCCCGAGTCACC 190
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db 191 AGGAAGGCCAACACGACATCACTTCTTGTCAAGCAACGCTGGGAGAGTGCAATGC 247

RESULT 23
US-11-331-019-8542
; Sequence 8542, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517,359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 8542
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3120-036-Q1-K1-C2
US-11-331-019-8542

Alignment Scores:
Pred. No.: 4.04e-22 Length: 433
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservatives: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-8542 (1-433)
Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 54 ATGGCTCTCTCCATGATCTCATCGGAGCAATTTGCCACCGCTCTCTCCCGGCA 113
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
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; SEQ ID NO 37716
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-020-P1-K1-E12
US-11-331-019-37716

Alignment Scores:
Pred. No.: 4,07e-22 Length: 435
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-37716 (1-435)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 54 ATGGCTCTCTCATGATCTCATCGGCAACCATTCGACCGTGAACCGCTCTCCCGGCA 113
QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 114 CAGGCCAACATGCTGGCCCCCTTCACCGGCTCAAAATCTGCCTCTGCTTTCCAGTCACC 173
QY 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 174 AGGAAGGCCAACACACGACATCACTTCTTGTGAAGCAACGGTGGGAGAGTGCAATGC 230

RESULT 26
US-11-331-019-38865
; Sequence 38865, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; PRIOR FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 38865
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-034-P1-K3-H11
US-11-331-019-38865

Alignment Scores:
Pred. No.: 4,08e-22 Length: 436
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-38865 (1-436)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 66 ATGGCTCTCTCATGATCTCATCGGCAACCATTCGACCGTGAACCGCTCTCCCGGCA 125
QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 126 CAGGCCAACATGCTGGCCCCCTTCACCGGCTCAAAATCTGCCTCTGCTTTCCAGTCACC 185

; SEQ ID NO 37716
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-020-P1-K1-E12
US-11-331-019-37716

Alignment Scores:
Pred. No.: 4,07e-22 Length: 435
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-37716 (1-435)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 54 ATGGCTCTCTCATGATCTCATCGGCAACCATTCGACCGTGAACCGCTCTCCCGGCA 113
QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 114 CAGGCCAACATGCTGGCCCCCTTCACCGGCTCAAAATCTGCCTCTGCTTTCCAGTCACC 173
QY 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 174 AGGAAGGCCAACACACGACATCACTTCTTGTGAAGCAACGGTGGGAGAGTGCAATGC 230

RESULT 26
US-11-331-019-38865
; Sequence 38865, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; PRIOR FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 38865
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-034-P1-K3-H11
US-11-331-019-38865

Alignment Scores:
Pred. No.: 4,08e-22 Length: 436
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-38865 (1-436)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 66 ATGGCTCTCTCATGATCTCATCGGCAACCATTCGACCGTGAACCGCTCTCCCGGCA 125
QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 126 CAGGCCAACATGCTGGCCCCCTTCACCGGCTCAAAATCTGCCTCTGCTTTCCAGTCACC 185
```

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; SEQ ID NO 37716
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-020-P1-K1-E12
US-11-331-019-37716

Alignment Scores:
Pred. No.: 4,07e-22 Length: 435
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-37716 (1-435)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 54 ATGGCTCTCTCATGATCTCATCGGCAACCATTCGACCGTGAACCGCTCTCCCGGCA 113
QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 114 CAGGCCAACATGCTGGCCCCCTTCACCGGCTCAAAATCTGCCTCTGCTTTCCAGTCACC 173
QY 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 174 AGGAAGGCCAACACACGACATCACTTCTTGTGAAGCAACGGTGGGAGAGTGCAATGC 230

RESULT 24
US-11-331-019-39634
; Sequence 39634, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; PRIOR FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 39634
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-042-Q1-K1-F10
US-11-331-019-39634

Alignment Scores:
Pred. No.: 4,06e-22 Length: 434
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-39634 (1-434)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 76 ATGGCTCTCTCATGATCTCATCGGCAACCATTCGACCGTGAACCGCTCTCCCGGCA 135
QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 136 CAGGCCAACATGCTGGCCCCCTTCACCGGCTCAAAATCTGCCTCTGCTTTCCAGTCACC 195
QY 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 196 AGGAAGGCCAACACACGACATCACTTCTTGTGAAGCAACGGTGGGAGAGTGCAATGC 252

RESULT 25
US-11-331-019-37716
; Sequence 37716, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; PRIOR FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; NUMBER OF SEQ ID NOS: 52949
```

QY 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 186 AGGAAGGCCAACACGACATCACTTCTTGTCAAGCAACGCTGGGAGAGTGCAATGC 242

## RESULT 27

US-11-331-019-39767  
 ; Sequence 39767, Application US/11331019  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fincher, Karen L.  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: McCarter, David W.  
 ; APPLICANT: Pear, Julie R.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants  
 ; FILE REFERENCE: 16517.359 - 38-21(51375)C/US  
 ; CURRENT APPLICATION NUMBER: US/11/331,019  
 ; CURRENT FILING DATE: 2006-01-13  
 ; PRIOR APPLICATION NUMBER: US 09/637,086  
 ; PRIOR FILING DATE: 2000-08-11  
 ; PRIOR APPLICATION NUMBER: US 60/149,881  
 ; PRIOR FILING DATE: 1999-08-19  
 ; NUMBER OF SEQ ID NOS: 52949  
 ; SEQ ID NO 39767  
 ; LENGTH: 437  
 ; TYPE: DNA  
 ; ORGANISM: Gossypium hirsutum  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: LIB3165-044-Q1-K1-C6  
 US-11-331-019-39767

Alignment Scores:  
 Pred. No.: 4.1e-22 Length: 437  
 Score: 212.50 Matches: 46  
 Percent Similarity: 89.8% Conservative: 7  
 Best Local Similarity: 78.0% Mismatches: 3  
 Query Match: 78.4% Indels: 3  
 DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-39767 (1-437)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18  
 Db 54 ATGGCTCTCTCCATGATCTCATCGCAACCATTCGCCACCGTGAACCGCTCTCTCCCGGCA 113  
 QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37  
 Db 114 CAGGCCAACATGTGTGGCCCTTCACCGGCTCAATCTGCCTCTGCTTCCAGTCACC 173  
 QY 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 174 AGGAAGGCCAACACGACATCACTTCTTGTCAAGCAACGCTGGGAGAGTGCAATGC 230

## RESULT 28

US-11-331-019-39351  
 ; Sequence 39351, Application US/11331019  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fincher, Karen L.  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: McCarter, David W.  
 ; APPLICANT: Pear, Julie R.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants  
 ; FILE REFERENCE: 16517.359 - 38-21(51375)C/US  
 ; CURRENT APPLICATION NUMBER: US/11/331,019  
 ; CURRENT FILING DATE: 2006-01-13  
 ; PRIOR APPLICATION NUMBER: US 09/637,086  
 ; PRIOR FILING DATE: 2000-08-11  
 ; PRIOR APPLICATION NUMBER: US 60/149,881  
 ; PRIOR FILING DATE: 1999-08-19  
 ; NUMBER OF SEQ ID NOS: 52949  
 ; SEQ ID NO 39351  
 ; LENGTH: 440

; TYPE: DNA  
 ; ORGANISM: Gossypium hirsutum  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: LIB3165-038-Q1-K1-H3  
 US-11-331-019-39351

Alignment Scores:  
 Pred. No.: 4.14e-22 Length: 440  
 Score: 212.50 Matches: 46  
 Percent Similarity: 89.8% Conservative: 7  
 Best Local Similarity: 78.0% Mismatches: 3  
 Query Match: 78.4% Indels: 3  
 DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-39351 (1-440)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18  
 Db 48 ATGGCTCTCTCCATGATCTCATCGCAACCATTCGCCACCGTGAACCGCTCTCTCCCGGCA 107  
 QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37  
 Db 108 CAGGCCAACATGTGTGGCCCTTCACCGGCTCAATCTGCCTCTGCTTCCAGTCACC 167  
 QY 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 168 AGGAAGGCCAACACGACATCACTTCTTGTCAAGCAACGCTGGGAGAGTGCAATGC 224

## RESULT 29

US-11-331-019-38846  
 ; Sequence 38846, Application US/11331019  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fincher, Karen L.  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: McCarter, David W.  
 ; APPLICANT: Pear, Julie R.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants  
 ; FILE REFERENCE: 16517.359 - 38-21(51375)C/US  
 ; CURRENT APPLICATION NUMBER: US/11/331,019  
 ; CURRENT FILING DATE: 2006-01-13  
 ; PRIOR APPLICATION NUMBER: US 09/637,086  
 ; PRIOR FILING DATE: 2000-08-11  
 ; PRIOR APPLICATION NUMBER: US 60/149,881  
 ; PRIOR FILING DATE: 1999-08-19  
 ; NUMBER OF SEQ ID NOS: 52949  
 ; SEQ ID NO 38846  
 ; LENGTH: 456  
 ; TYPE: DNA  
 ; ORGANISM: Gossypium hirsutum  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: LIB3165-034-PI-K3-P3  
 US-11-331-019-38846

Alignment Scores:  
 Pred. No.: 4.36e-22 Length: 456  
 Score: 212.50 Matches: 46  
 Percent Similarity: 89.8% Conservative: 7  
 Best Local Similarity: 78.0% Mismatches: 3  
 Query Match: 78.4% Indels: 3  
 DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-38846 (1-456)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18  
 Db 48 ATGGCTCTCTCCATGATCTCATCGCAACCATTCGCCACCGTGAACCGCTCTCTCCCGGCA 107  
 QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37  
 Db 108 CAGGCCAACATGTGTGGCCCTTCACCGGCTCAATCTGCCTCTGCTTCCAGTCACC 167  
 QY 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

```
||||| ||| |||||||||:|||||
Db 168 AGGAGGCCAACACACATCACTTCTTGTGCAAGCAACGGTGGGAGAGTGCAATGC 224

RESULT 30
US-11-331-019-8383
; Sequence 8383, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 8383
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3120-033-PI-K1-B2
US-11-331-019-8383

Alignment Scores:
Pred. No.: 4.43e-22 Length: 461
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-8383 (1-461)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 58 ATGGGGTCTCTCCATGATCTCATCGGCAGGCATTCGCCACCGCTCCTCCCGGCA 117
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 118 CAGGCCACATGTGTGGCCCTTCACCGCCCTCAAAATCTGCTCTCTCTCTCCAGTCACC 177
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 178 AGGAGGCCAACACACATCACTTCTTGTGCAAGCAACGGTGGGAGAGTGCAATGC 234
```

Search completed: April 2, 2006, 03:51:41  
Job time : 107.728 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search using frame plus p2n model

Run on: April 1, 2006, 04:29:01 ; Search time 1155.21 Seconds  
(without alignments)  
2853.949 Million cell updates/sec

Title: US-10-628-525A-34

Perfect score: 282

Sequence: 1 MPTVMASATATRTNPAQ.....ARRSRSLGNVASNGGRIRC 58

Scoring table:

|             | BLOSUM62 | Xgapop 10.0 | Xgapext 0.5 |
|-------------|----------|-------------|-------------|
| Ygapop 10.0 |          |             | 0.5         |
| Ygapext 0.5 |          |             |             |
| Fgapop 6.0  |          |             | 7.0         |
| Delop 6.0   |          |             |             |

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-MODEL=frame+ p2n.model -DRV=xlh
-Q=/abes/ABSSWEB spool/US10628525/runat_31032006_095113_16622/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes06h
-USER=US10628525 @CGN_1_1_4375 @runat_31032006_095113_16622 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database :

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GenEmbl:*
1: gb.ba:*
2: gb.in:*
3: gb.in:*
4: gb.env:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pr:*
9: gb.ro:*
10: gb.sts:*
11: gb.sy:*
12: gb.un:*
13: gb.vi:*
14: gb.htg:*
15: gb.pli:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
| 1          | 203.5 | 72.2        | 183    | 6  | AX147212 Sequence |
| 2          | 203.5 | 72.2        | 185    | 6  | AR212567 Sequence |
| 3          | 203.5 | 72.2        | 185    | 6  | AR590636 Sequence |

|    |       |      |       |    |           |                     |
|----|-------|------|-------|----|-----------|---------------------|
| 4  | 203.5 | 72.2 | 405   | 6  | A44435    | A44435 Sequence 4   |
| 5  | 203.5 | 72.2 | 405   | 6  | I44914    | I44914 Sequence 4   |
| 6  | 203.5 | 72.2 | 830   | 15 | MZRPCCSU  | D00170 Zea mays mr  |
| 7  | 203.5 | 72.2 | 830   | 15 | ZMRUBSU   | X06535 Maize mRNA   |
| 8  | 203.5 | 72.2 | 1648  | 15 | ZMRBCS    | Y00322 Maize rbcS   |
| 9  | 203.5 | 72.2 | 1868  | 6  | CQ828194  | CQ828194 Sequence   |
| 10 | 203.5 | 72.2 | 2318  | 6  | BD014494  | BD014494 Transgeni  |
| 11 | 203.5 | 72.2 | 5281  | 6  | AR581878  | AR581878 Sequence   |
| 12 | 203.5 | 72.2 | 5281  | 6  | AX394256  | AX394256 Sequence   |
| 13 | 203.5 | 72.2 | 5909  | 6  | AR581879  | AR581879 Sequence   |
| 14 | 203.5 | 72.2 | 5909  | 6  | AX394257  | AX394257 Sequence   |
| 15 | 196.5 | 69.7 | 415   | 6  | AR206035  | AR206035 Sequence   |
| 16 | 196.5 | 69.7 | 415   | 6  | AR229545  | AR229545 Sequence   |
| 17 | 196.5 | 69.7 | 415   | 6  | AR260580  | AR260580 Sequence   |
| 18 | 196.5 | 69.7 | 416   | 6  | AR271024  | AR271024 Sequence   |
| 19 | 196.5 | 69.7 | 416   | 6  | AR271026  | AR271026 Sequence   |
| 20 | 196.5 | 69.7 | 3450  | 6  | AR271020  | AR271020 Sequence   |
| 21 | 196.5 | 69.7 | 3455  | 6  | AR271032  | AR271032 Sequence   |
| 22 | 196.5 | 69.7 | 4149  | 6  | AR271018  | AR271018 Sequence   |
| 23 | 196.5 | 69.7 | 8349  | 6  | AR260588  | AR260588 Sequence   |
| 24 | 195.5 | 69.3 | 1274  | 15 | ZMRUBSMU  | Y09214 Z. mays rubi |
| 25 | 187.5 | 66.5 | 195   | 6  | AR088975  | AR088975 Sequence   |
| 26 | 187.5 | 66.5 | 195   | 6  | AR577398  | AR577398 Sequence   |
| 27 | 171.5 | 60.8 | 1386  | 15 | STRBCS2C  | X69762 S.tuberosum  |
| 28 | 169.5 | 60.1 | 723   | 15 | SLARBCS   | L26605 Stellaria l  |
| 29 | 166.5 | 59.0 | 1629  | 15 | STRBCS2   | X69760 S.tuberosum  |
| 30 | 165.5 | 58.7 | 1027  | 15 | TOMRBCSC  | M13544 Tomato (L.e  |
| 31 | 165.5 | 58.7 | 1261  | 15 | BT012936  | BT012936 Lycopersi  |
| 32 | 165.5 | 58.7 | 1341  | 15 | LERBCS3C  | X05986 Tomato rbcS  |
| 33 | 165.5 | 58.7 | 1520  | 15 | LERBCS3A  | X05984 Tomato rbcS  |
| 34 | 164.5 | 58.3 | 1314  | 15 | PERBCS11  | X03821 Petunia x h  |
| 35 | 164.5 | 58.3 | 1703  | 15 | STRBCS2B  | X69761 S.tuberosum  |
| 36 | 163.5 | 58.0 | 806   | 15 | AY220079  | AY220079 Nicotiana  |
| 37 | 162.5 | 57.6 | 22574 | 11 | CVE18556  | Y18556 Cloning vec  |
| 38 | 161   | 57.1 | 808   | 15 | RCCPRBCUA | L22155 Oryza sativ  |
| 39 | 160.5 | 56.9 | 591   | 15 | AB020942  | AB020942 Secale ce  |
| 40 | 160.5 | 56.9 | 1054  | 15 | LERBCS3B  | X05985 Tomato rbcS  |
| 41 | 160.5 | 56.9 | 4124  | 15 | TOMRBCO   | D11112 Tomato ribu  |
| 42 | 159.5 | 56.6 | 177   | 6  | I24839    | I24839 Sequence 8   |
| 43 | 159.5 | 56.6 | 177   | 6  | I40228    | I40228 Sequence 6   |
| 44 | 159.5 | 56.6 | 177   | 6  | I76855    | I76855 Sequence 12  |
| 45 | 159.5 | 56.6 | 204   | 6  | AR528363  | AR528363 Sequence   |
| 46 | 159.5 | 56.6 | 225   | 11 | ARPPECA2  | X05923 Hybrid rbc-  |
| 47 | 159.5 | 56.6 | 499   | 6  | AR205973  | AR205973 Sequence   |
| 48 | 159.5 | 56.6 | 796   | 15 | NSRUB1    | X01722 Nicotiana s  |
| 49 | 159.5 | 56.6 | 979   | 15 | TOBRUBPA  | M32419 Tobacco rib  |
| 50 | 159.5 | 56.6 | 2293  | 15 | NRBCS8B   | X13711 Nicotiana p  |
| 51 | 159.5 | 56.6 | 2293  | 15 | TOBRBCS8B | M3685 N.plumbagin   |
| 52 | 159.5 | 56.6 | 2362  | 15 | NTRUBSS   | X02353 Tobacco gen  |
| 53 | 159   | 56.4 | 638   | 15 | AB042065  | AB042065 Triticum   |
| 54 | 159   | 56.4 | 853   | 15 | AF008214  | AF008214 Musa acum  |
| 55 | 159   | 56.4 | 2795  | 15 | NSRUBSU   | X53426 Nicotiana s  |
| 56 | 159   | 56.4 | 5980  | 15 | AB042069  | AB042069 Triticum   |
| 57 | 158.5 | 56.2 | 2328  | 15 | SCFBCS1A  | M86717 Saccharum h  |
| 58 | 156.5 | 55.5 | 2242  | 15 | PERBCS08  | X03820 Petunia x h  |
| 59 | 156   | 55.3 | 595   | 15 | AF039012  | AF039012 Fritillar  |
| 60 | 156   | 55.3 | 595   | 15 | AF039013  | AF039013 Fritillar  |
| 61 | 155   | 55.0 | 2205  | 15 | WTRUB1AA  | M37328 T.aestivum   |
| 62 | 154.5 | 54.8 | 504   | 15 | AF192777  | AF192777 Avena cia  |
| 63 | 154   | 54.6 | 592   | 15 | AF039008  | AF039008 Fritillar  |
| 64 | 154   | 54.6 | 592   | 15 | AF039014  | AF039014 Fritillar  |
| 65 | 154   | 54.6 | 595   | 15 | AF039010  | AF039010 Fritillar  |
| 66 | 153.5 | 54.4 | 837   | 15 | ASRBCSSS  | X83095 A. squarrosa |
| 67 | 153.5 | 54.4 | 875   | 15 | SCS131738 | AJ131738 Secale ce  |
| 68 | 153   | 54.3 | 789   | 15 | AB006080  | AB006080 Fagus cre  |
| 69 | 152.5 | 54.1 | 504   | 15 | AF097361  | AF097361 Avena cia  |
| 70 | 152.5 | 54.1 | 605   | 15 | AB020934  | AB020934 Aegilops   |
| 71 | 152.5 | 54.1 | 605   | 15 | AB020943  | AB020943 Hordeum v  |
| 72 | 152.5 | 54.1 | 781   | 15 | AB020958  | AB020958 Triticum   |
| 73 | 152.5 | 54.1 | 787   | 15 | AB020946  | AB020946 Aegilops   |
| 74 | 152.5 | 54.1 | 789   | 15 | AB020959  | AB020959 Secale ce  |
| 75 | 152.5 | 54.1 | 792   | 15 | AB020949  | AB020949 Aegilops   |
| 76 | 152.5 | 54.1 | 860   | 15 | AY445627  | AY445627 Oryza sat  |



77 152.5 54.1 899 15 AK068555 Oryza sat  
78 152.5 54.1 110000 15 AP008218\_112  
79 152.5 54.1 127267 15 CNS0954U\_112  
80 152.5 53.9 816 15 HVU43493  
81 151.5 53.7 504 15 AF097359  
82 151.5 53.7 604 15 AB020944  
83 151.5 53.7 605 15 AB020932  
84 151.5 53.7 605 15 AB020933  
85 151.5 53.7 605 15 AB020935  
86 151.5 53.7 605 15 AB020936  
87 151.5 53.7 607 15 AB020938  
88 151.5 53.7 720 15 AF360124  
89 151.5 53.7 724 6 AF364047  
90 151.5 53.7 724 6 AX366136  
91 151.5 53.7 726 6 AX364195  
92 151.5 53.7 728 15 AB020952  
93 151.5 53.7 728 15 AF410314  
94 151.5 53.7 764 15 AF462822  
95 151.5 53.7 772 15 AY054552  
96 151.5 53.7 772 15 BT000721  
97 151.5 53.7 781 15 AB020953  
98 151.5 53.7 787 15 AB020954  
99 151.5 53.7 787 15 AB020955  
100 151.5 53.7 83646 15 BT005730  
101 151.5 53.7 83646 15 AB005248  
102 151.5 53.5 546 15 POTRBCS  
103 151.5 53.5 546 15 TOMRBCSD  
104 151.5 53.5 1032 15 TOMRBCSA  
105 151.5 53.5 1454 15 LERBCS1  
106 151.5 53.5 1598 15 STRBCS3  
107 151.5 53.5 3323 15 STRBCS1  
108 150.5 53.4 153 6 AR390846  
109 150.5 53.4 586 15 AF202646  
110 150.5 53.4 600 15 AF202645  
111 150.5 53.4 604 15 AB020939  
112 150.5 53.4 605 15 AB020940  
113 150.5 53.4 605 15 AB020941  
114 150.5 53.4 611 15 AB020937  
115 150.5 53.4 738 15 AB020947  
116 150.5 53.4 772 15 AB020948  
117 150.5 53.4 828 15 AK119219  
118 150.5 53.4 830 15 D00643  
119 150.5 53.4 830 15 AK061611  
120 150.5 53.4 835 15 AF052305  
121 150.5 53.4 845 15 AK070257  
122 150.5 53.4 854 15 AF017364  
123 150.5 53.4 884 15 AK121444  
124 150.5 53.4 1815 15 AB067656  
125 150.5 53.4 1999 15 AK068266  
126 150.5 53.4 2109 6 E11082  
127 150.5 53.4 110000 15 AP008218\_100  
128 150.5 53.4 110000 15 AP008218\_113  
129 150.5 53.4 145890 15 CNS08C70  
130 150.5 53.2 594 15 AF039004  
131 150.5 53.2 1337 15 TOMRBCPB  
132 149.5 53.0 599 15 TOMRBCSB  
133 149.5 53.0 684 6 AR428736  
134 149.5 53.0 684 6 AR455412  
135 149.5 53.0 684 6 AX329368  
136 149.5 53.0 684 6 AX382258  
137 149.5 53.0 720 15 AY062458  
138 149.5 53.0 721 15 AY062543  
139 149.5 53.0 728 15 AY062437  
140 149.5 53.0 742 15 TOMRBCSE  
141 149.5 53.0 758 15 AY059339  
142 149.5 53.0 1097 15 BT013023  
143 149.5 53.0 2006 15 BNRBCSF1  
144 149.5 53.0 2776 15 LERBCS2  
145 149.5 53.0 9647 15 AYATSGS  
146 149.5 52.8 562 15 AY05444  
147 148.5 52.7 586 15 AY093288  
148 148.5 52.7 586 15 BT002094  
149 148.5 52.7 586 15 BT002554

AK068555 Oryza sat  
Continuation (113)  
BX119951 Oryza sat  
U43493 Hordeum vul  
AF097359 Avena aga  
AB020944 Agropyron  
AB020932 Aegilops  
AB020933 Aegilops  
AB020935 Aegilops  
AB020936 Aegilops  
AB020938 Aegilops  
AF360124 Arabidops  
AX364047 Sequence  
AX366136 Sequence  
AX364195 Sequence  
AB020952 Aegilops  
AF410314 Arabidops  
AF462822 Arabidops  
AY054552 Arabidops  
BT000721 Arabidops  
AB020953 Aegilops  
AB020954 Triticum  
AB020955 Triticum  
BT005730 Arabidops  
AB005248 Arabidops  
J03613 Potato (S.t  
M15235 Tomato RUBP  
M13542 Tomato (L.e  
X05982 Tomato rbcs  
X69763 S.tuberosum  
X69759 S.tuberosum  
AR390846 Sequence  
AF202646 Avena cla  
AF202645 Avena cla  
AB020939 Triticum  
AB020940 Triticum  
AB020941 Triticum  
AB020937 Aegilops  
AB020947 Aegilops  
AB020948 Aegilops  
AK119219 Oryza sat  
D00643 Oryza sativ  
AK061611 Oryza sat  
AF052305 Oryza sat  
AK070257 Oryza sat  
AF017364 Oryza sat  
AK121444 Oryza sat  
AB067656 Oryza sat  
AK068266 Oryza sat  
E11082 DNA encodin  
Continuation (101)  
AL731739 Oryza sat  
AF039004 Fritillar  
M32420 Tobacco rib  
M13543 Tomato (L.e  
AR428736 Sequence  
AR455412 Sequence  
AX329368 Sequence  
AX382258 Sequence  
AY062458 Arabidops  
AY062543 Arabidops  
AY062437 Arabidops  
M15236 Tomato RUBP  
AY059339 Arabidops  
BT013023 Lycopersi  
X55937 Brassica na  
X05983 Tomato rbcs  
X14564 A.thaliana  
AY05444 Fagus syl  
AY093288 Arabidops  
BT002094 Arabidops  
BT002554 Arabidops

150 148.5 52.7 587 15 BT003356 Arabidops

ALIGNMENTS

RESULT 1  
AX147212  
LOCUS AX147212 183 bp DNA linear PAT 08-JUN-2001  
DEFINITION Sequence 1 from Patent WO0136622.  
ACCESSION AX147212  
VERSION AX147212.1 GI:14346383  
KEYWORDS Zea mays  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1  
AUTHORS Calmi,P.G. and Lightner,J.  
TITLE Fructose polymer synthesis in monocot plastids  
JOURNAL Patent: WO 0136622-A 1 25-MAY-2001;  
E.I. DU PONT DE NEMOURS AND COMPANY (US)  
FEATURES  
Location/Qualifiers  
source  
1..183  
/organism="Zea mays"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:4577"

ORIGIN

Alignment Scores:  
Pred. No.: 3.58e-10 Length: 183  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x AX147212 (1-183)

QY 1 MetaLapThValMetMetAlaSerSerAlaThAlaThArgThrAsnProAlaGln 20  
Db 1 ATGGGCGCCACCGTATGATGGCTCGTGGCCACC----- 36  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 37 -----GCCGTCGCTCCGTTCCAGGGGCTTAAGTCCACGCCGAGCTCCCGTCGCCCGC 90  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58  
Db 91 CGCTCTCTAGAGCTCGGCAACGTC---AGCAACGGCGGAAGATCGGTGC 141

RESULT 2  
AR212567  
LOCUS AR212567 185 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 14 from patent US 6399861.  
ACCESSION AR212567  
VERSION AR212567.1 GI:21516176  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 185)  
AUTHORS Anderson,P.C., Flick,C.E., Gordon-Kamm,W.J., Kausch,A.P.,  
Mackey,C.J., Orozco,E.M., Orr,P., Stephens,M.A., Walters,D.A. and  
Walters,D.S.  
TITLE Methods and compositions for the production of stably transformed,  
fertilile monocot plants and cells thereof  
JOURNAL Patent: US 6399861-A 14 04-JUN-2002;  
FEATURES  
Location/Qualifiers  
source  
1..185  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
 Pred. No.: 3.62e-10 Length: 185  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x AR212567 (1-185)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 Db 42 ATGGCGCCACCGTGATGGCTCTGTGGCCACC----- 77

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuYleSerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 78 -----GCCGTCGCTCGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGTCCGCCGC 131

Qy 41 ArgSerSerArgSerLeuGlyAnValAlaSerAnGlyGlyArgIleArgCys 58  
 |||||  
 Db 132 CGGTCTCTCAGAACGCTCGGCACGTC---AGCAACGGCGGAAGGATCCGGTGC 182

RESULT 3  
 AR590636 185 bp DNA linear PAT 15-DEC-2004  
 LOCUS  
 DEFINITION Sequence 14 from patent US 6803499.  
 ACCESSION AR590636  
 VERSION AR590636.1 GI:56638304  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 185)  
 AUTHORS Anderson,P.C., Flick,C.E., Gordon-Kamm,W.J., Kausch,A.P., Mackey,C.J., Orozco,E.M., Orr,P., Stephens,M.A., Walters,D.A. and Walters,D.S.  
 TITLE Methods and compositions for the production of stably transformed, fertile monocot plants and cells thereof  
 JOURNAL Patent: US 6803499-A 14 12-OCT-2004;  
 DeKalb Genetics Corporation; DeKalb, IL

FEATURES  
 source  
 1..185  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
 Pred. No.: 3.62e-10 Length: 185  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x AR590636 (1-185)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 Db 42 ATGGCGCCACCGTGATGGCTCTGTGGCCACC----- 77

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuYleSerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 78 -----GCCGTCGCTCGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGTCCGCCGC 131

Qy 41 ArgSerSerArgSerLeuGlyAnValAlaSerAnGlyGlyArgIleArgCys 58  
 |||||  
 Db 132 CGGTCTCTCAGAACGCTCGGCACGTC---AGCAACGGCGGAAGGATCCGGTGC 182

RESULT 4  
 A44435 405 bp DNA linear PAT 07-MAR-1997  
 LOCUS  
 DEFINITION Sequence 4 from Patent EP0652286.

ACCESSION A44435  
 VERSION A44435.1 GI:2299261  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1 (bases 1 to 405)  
 AUTHORS Capellades,M., De,R.R., Montoliu,L., Puigdomenech,P., Torres,M.A., Rigau,J. and Uribe,J.  
 TITLE Promoter elements of chimaeric alpha tubulines  
 JOURNAL Patent: EP 0652286-A 4 10-MAY-1995;  
 COMMENT RHONE-POULENC AGROCHIMIE (FR)  
 Other publication CN 1121958 960508  
 Other publication ZA 9408826 950717  
 Other publication SK 134094 950607  
 Other publication HU 70464 951030  
 Other publication BG 99169 950728  
 Other publication CZ 9402743 950913  
 Other publication BR 9404562 950620  
 Other publication JP 7184664 950725  
 Other publication PL 305775 950515  
 Other publication FR 2712302 950519  
 Other publication CA 2135461 950511  
 Other publication AU 7775194 950518.  
 Location/Qualifiers  
 1..405  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"

ORIGIN

Alignment Scores:  
 Pred. No.: 7.56e-10 Length: 405  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x A44435 (1-405)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 Db 262 ATGGCGCCACCGTGATGGCTCTGTGGCCACC----- 297

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuYleSerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 298 -----GCCGTCGCTCGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGTCCGCCGC 351

Qy 41 ArgSerSerArgSerLeuGlyAnValAlaSerAnGlyGlyArgIleArgCys 58  
 |||||  
 Db 352 CGCTCTCTCAGAACGCTCGGCACGTC---AGCAACGGCGGAAGGATCCGGTGC 402

RESULT 5  
 I44914 405 bp DNA linear PAT 07-OCT-1997  
 LOCUS  
 DEFINITION Sequence 4 from patent US 5635618.  
 ACCESSION I44914  
 VERSION I44914.1 GI:2469627  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 405)  
 AUTHORS Capellades,M., De Rose,R., Montoliu,L., Puigdomenech,P., Torres,M.A., Uribe,J. and Rigau,J.  
 TITLE Promoter elements of chimeric genes of .alpha.-tubulin  
 JOURNAL Patent: US 5635618-A 4 03-JUN-1997;  
 FEATURES  
 source  
 1..405  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN

|                                                                                                                                                                                                                                                                                                                                     |          |                                                              |               |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------|--------------------------------------------------------------|---------------|-----|
| Alignment Scores:                                                                                                                                                                                                                                                                                                                   |          | 7.56e-10                                                     | Length:       | 405 |
| Pred. No.:                                                                                                                                                                                                                                                                                                                          |          | 203.50                                                       | Matches:      | 47  |
| Score:                                                                                                                                                                                                                                                                                                                              |          | 81.0%                                                        | Conservative: | 0   |
| Percent Similarity:                                                                                                                                                                                                                                                                                                                 |          | 81.0%                                                        | Mismatches:   | 0   |
| Best Local Similarity:                                                                                                                                                                                                                                                                                                              |          | 72.2%                                                        | Indels:       | 11  |
| Query Match:                                                                                                                                                                                                                                                                                                                        |          | 6                                                            | Gaps:         | 2   |
| DB:                                                                                                                                                                                                                                                                                                                                 |          |                                                              |               |     |
| US-10-628-525A-34 (1-58) x I44914 (1-405)                                                                                                                                                                                                                                                                                           |          |                                                              |               |     |
| QY                                                                                                                                                                                                                                                                                                                                  | 1        | MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln | 20            |     |
| Db                                                                                                                                                                                                                                                                                                                                  | 262      | ATGGCGCCACCGTGATGCGCTCGTGGCCACC-----                         | 297           |     |
| QY                                                                                                                                                                                                                                                                                                                                  | 21       | AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg | 40            |     |
| Db                                                                                                                                                                                                                                                                                                                                  | 298      | -----GCCGTGCGCTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTGGCCGC         | 351           |     |
| QY                                                                                                                                                                                                                                                                                                                                  | 41       | ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys       | 58            |     |
| Db                                                                                                                                                                                                                                                                                                                                  | 352      | CGCTCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC        | 402           |     |
| RESULT 6                                                                                                                                                                                                                                                                                                                            |          |                                                              |               |     |
| MZEPCCSSU                                                                                                                                                                                                                                                                                                                           |          |                                                              |               |     |
| LOCUS                                                                                                                                                                                                                                                                                                                               |          |                                                              |               |     |
| DEFINITION                                                                                                                                                                                                                                                                                                                          |          |                                                              |               |     |
| Zea mays mRNA for ribulose 1,5-bisphosphate carboxylase small subunit, complete cds.                                                                                                                                                                                                                                                |          |                                                              |               |     |
| D00170                                                                                                                                                                                                                                                                                                                              |          |                                                              |               |     |
| ACCESSION                                                                                                                                                                                                                                                                                                                           |          |                                                              |               |     |
| VERSION                                                                                                                                                                                                                                                                                                                             |          |                                                              |               |     |
| KEYWORDS                                                                                                                                                                                                                                                                                                                            |          |                                                              |               |     |
| SOURCE                                                                                                                                                                                                                                                                                                                              |          |                                                              |               |     |
| ORGANISM                                                                                                                                                                                                                                                                                                                            |          |                                                              |               |     |
| Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.                                                                                                                                                        |          |                                                              |               |     |
| REFERENCE                                                                                                                                                                                                                                                                                                                           |          |                                                              |               |     |
| AUTHORS                                                                                                                                                                                                                                                                                                                             |          |                                                              |               |     |
| TITLE                                                                                                                                                                                                                                                                                                                               |          |                                                              |               |     |
| JOURNAL                                                                                                                                                                                                                                                                                                                             |          |                                                              |               |     |
| PUBMED                                                                                                                                                                                                                                                                                                                              |          |                                                              |               |     |
| COMMENT                                                                                                                                                                                                                                                                                                                             |          |                                                              |               |     |
| Comparison with the RuBPC small subunit genes from other plants revealed that the maize small subunit is similar to the wheat one, there being 73% homology between the transit peptides and 64% between the mature proteins. This indicates that there is no noteworthy difference between the C3 and C4 small subunit structures. |          |                                                              |               |     |
| FEATURES                                                                                                                                                                                                                                                                                                                            |          |                                                              |               |     |
| source                                                                                                                                                                                                                                                                                                                              |          |                                                              |               |     |
| 1. .830                                                                                                                                                                                                                                                                                                                             |          |                                                              |               |     |
| /organism="Zea mays"                                                                                                                                                                                                                                                                                                                |          |                                                              |               |     |
| /mol_type="mRNA"                                                                                                                                                                                                                                                                                                                    |          |                                                              |               |     |
| /db_xref="taxon:4577"                                                                                                                                                                                                                                                                                                               |          |                                                              |               |     |
| /tissue_type="leaf"                                                                                                                                                                                                                                                                                                                 |          |                                                              |               |     |
| 66. .578                                                                                                                                                                                                                                                                                                                            |          |                                                              |               |     |
| /note="SSU"                                                                                                                                                                                                                                                                                                                         |          |                                                              |               |     |
| /codon_start=1                                                                                                                                                                                                                                                                                                                      |          |                                                              |               |     |
| /product="ribulose 1,5-bisphosphate carboxylase small subunit"                                                                                                                                                                                                                                                                      |          |                                                              |               |     |
| /protein_id="BAA00120.1"                                                                                                                                                                                                                                                                                                            |          |                                                              |               |     |
| /db_xref="GI:217964"                                                                                                                                                                                                                                                                                                                |          |                                                              |               |     |
| /translation="NAPVTMMASATAVAPFGLKSTASLPVARSRSRLGNVSNNGR IRCMQVPAYGNKKFETLSYLPPLSTDLLKQVDLLRNGWIPCLFESKVGVTRENS TSPCYDGRYWTMWKLPMPGNCDAIQVKELQEAIKSYDPDFHRVIGFDNIKQTQCVS FIAYKPPGSD"                                                                                                                                                 |          |                                                              |               |     |
| CDS                                                                                                                                                                                                                                                                                                                                 |          |                                                              |               |     |
| transit_peptide 66. .206                                                                                                                                                                                                                                                                                                            |          |                                                              |               |     |
| mat_peptide 207. .575                                                                                                                                                                                                                                                                                                               |          |                                                              |               |     |
| /product="mature Ru BPC"                                                                                                                                                                                                                                                                                                            |          |                                                              |               |     |
| ORIGIN                                                                                                                                                                                                                                                                                                                              |          |                                                              |               |     |
| Alignment Scores:                                                                                                                                                                                                                                                                                                                   |          |                                                              |               |     |
| Pred. No.:                                                                                                                                                                                                                                                                                                                          | 1.48e-09 | Length:                                                      | 830           |     |
| Score:                                                                                                                                                                                                                                                                                                                              | 203.50   | Matches:                                                     | 47            |     |
| Percent Similarity:                                                                                                                                                                                                                                                                                                                 | 81.0%    | Conservative:                                                | 0             |     |
| Best Local Similarity:                                                                                                                                                                                                                                                                                                              | 81.0%    | Mismatches:                                                  | 0             |     |
| Query Match:                                                                                                                                                                                                                                                                                                                        | 72.2%    | Indels:                                                      | 11            |     |
| DB:                                                                                                                                                                                                                                                                                                                                 | 15       | Gaps:                                                        | 2             |     |
| US-10-628-525A-34 (1-58) x ZMRUBSSU (1-830)                                                                                                                                                                                                                                                                                         |          |                                                              |               |     |
| QY                                                                                                                                                                                                                                                                                                                                  | 1        | MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln | 20            |     |
|                                                                                                                                                                                                                                                                                                                                     |          |                                                              |               |     |

```

Db      66  ATGGGGCCACCGTGATGGCTCGTCGGCCACC----- 101
Qy      21  AlaSerAlaValAlaProPheGlnGlyLeuLyseSerThrAlaSerLeuProValAlaArg 40
Db      102 -----GCCGTCGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 155
Qy      41  ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyVclyArgIleArgCys 58
Db      156 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 206

RESULT 8
ZMRBCS
LOCUS      1648 bp      DNA      linear      PLN 10-FEB-1999
DEFINITION Maize rbcS gene for ribulose-1,5-bisphosphate carboxylase/oxygenase
            small subunit (EC 4.1.1.39).
ACCESSION  Y00322.1 GI:22464
VERSION     rbcS gene; ribulose bisphosphate carboxylase.
KEYWORDS    Zea mays
SOURCE      Zea mays
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 1648)
AUTHORS     Lebrun, M., Wakeman, G. and Freyssinet, G.
TITLE       Nucleotide sequence of a gene encoding corn
            ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit
            (rbcS)
JOURNAL     Nucleic Acids Res. 15 (10), 4360 (1987)
PUBMED      3588298
REFERENCE   2 (bases 1 to 1648)
AUTHORS     Freyssinet, G.
TITLE       Direct Submission
JOURNAL     Submitted (16-OCT-1987)
FEATURES    Location/Qualifiers
            1..1648
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /strain="F2"
            /db_xref="taxon:4577"
            CAAT_signal 359..362
            TATA_signal 398..403
            gene        join(491..637,801..1163)
            CDS         join(491..637,801..1163)
            /EC_number="4.1.1.39"
            /product="ribulose 1,5-bisphosphate carboxylase/oxygenase"
            /protein_id="CAA68419.1"
            /db_xref="GI:22465"
            /db_xref="GOA:P05348"
            /translacion="MAPTVMASATATAVAPROGLKSTASLPVARRSSRLGNVSNCR
            IRCMQWPAYKXKFTLSYLPPLSTDDLKQVDYLRNGWIPCLFSKVGFTVRENT
            SPICYDRYWTWKLPMFGNDATQVYKSLQELAIKSYPDAPFHRVIGFDNIKQTQCVSF
            IAYKPGSPD"
            exon         491..637
            /genes="rbcS"
            /number=1
            misc_feature 631..632
            /genes="rbcS"
            /notes="pot. site of cleavage of transit peptide"
            intron       638..800
            /genes="rbcS"
            /number=1
            exon         801..1160
            /genes="rbcS"
            /number=2

ALIGNMENT Scores:
Pred. No.:      2.83e-09      Length:      1648
Score:          359.362
Percent Similarity: 81.0%
Best Local Similarity: 81.0%
Query Match:    11
DB:             2

ORIGIN
1
//

```

```

Score:          203.50      Matches:      47
Percent Similarity: 81.0%
Best Local Similarity: 81.0%
Query Match:    15
DB:             2

US-10-628-525A-34 (1-58) x ZMRBCS (1-1648)
Qy      1  MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db      491 ATGGCGCCACCGTGATGGCTCGTCGGCCACC----- 526
Qy      21  AlaSerAlaValAlaProPheGlnGlyLeuLyseSerThrAlaSerLeuProValAlaArg 40
Db      527 -----GCCGTCGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 580
Qy      41  ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyVclyArgIleArgCys 58
Db      581 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 631

RESULT 9
CQ828194
LOCUS      1868 bp      DNA      linear      PAT 05-JUL-2004
DEFINITION Sequence 6 from Patent WO2004053135.
ACCESSION  CQ828194
VERSION     CQ828194.1 GI:49731677
KEYWORDS    synthetic construct
SOURCE      other sequences; artificial sequences.
ORGANISM    Ferullo, J.M., Sailland, A., Schmitt, F. and Paget, E.
REFERENCE   1
AUTHORS     Expression cassette encoding a hydroxyphenylpyruvate dioxygenase
            and herbicide-tolerant plants containing such a gene
            Patent: WO 2004053135-A 6 24-JUN-2004;
            Bayer CropScience S.A. (FR)
JOURNAL     Location/Qualifiers
            1..1868
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Cassette d'expression actine intron -OTF-HPPD-tnos"

ORIGIN
1
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ALIGNMENT Scores:
Pred. No.:      3.18e-09      Length:      1868
Score:          203.50      Matches:      47
Percent Similarity: 81.0%
Best Local Similarity: 81.0%
Query Match:    11
DB:             2

US-10-628-525A-34 (1-58) x CQ828194 (1-1868)
Qy      1  MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db      234 ATGGCGCCACCGTGATGGCTCGTCGGCCACC----- 269
Qy      21  AlaSerAlaValAlaProPheGlnGlyLeuLyseSerThrAlaSerLeuProValAlaArg 40
Db      270 -----GCCGTCGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 323
Qy      41  ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyVclyArgIleArgCys 58
Db      324 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 374

RESULT 10
BD014494
LOCUS      2318 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Transgenic corn and method of detecting recombinant gene from foods
            containing the same.
ACCESSION  BD014494
VERSION     BD014494.1 GI:22555277

```

```
KEYWORDS      JP 2001136983-A/36.
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1 (bases 1 to 2318)
AUTHORS        Hino,A., Matsuoka,T., Kurihara,H., Masatake, Toyota, Aida,Y. and
                Akiyama,H.
TITLE          Transgenic corn and method of detecting recombinant gene from foods
                containing the same
JOURNAL        Patent: JP 2001136983-A 36 22-MAY-2001;
                NATL FOOD RES INST, DIRECTOR GENERAL OF NATIONAL INSTITUTE OF
                HEALTH SCIENCES
COMMENT        OS Artificial Sequence
                PN JP 2001136983-A/36
                PD 22-MAY-2001
                PF 30-AUG-2000 JP 2000261106
                PI AKIHIRO HINO,TAKESHI MATSUOKA,HIDEO KURIHARA,MASATAKE PI
                TOYOTA,YUKIHIRO AIDA,
                PC HIROSHI AKIYAMA
                CC C12N15/09,C12M1/00,C12Q1/68,C12N15/00
                CC Description of Artificial Sequence:Partial sequence of CC
                recombinant gene in
                CC genetically modified maize
                FH Key Location/Qualifiers
                FT source 1. .2318
                FT Location/Qualifiers
                FT 1. .2318 /organism='Artificial Sequence'.

FEATURES      source
                Location/Qualifiers
                1. .2318
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.:      3,9e-09      Length:      2318
Score:          203.50      Matches:      47
Percent Similarity: 81.0%      Conservative: 0
Best Local Similarity: 81.0%      Mismatches: 0
Query Match:    72.2%      Indels:      11
DB:             6          Gaps:         2

US-10-628-525A-34 (1-58) x BD014494 (1-2318)

QY      1 MetAlaProThrValMetMetAlaSerSerAlaThraAlaThraArgThrAsnProAlaGln 20
Db      665 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC-----700
QY      21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValaAlaArg 40
Db      701 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 754
QY      41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db      755 CGCTCTCTCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 805

RESULT 11
AR581878/c
LOCUS      AR581878      5281 bp      DNA      linear      PAT 15-DEC-2004
DEFINITION Sequence 1 from patent US 6791014.
ACCESSION  AR581878
VERSION     AR581878.1 GI:56613881
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 5281)
AUTHORS      Garcon,F. and Pelissier,B.
TITLE        Use of HPPd inhibitors as selection agents in plant transformation
JOURNAL      Patent: US 6791014-A 1 14-SEP-2004;
                Aventis Cropsience, S.A.;;
                FRX;
FEATURES     Location/Qualifiers
                source
                1. .5281
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="gene chimere"

ORIGIN
Alignment Scores:
Pred. No.:      8,45e-09      Length:      5281
Score:          203.50      Matches:      47
Percent Similarity: 81.0%      Conservative: 0
Best Local Similarity: 81.0%      Mismatches: 0
Query Match:    72.2%      Indels:      11
DB:             6          Gaps:         2

US-10-628-525A-34 (1-58) x AX394256 (1-5281)

QY      1 MetAlaProThrValMetMetAlaSerSerAlaThraAlaThraArgThrAsnProAlaGln 20
Db      4260 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC-----4225
QY      21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValaAlaArg 40
Db      4224 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 4171
QY      41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db      4170 CGCTCTCTCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 4120

RESULT 12
AX394256/c
LOCUS      AX394256      5281 bp      DNA      linear      PAT 18-MAY-2002
DEFINITION Sequence 1 from Patent EP1186666.
ACCESSION  AX394256
VERSION     AX394256.1 GI:21065463
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Garcon,F. and Pelissier,B.
TITLE        Use of hppd inhibitors as selection agents in plant transformation
JOURNAL      Patent: EP 1186666-A 1 13-MAR-2002;
                AVENTIS CROPSCIENCE S.A. (FR)
FEATURES     Location/Qualifiers
                source
                1. .5281
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="gene chimere"

ORIGIN
Alignment Scores:
Pred. No.:      8,45e-09      Length:      5281
Score:          203.50      Matches:      47
Percent Similarity: 81.0%      Conservative: 0
Best Local Similarity: 81.0%      Mismatches: 0
Query Match:    72.2%      Indels:      11
DB:             6          Gaps:         2

US-10-628-525A-34 (1-58) x AR581878 (1-5281)

QY      1 MetAlaProThrValMetMetAlaSerSerAlaThraAlaThraArgThrAsnProAlaGln 20
Db      4260 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC-----4225
QY      21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValaAlaArg 40
Db      4224 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 4171
QY      41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db      4170 CGCTCTCTCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 4120

RESULT 13
AR581879
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LOCUS AR581879 5909 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 2 from patent US 6791014.
ACCESSION AR581879
VERSION AR581879.1 GI:56613883
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5909)
AUTHORS Garcon,F. and Pelissier,B.
TITLE Use of HPPD inhibitors as selection agents in plant transformation
JOURNAL Patent: US 6791014-A 2 14-SEP-2004;
Aventis Cropscience, S.A.;;
FRX;
FEATURES             Location/Qualifiers
     source           1..5909
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.:          9.39e-09          Length:          5909
Score:              203.50            Matches:          47
Percent Similarity: 81.0%             Conservative:     0
Best Local Similarity: 81.0%          Mismatches:      0
Query Match:        72.2%             Indels:          11
DB:                 6                 Gaps:            2
US-10-628-525A-34 (1-58) x AR581879 (1-5909)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 1655 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 1690
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 1691 -----GCCGTGCTCGTTCAGGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 1744
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 1745 CGCTCCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 1795
RESULT 14
AX394257
LOCUS AX394257 5909 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 2 from Patent EP1186666.
ACCESSION AX394257
VERSION AX394257.1 GI:21065464
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Garcon,F. and Pelissier,B.
TITLE Use of hppd inhibitors as selection agents in plant transformation
JOURNAL Patent: EP 1186666-A 2 13-MAR-2002;
AVENTIS CROPSCIENCE S.A. (FR)
FEATURES             Location/Qualifiers
     source           1..5909
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="gene chimera"
ORIGIN
Alignment Scores:
Pred. No.:          9.39e-09          Length:          5909
Score:              203.50            Matches:          47
Percent Similarity: 81.0%             Conservative:     0
Best Local Similarity: 81.0%          Mismatches:      0
Query Match:        72.2%             Indels:          11
DB:                 6                 Gaps:            2
US-10-628-525A-34 (1-58) x AR581879 (1-5909)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 1655 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 1690
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 1691 -----GCCGTGCTCGTTCAGGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 1744
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 1745 CGCTCCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 1795
RESULT 15
AX206035
LOCUS AR206035 415 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 49 from patent US 6372211.
ACCESSION AR206035
VERSION AR206035.1 GI:21504517
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 415)
AUTHORS Isaac,B.G., Greenplate,J.T., Purcell,J.P. and Romano,C.P.
TITLE Methods and compositions for controlling insects
JOURNAL Patent: US 6372211-A 49 16-APR-2002;
FEATURES             Location/Qualifiers
     source           1..415
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.:          3.33e-09          Length:          415
Score:              196.50            Matches:          46
Percent Similarity: 79.3%             Conservative:     0
Best Local Similarity: 79.3%          Mismatches:      1
Query Match:        69.7%             Indels:          11
DB:                 6                 Gaps:            2
US-10-628-525A-34 (1-58) x AR206035 (1-415)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 15 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 50
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 51 -----GCCGTGCTCGTTCCTGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 104
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 105 CGCTCCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 155
RESULT 16
AR229545
LOCUS AR229545 415 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 13 from patent US 6448476.
ACCESSION AR229545
VERSION AR229545.1 GI:27269161
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 415)
AUTHORS Barry,G.F.
TITLE Plants and plant cells transformation to express an
JOURNAL AMPA-N-acetyltransferase
Patent: US 6448476-A 13 10-SEP-2002;
Monsanto Technology LLC; St. Louis, MO
FEATURES             Location/Qualifiers
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US-10-628-525A-34 (1-58) x AX394257 (1-5909)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 1655 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 1690
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 1691 -----GCCGTGCTCGTTCAGGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 1744
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 1745 CGCTCCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 1795
RESULT 15
AR206035
LOCUS AR206035 415 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 49 from patent US 6372211.
ACCESSION AR206035
VERSION AR206035.1 GI:21504517
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 415)
AUTHORS Isaac,B.G., Greenplate,J.T., Purcell,J.P. and Romano,C.P.
TITLE Methods and compositions for controlling insects
JOURNAL Patent: US 6372211-A 49 16-APR-2002;
FEATURES             Location/Qualifiers
     source           1..415
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.:          3.33e-09          Length:          415
Score:              196.50            Matches:          46
Percent Similarity: 79.3%             Conservative:     0
Best Local Similarity: 79.3%          Mismatches:      1
Query Match:        69.7%             Indels:          11
DB:                 6                 Gaps:            2
US-10-628-525A-34 (1-58) x AR206035 (1-415)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 15 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 50
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 51 -----GCCGTGCTCGTTCCTGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 104
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 105 CGCTCCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 155
RESULT 16
AR229545
LOCUS AR229545 415 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 13 from patent US 6448476.
ACCESSION AR229545
VERSION AR229545.1 GI:27269161
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 415)
AUTHORS Barry,G.F.
TITLE Plants and plant cells transformation to express an
JOURNAL AMPA-N-acetyltransferase
Patent: US 6448476-A 13 10-SEP-2002;
Monsanto Technology LLC; St. Louis, MO
FEATURES             Location/Qualifiers
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source 1. .415  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 3.33e-09 Length: 415  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservative: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x AR229545 (1-415)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
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Db 15 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC----- 50

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuYleuSerThrAlaSerLeuProValAlaArg 40  
Db 51 -----GCCGTGCGTCGCTTCTGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 104

Qy 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 105 CGTCTCTCCAGAGCCTCGGCACGTC---AGCAACGGCGGAGGATCCGGTGC 155

RESULT 17  
AR260580

LOCUS AR260580 415 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 3 from patent US 6489542.  
ACCESSION AR260580  
VERSION AR260580.1 GI:27311135  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 415)  
AUTHORS Corbin,D.R. and Romano,C.P.  
TITLE Methods for transforming plants to express Cry2Ab  
delta-endotoxins targeted to the plastids  
JOURNAL Patent: US 6489542-A 3 03-DEC-2002;  
Monsanto Technology LLC; St. Louis, MO  
FEATURES  
source 1. .415  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 3.33e-09 Length: 415  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservative: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x AR260580 (1-415)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
|||||  
Db 15 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC----- 50

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuYleuSerThrAlaSerLeuProValAlaArg 40  
Db 51 -----GCCGTGCGTCGCTTCTGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 104

Qy 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 105 CGTCTCTCCAGAGCCTCGGCACGTC---AGCAACGGCGGAGGATCCGGTGC 155

RESULT 18  
AR271024

LOCUS AR271024 416 bp DNA linear PAT 10-APR-2000  
DEFINITION Sequence 25 from patent US 6501009.  
ACCESSION AR271024  
VERSION AR271024.1 GI:29702290  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 416)  
AUTHORS Romano,C.P.  
TITLE Expression of Cry3B insecticidal protein in plants  
JOURNAL Patent: US 6501009-A 25 31-DEC-2002;  
Monsanto Technology LLC; St. Louis, MO  
FEATURES  
source 1. .416  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 3.34e-09 Length: 416  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservative: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x AR271024 (1-416)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
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Db 16 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC----- 51

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuYleuSerThrAlaSerLeuProValAlaArg 40  
Db 52 -----GCCGTGCGTCGCTTCTGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 105

Qy 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 106 CGCTCTCTCCAGAGCCTCGGCACGTC---AGCAACGGCGGAGGATCCGGTGC 156

RESULT 19  
AR271026

LOCUS AR271026 416 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 30 from patent US 6501009.  
ACCESSION AR271026  
VERSION AR271026.1 GI:29702292  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 416)  
AUTHORS Romano,C.P.  
TITLE Expression of Cry3B insecticidal protein in plants  
JOURNAL Patent: US 6501009-A 30 31-DEC-2002;  
Monsanto Technology LLC; St. Louis, MO  
FEATURES  
source 1. .416  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 3.34e-09 Length: 416  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservative: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x AR271026 (1-416)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20



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Db      16 ATGGGCCCCACCGTGATGAGCGCTCGTCGGCCACC----- 51
Qy      21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db      52 -----GCCGTGCTCGTTCTCGTGGGGCTCAAGTCCACGCCAGCTCCCGTCGGCCGC 105
Qy      41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db      106 CGCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 156

RESULT 20
AR271020
LOCUS      AR271020
DEFINITION Sequence 17 from patent US 6501009.
ACCESSION AR271020
VERSION    AR271020.1 GI:29702286
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 3450)
AUTHORS     Romano, C.P.
TITLE       Expression of Cry3B insecticidal protein in plants
JOURNAL     Monsanto Technology LLC; St. Louis, MO
FEATURES    Location/Qualifiers
             source
               1..3450
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.:      2,44e-08      Length:      3450
Score:          196.50      Matches:    46
Percent Similarity: 79.3%      Conservative: 0
Best Local Similarity: 79.3%      Mismatches: 1
Query Match:    69.7%      Indels:    11
DB:             6          Gaps:          2

US-10-628-525A-34 (1-58) x AR271020 (1-3450)

Qy      1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db      825 ATGGGCCCCACCGTGATGAGCGCTCGTCGGCCACC----- 860
Qy      21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db      861 -----GCCGTGCTCGTTCTCGTGGGGCTCAAGTCCACGCCAGCTCCCGTCGGCCGC 914
Qy      41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db      915 CGCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 965

RESULT 21
AR271032
LOCUS      AR271032
DEFINITION Sequence 36 from patent US 6501009.
ACCESSION AR271032
VERSION    AR271032.1 GI:29702298
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 3455)
AUTHORS     Romano, C.P.
TITLE       Expression of Cry3B insecticidal protein in plants
JOURNAL     Monsanto Technology LLC; St. Louis, MO
FEATURES    Location/Qualifiers
             source
               1..3455
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.:      2,44e-08      Length:      3450
Score:          196.50      Matches:    46
Percent Similarity: 79.3%      Conservative: 0
Best Local Similarity: 79.3%      Mismatches: 1
Query Match:    69.7%      Indels:    11
DB:             6          Gaps:          2

US-10-628-525A-34 (1-58) x AR271020 (1-3450)

Qy      1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db      825 ATGGGCCCCACCGTGATGAGCGCTCGTCGGCCACC----- 860
Qy      21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db      861 -----GCCGTGCTCGTTCTCGTGGGGCTCAAGTCCACGCCAGCTCCCGTCGGCCGC 914
Qy      41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db      915 CGCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 965

RESULT 22
AR271018
LOCUS      AR271018
DEFINITION Sequence 13 from patent US 6501009.
ACCESSION AR271018
VERSION    AR271018.1 GI:29702284
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 4149)
AUTHORS     Romano, C.P.
TITLE       Expression of Cry3B insecticidal protein in plants
JOURNAL     Patent: US 6501009-A 13 31-DEC-2002;
             Monsanto Technology LLC; St. Louis, MO
FEATURES    Location/Qualifiers
             source
               1..4149
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.:      2,9e-08      Length:      4149
Score:          196.50      Matches:    46
Percent Similarity: 79.3%      Conservative: 0
Best Local Similarity: 79.3%      Mismatches: 1
Query Match:    69.7%      Indels:    11
DB:             6          Gaps:          2

US-10-628-525A-34 (1-58) x AR271018 (1-4149)

Qy      1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db      1488 ATGGGCCCCACCGTGATGAGCGCTCGTCGGCCACC----- 1523
Qy      21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db      1524 -----GCCGTGCTCGTTCTCGTGGGGCTCAAGTCCACGCCAGCTCCCGTCGGCCGC 1577
Qy      41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db      1578 CGCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 1628

RESULT 23
AR260588
LOCUS      AR260588
DEFINITION Sequence 16 from patent US 6485542.
ACCESSION AR260588
VERSION    AR260588.1 GI:27311143

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ORIGIN
Alignment Scores:
Pred. No.:      2,44e-08      Length:      3455
Score:          196.50      Matches:    46
Percent Similarity: 79.3%      Conservative: 0
Best Local Similarity: 79.3%      Mismatches: 1
Query Match:    69.7%      Indels:    11
DB:             6          Gaps:          2

US-10-628-525A-34 (1-58) x AR271032 (1-3455)

Qy      1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db      825 ATGGGCCCCACCGTGATGAGCGCTCGTCGGCCACC----- 860
Qy      21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db      861 -----GCCGTGCTCGTTCTCGTGGGGCTCAAGTCCACGCCAGCTCCCGTCGGCCGC 914
Qy      41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db      915 CGCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 965

RESULT 22
AR271018
LOCUS      AR271018
DEFINITION Sequence 13 from patent US 6501009.
ACCESSION AR271018
VERSION    AR271018.1 GI:29702284
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 4149)
AUTHORS     Romano, C.P.
TITLE       Expression of Cry3B insecticidal protein in plants
JOURNAL     Patent: US 6501009-A 13 31-DEC-2002;
             Monsanto Technology LLC; St. Louis, MO
FEATURES    Location/Qualifiers
             source
               1..4149
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.:      2,9e-08      Length:      4149
Score:          196.50      Matches:    46
Percent Similarity: 79.3%      Conservative: 0
Best Local Similarity: 79.3%      Mismatches: 1
Query Match:    69.7%      Indels:    11
DB:             6          Gaps:          2

US-10-628-525A-34 (1-58) x AR271018 (1-4149)

Qy      1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db      1488 ATGGGCCCCACCGTGATGAGCGCTCGTCGGCCACC----- 1523
Qy      21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db      1524 -----GCCGTGCTCGTTCTCGTGGGGCTCAAGTCCACGCCAGCTCCCGTCGGCCGC 1577
Qy      41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db      1578 CGCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 1628

RESULT 23
AR260588
LOCUS      AR260588
DEFINITION Sequence 16 from patent US 6485542.
ACCESSION AR260588
VERSION    AR260588.1 GI:27311143

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KEYWORDS      .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 8349)
AUTHORS        Corbin,D.R. and Romano,C.P.
TITLE          Methods for transforming plants to express Cry2ab
               .delta.-endotoxins targeted to the plastids
JOURNAL        Patent: US 6489542-A 16 03-DEC-2002;
               Monsanto Technology LLC; St. Louis, MO
FEATURES       Location/Qualifiers
                source
                1..8349
                /organism="unknown"
                /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.:      5.6e-08      Length:      8349
Score:          196.50      Matches:      46
Percent Similarity: 79.3%      Conservative: 0
Best Local Similarity: 79.3%      Mismatches: 1
Query Match:     69.7%      Indels:      11
DB:              6          Gaps:          2

US-10-628-525A-34 (1-58) x AR260588 (1-8349)

QY      1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db      3259 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 3304
QY      21 AlaSerAlaValAlaProPheGlnGlyLeuIysSerThrAlaSerLeuProValAlaArg 40
Db      3305 -----GCCGTGCTCGTCTCTCGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 3358
QY      41 ArgSerSerArgSerLeuGlyAsnValAlaSerAlaSerAenGlyGlyArgIleArgCys 58
Db      3359 CGCTCTCCAGAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 3409

RESULT 24
ZMRUBSMSU      1274 bp      DNA      linear      PLN 15-NOV-1996
LOCUS          Z.mays rubisco small subunit gene.
DEFINITION     Y09214
ACCESSION      Y09214.1 GI:1673455
VERSION        rubisco small subunit.
KEYWORDS       Zea mays
SOURCE         Zea mays
ORGANISM       Zea mays

REFERENCE      1
AUTHORS        Ewing,R.M.
JOURNAL        Thesis (1996) Department of Plant Sciences, University of Oxford,
               U.K.
REFERENCE      2 (bases 1 to 1274)
AUTHORS        Ewing,R.M.
TITLE          Direct Submission
JOURNAL        Submitted (05-NOV-1996) R.M. Ewing, University of Oxford, Plant
               Sciences, South Parks Road, Oxford, OX1 3RB, UK
FEATURES       Location/Qualifiers
                1..1274
                /organism="Zea mays"
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                /db_xref="taxon:4577"
                /chromosome="21"
                /cell_line="b73"
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                /product="rubisco small subunit"
                /protein_id="CAA70416.1"
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                /db_xref="GOA:O24574"
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CDS

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343..460
/number=1
461..826
/number=2

exon
intron
exon

ORIGIN
Alignment Scores:
Pred. No.:      1.18e-08      Length:      1274
Score:          195.50      Matches:      45
Percent Similarity: 79.3%      Conservative: 1
Best Local Similarity: 77.6%      Mismatches: 1
Query Match:     69.3%      Indels:      11
DB:              15          Gaps:          2

US-10-628-525A-34 (1-58) x ZMRUBSMSU (1-1274)

QY      1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db      196 ATGGCGCCACCGTGATGATGGCTCGTCGGCAACC----- 231
QY      21 AlaSerAlaValAlaProPheGlnGlyLeuIysSerThrAlaSerLeuProValAlaArg 40
Db      232 -----GCCGTGCGCCCGTTCAGGGTCTCAAGTCCGCCAGCTCCCGTCGCCCGC 285
QY      41 ArgSerSerArgSerLeuGlyAsnValAlaSerAenGlyGlyArgIleArgCys 58
Db      286 CGCAGCACGAGGAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 336

RESULT 25
AR088975      195 bp      DNA      linear      PAT 07-SEP-2000
LOCUS          AR088975
DEFINITION     Sequence 9 from patent US 5990390.
ACCESSION      AR088975
VERSION        AR088975.1 GI:10015732
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 195)
AUTHORS        Lundquist,R.C., Walters,D.A. and Kiriwara,J.A.
TITLE          Methods and compositions for the production of stably transformed,
               fertile monocot plants and cells thereof
JOURNAL        Patent: US 5990390-A 9 23-NOV-1999;
FEATURES       Location/Qualifiers
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                /organism="unknown"
                /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      1.07e-08      Length:      195
Score:          187.50      Matches:      44
Percent Similarity: 80.0%      Conservative: 0
Best Local Similarity: 80.0%      Mismatches: 0
Query Match:     66.5%      Indels:      11
DB:              6          Gaps:          2

US-10-628-525A-34 (1-58) x AR088975 (1-195)

QY      4 ThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAlaSerAla 23
Db      61 ACCGTGATGATGGCTCGTCGGCCACC-----GCC 90
QY      24 ValAlaProPheGlnGlyLeuIysSerThrAlaSerLeuProValAlaArgSerSer 43
Db      91 GTCGCTCGGTTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGCGCGGCTCCTCC 150

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Qy 44 ArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58  
Db 151 AGAAGCCTCGCAACGTC---AGCACGGCGGAGGATCGGTGC 192

RESULT 26  
AR577398  
LOCUS AR577398 195 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 9 from patent US 6777589.  
ACCESSION AR577398  
VERSION AR577398.1 GI:56579942  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 195)  
AUTHORS Lundquist,R.C. and Walters,D.A.  
TITLE Methods and compositions for the production of stably transformed,  
fertilile monocot plants and cells thereof  
JOURNAL Patent: US 6777589-A 9 17-AUG-2004;  
DeKalb Genetics Corporation; DeKalb, IL

FEATURES  
source  
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/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.07e-08 Length: 195  
Score: 187.50 Matches: 44  
Percent Similarity: 80.0% Conservative: 0  
Best Local Similarity: 80.0% Mismatches: 0  
Query Match: 66.5% Indels: 11  
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x AR577398 (1-195)

Qy 4 ThrValMetMetAlaSerSerAlaThrAlaThrArgThrAenProAlaGlnAlaSerAla 23  
Db 61 ACCGTGATGATGCCCTCGTCCGCCACC-----GCC 90

Qy 24 ValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArgArgSer 43  
Db 91 GTGCTTCGGTTCAGGGGCTCAGTCCACGCCAGCTCCCGTCCCGCGGTCTCTCC 150

Qy 44 ArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58  
Db 151 AGAAGCCTCGCAACGTC---AGCACGGCGGAGGATCGGTGC 192

RESULT 27  
STRBCS2C  
LOCUS STRBCS2C 1386 bp DNA linear PLN 09-OCT-1996  
DEFINITION S.tuberosum rbcS2c gene for ribulose-(1,5)-bisphosphate  
carboxylase/oxygenase small subunit.

ACCESSION X69762.1 GI:21568  
VERSION X69762.1  
KEYWORDS chloroplast; gene expression; gene family; photosynthesis; protein  
transport; rbcS2c gene.  
SOURCE S.tuberosum (potato)  
ORGANISM S.tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanales; Solanaceae; Solanum.  
REFERENCE 1 (bases 1 to 1386)  
AUTHORS Fritts,C.C., Wolter,P.P., Schenkemeyer,V., Hergert,T. and  
Schreier,P.H.  
TITLE The gene family encoding the ribulose-(1,5)-bisphosphate  
carboxylase/oxygenase (Rubisco) small subunit of potato  
JOURNAL Gene 137 (2), 271-274 (1993)  
PUBLISHED 829958  
REFERENCE 2 (bases 1 to 1386)  
AUTHORS Schreier,P.H.  
TITLE Direct Submission  
JOURNAL Submitted (01-DEC-1992) P.H. Schreier, Bayer AG, PF-E/FU Gebaeude

6240, 5090 Leverkusen-Bayerwerk, FRG  
Related sequence: Fritts, C.C., Proc. Natl. Acad. Sci. 88:4458-4462 (91).

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1..428  
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429..605  
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606..694  
/gene="rbcS2c"  
/number=1  
695..829  
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/product="ribulose biphosphate carboxylase"  
/number=2  
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830..914  
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/number=3  
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/gene="rbcS2c"

ORIGIN  
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Pred. No.: 1.91e-06 Length: 1386  
Score: 171.50 Matches: 36  
Percent Similarity: 79.3% Conservative: 10  
Best Local Similarity: 62.1% Mismatches: 11  
Query Match: 60.8% Indels: 1  
DB: 15 Gaps: 1

US-10-628-525A-34 (1-58) x STRBCS2C (1-1386)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAenProAlaGln 20  
Db 429 ATGGCTTCTTCAGTA---ATGTCCTCAGCGCTGTGCCACCGCGGCAATGTGCACAA 485

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 486 GCCAGCATGTTGCACCTTCACTGGCTCAAGTCCACCGCTCTTTCCTGTTTCAGG 545

Qy 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58  
Db 486 GCCAGCATGTTGCACCTTCACTGGCTCAAGTCCACCGCTCTTTCCTGTTTCAGG 545

|                                            |                                                                                                                                                                                          |                                                              |      |        |                 |
|--------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------|------|--------|-----------------|
| Db                                         | 546                                                                                                                                                                                      | AAGCAAAACCTTGACATTACCTCATTGCTAGCAATGGTGAAGAGTCAGATGC         | 599  |        |                 |
| RESULT 28                                  | SLARBCS                                                                                                                                                                                  | 723 bp                                                       | mRNA | linear | PLN 30-JUN-1995 |
| LOCUS                                      | Stellaria longipes ribulose-1,5-bisphosphate carboxylase/oxygenase                                                                                                                       |                                                              |      |        |                 |
| DEFINITION                                 | (rbcS) mRNA, complete cds.                                                                                                                                                               |                                                              |      |        |                 |
| ACCESSION                                  | L26605                                                                                                                                                                                   |                                                              |      |        |                 |
| VERSION                                    | L26605.1                                                                                                                                                                                 | GI:556417                                                    |      |        |                 |
| KEYWORDS                                   | rbcS gene; ribulose 1,5-bisphosphate carboxylase/oxygenase small subunit.                                                                                                                |                                                              |      |        |                 |
| SOURCE                                     | Stellaria longipes                                                                                                                                                                       |                                                              |      |        |                 |
| ORGANISM                                   | Stellaria longipes                                                                                                                                                                       |                                                              |      |        |                 |
| REFERENCE                                  | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Caryophyllaceae; Stellaria.        |                                                              |      |        |                 |
| AUTHORS                                    | Zhang,X.-H., Muhammad,N. and Chinnappa,C.C.                                                                                                                                              |                                                              |      |        |                 |
| TITLE                                      | Characterization and evolution of a cDNA encoding the small subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (rbcS) of Stellaria longipes (Caryophyllaceae)                    |                                                              |      |        |                 |
| JOURNAL                                    | Plant Species Biol. 10, 39-51 (1995)                                                                                                                                                     |                                                              |      |        |                 |
| REFERENCE                                  | 2 (bases 1 to 723)                                                                                                                                                                       |                                                              |      |        |                 |
| AUTHORS                                    | Zhang,X.-H.                                                                                                                                                                              |                                                              |      |        |                 |
| TITLE                                      | Direct Submission                                                                                                                                                                        |                                                              |      |        |                 |
| JOURNAL                                    | Submitted (04-OCT-1994) King-Hai Zhang, Department of Biological Sciences, University of Calgary, Alberta, Canada                                                                        |                                                              |      |        |                 |
| COMMENT                                    | Original source text: Stellaria longipes cDNA to mRNA.                                                                                                                                   |                                                              |      |        |                 |
| FEATURES                                   | Location/Qualifiers                                                                                                                                                                      |                                                              |      |        |                 |
| source                                     | 1..723                                                                                                                                                                                   |                                                              |      |        |                 |
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| gene                                       | 1..723                                                                                                                                                                                   |                                                              |      |        |                 |
| 5'UTR                                      | 1..32                                                                                                                                                                                    |                                                              |      |        |                 |
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| CDS                                        | 33..575                                                                                                                                                                                  |                                                              |      |        |                 |
|                                            | /gene="rbcS"                                                                                                                                                                             |                                                              |      |        |                 |
|                                            | /notes="putative"                                                                                                                                                                        |                                                              |      |        |                 |
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| transit_peptide                            | 33..203                                                                                                                                                                                  |                                                              |      |        |                 |
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|                                            | /notes="putative"                                                                                                                                                                        |                                                              |      |        |                 |
| 3'UTR                                      | 576..723                                                                                                                                                                                 |                                                              |      |        |                 |
|                                            | /gene="rbcS"                                                                                                                                                                             |                                                              |      |        |                 |
|                                            | /notes="putative"                                                                                                                                                                        |                                                              |      |        |                 |
| polyA_signal                               | 640..645                                                                                                                                                                                 |                                                              |      |        |                 |
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|                                            | /notes="putative"                                                                                                                                                                        |                                                              |      |        |                 |
| ORIGIN                                     |                                                                                                                                                                                          |                                                              |      |        |                 |
| Alignment Scores:                          |                                                                                                                                                                                          |                                                              |      |        |                 |
| Pred. No.:                                 | 1.57e-06                                                                                                                                                                                 | Length:                                                      | 723  |        |                 |
| Score:                                     | 169.50                                                                                                                                                                                   | Matches:                                                     | 34   |        |                 |
| Percent Similarity:                        | 81.0%                                                                                                                                                                                    | Conservative:                                                | 13   |        |                 |
| Best Local Similarity:                     | 58.6%                                                                                                                                                                                    | Mismatches:                                                  | 10   |        |                 |
| Query Match:                               | 60.1%                                                                                                                                                                                    | Indels:                                                      | 1    |        |                 |
| DB:                                        | 15                                                                                                                                                                                       | Gaps:                                                        | 1    |        |                 |
| US-10-628-525A-34 (1-58) x SLARBCS (1-723) |                                                                                                                                                                                          |                                                              |      |        |                 |
| Qy                                         | 1                                                                                                                                                                                        | MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln | 20   |        |                 |

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/EC number="4.1.1.39"
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Alignment Scores:
Pred. No.: 6.3e-06 Length: 1629
Score: 166.50 Matches: 35
Percent Similarity: 77.6% Conservative: 10
Best Local Similarity: 60.3% Mismatches: 12
Query Match: 59.0% Indels: 1
DB: 15 Gaps: 1

US-10-628-525A-34 (1-58) x STRBCS2 (1-1629)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrArgProAlaGln 20
Db 630 ATGGCTTCTTCAGTG---ATGCTCTCAGCAGCTGTTGCCACCGCGCAATGGTGCAAA 686

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 687 GCAGCATGTTGGACCCCTTCATGGACTTAAGTCGCCGCCCTCTTTCCCTGTTTCAAGG 746

Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58
Db 747 AAGCAAAACCTTGACATTACCTCCATTGCTAGCAATGGTGGAAAGTCAATGC 800

RESULT 30
TOMRBCSC
LOCUS
DEFINITION
Tomato (L.esculentum) ribulose-1,5-bisphosphate
carboxylase/oxygenase (RBCS) small subunit gene, clone Rbcs-3A.
MI3544
ACCESSION
MI3544.1 GI:170499
VERSION
ribulose 1,5-bisphosphate carboxylase/oxygenase.
KEYWORDS
Lycopersicon esculentum (solanum lycopersicum)
SOURCE
Lycopersicon esculentum
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
Pichersky, E., Bernatzky, R., Tanksley, S.D. and Cashmore, A.R.
EVIDENCE
Evidence for selection as a mechanism in the concerted evolution of
Lycopersicon esculentum (tomato) genes encoding the small subunit
of ribulose-1,5-bisphosphate carboxylase/oxygenase
Proc. Natl. Acad. Sci. U.S.A. 83 (11), 3880-3884 (1986)
3012537
JOURNAL
PUBMED
COMMENT
Original source text: Tomato (L.esculentum) DNA, clone Rbcs-3A.
Clean copy sequence for [1] kindly provided by E.Pichersky,
31-OCT-1986.

FEATURES
Location/Qualifiers
1. .1027
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/mol_type="genomic DNA"
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join(136. .312,405. .539,627. .857)
/notes="ribulose-1,5-bisphosphate carboxylase/ oxygenase
small subunit"
/codon_start=1
/protein_id="AAA34190.1"
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CDS
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/notes="ribulose-1,5-bisphosphate carboxylase/ oxygenase
small subunit, (EC 4.1.1.39)"
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313. .404
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405. .539
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small subunit"
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540. .626
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627. .857
/notes="ribulose-1,5-bisphosphate carboxylase/ oxygenase
small subunit"
/number=3

ORIGIN 525 bp upstream of EcoRI site; chromosome 2, Rbcs-3 locus.

Alignment Scores:
Pred. No.: 5.03e-06 Length: 1027
Score: 165.50 Matches: 35
Percent Similarity: 77.6% Conservative: 10
Best Local Similarity: 60.3% Mismatches: 12
Query Match: 58.7% Indels: 1
DB: 15 Gaps: 1

US-10-628-525A-34 (1-58) x TOMRBCSC (1-1027)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrArgProAlaGln 20
Db 136 ATGGCTTCTTCAGTA---ATGCTCTCAGCAGCTGTTGCCACCGCGCAATGGTGCAAA 192

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 193 GCTAGCATGTTGGACCCCTTCATGGACTCAAGTCCACCGCTTCTTTCCCTGTTTCAAGG 252

Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58
Db 253 AAGCAAAACCTTGACATTACCTCCATTGCTAGCAACGGTGGAAAGTCAAGTTC 306

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Job time : 1160.21 secs
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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 00:15:06 ; Search time 136.553 Seconds  
(without alignments)  
2830.777 Million cell updates/sec

Title: US-10-628-525A-34

Perfect score: 282

Sequence: 1 MATVMWASSATATRTNPAQ.....ARRSRSLGNVAGGRIRC 58

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 203.5 | 72.2        | 183    | 4  | Aah27499 Small sub |
| 2          | 203.5 | 72.2        | 183    | 10 | Aad79096 Corn RUBI |
| 3          | 203.5 | 72.2        | 185    | 2  | Aaq82917 Maize chl |
| 4          | 203.5 | 72.2        | 228    | 12 | Adp57000 Maize car |

|    |       |      |      |    |          |                    |
|----|-------|------|------|----|----------|--------------------|
| 5  | 203.5 | 72.2 | 229  | 12 | ADP57015 | Adp57015 Maize car |
| 6  | 203.5 | 72.2 | 230  | 12 | ADP57195 | Adp57195 Maize car |
| 7  | 203.5 | 72.2 | 235  | 12 | ADP57010 | Adp57010 Maize car |
| 8  | 203.5 | 72.2 | 236  | 12 | ADP57001 | Adp57001 Maize car |
| 9  | 203.5 | 72.2 | 238  | 12 | ADP56997 | Adp56997 Maize car |
| 10 | 203.5 | 72.2 | 249  | 12 | ADP57002 | Adp57002 Maize car |
| 11 | 203.5 | 72.2 | 264  | 12 | ADP56984 | Adp56984 Maize car |
| 12 | 203.5 | 72.2 | 265  | 12 | ADP56971 | Adp56971 Maize car |
| 13 | 203.5 | 72.2 | 272  | 12 | ADP56976 | Adp56976 Maize car |
| 14 | 203.5 | 72.2 | 276  | 12 | ADP56957 | Adp56957 Maize car |
| 15 | 203.5 | 72.2 | 276  | 12 | ADP56982 | Adp56982 Maize car |
| 16 | 203.5 | 72.2 | 284  | 12 | ADP56963 | Adp56963 Maize car |
| 17 | 203.5 | 72.2 | 286  | 12 | ADP56968 | Adp56968 Maize car |
| 18 | 203.5 | 72.2 | 291  | 12 | ADP56978 | Adp56978 Maize car |
| 19 | 203.5 | 72.2 | 297  | 12 | ADP56945 | Adp56945 Maize car |
| 20 | 203.5 | 72.2 | 298  | 12 | ADP56952 | Adp56952 Maize car |
| 21 | 203.5 | 72.2 | 305  | 12 | ADP56947 | Adp56947 Maize car |
| 22 | 203.5 | 72.2 | 307  | 12 | ADP56960 | Adp56960 Maize car |
| 23 | 203.5 | 72.2 | 309  | 12 | ADP56946 | Adp56946 Maize car |
| 24 | 203.5 | 72.2 | 311  | 12 | ADP56961 | Adp56961 Maize car |
| 25 | 203.5 | 72.2 | 312  | 12 | ADP56999 | Adp56999 Maize car |
| 26 | 203.5 | 72.2 | 315  | 12 | ADP56942 | Adp56942 Maize car |
| 27 | 203.5 | 72.2 | 317  | 12 | ADP56941 | Adp56941 Maize car |
| 28 | 203.5 | 72.2 | 319  | 12 | ADP56935 | Adp56935 Maize car |
| 29 | 203.5 | 72.2 | 344  | 12 | ADP57162 | Adp57162 Maize car |
| 30 | 203.5 | 72.2 | 405  | 2  | AAQ88331 | Aaq88331 Optimal   |
| 31 | 203.5 | 72.2 | 409  | 12 | ADP57146 | Adp57146 Maize car |
| 32 | 203.5 | 72.2 | 415  | 12 | ADP57175 | Adp57175 Maize car |
| 33 | 203.5 | 72.2 | 438  | 12 | ADP57141 | Adp57141 Maize car |
| 34 | 203.5 | 72.2 | 441  | 12 | ADP57160 | Adp57160 Maize car |
| 35 | 203.5 | 72.2 | 443  | 12 | ADP57156 | Adp57156 Maize car |
| 36 | 203.5 | 72.2 | 1449 | 3  | AAZ36874 | Aaz36874 cDNA enco |
| 37 | 203.5 | 72.2 | 1868 | 12 | ADQ54814 | Adq54814 DNA expre |
| 38 | 203.5 | 72.2 | 2318 | 5  | AAH49585 | Aah49585 Partial s |
| 39 | 203.5 | 72.2 | 5281 | 6  | ABL56341 | AbL56341 Nucleotid |
| 40 | 203.5 | 72.2 | 5909 | 6  | ABL56342 | AbL56342 Nucleotid |
| 41 | 202.5 | 71.8 | 197  | 12 | ADP57201 | Adp57201 Maize car |
| 42 | 202.5 | 71.8 | 198  | 12 | ADP57030 | Adp57030 Maize car |
| 43 | 202.5 | 71.8 | 258  | 12 | ADP56979 | Adp56979 Maize car |
| 44 | 202.5 | 71.8 | 268  | 12 | ADP56985 | Adp56985 Maize car |
| 45 | 202.5 | 71.8 | 269  | 12 | ADP56993 | Adp56993 Maize car |
| 46 | 202.5 | 71.8 | 276  | 12 | ADP56975 | Adp56975 Maize car |
| 47 | 202.5 | 71.8 | 278  | 12 | ADP56953 | Adp56953 Maize car |
| 48 | 202.5 | 71.8 | 283  | 12 | ADP56962 | Adp56962 Maize car |
| 49 | 202.5 | 71.8 | 286  | 12 | ADP56972 | Adp56972 Maize car |
| 50 | 202.5 | 71.8 | 290  | 12 | ADP56966 | Adp56966 Maize car |
| 51 | 202.5 | 71.8 | 291  | 12 | ADP56980 | Adp56980 Maize car |
| 52 | 202.5 | 71.8 | 291  | 12 | ADP56956 | Adp56956 Maize car |
| 53 | 202.5 | 71.8 | 291  | 12 | ADP56965 | Adp56965 Maize car |
| 54 | 202.5 | 71.8 | 296  | 12 | ADP56969 | Adp56969 Maize car |
| 55 | 202.5 | 71.8 | 310  | 12 | ADP56954 | Adp56954 Maize car |
| 56 | 202.5 | 71.8 | 310  | 12 | ADP56958 | Adp56958 Maize car |
| 57 | 202.5 | 71.8 | 316  | 12 | ADP56940 | Adp56940 Maize car |
| 58 | 202.5 | 71.8 | 381  | 12 | ADP57151 | Adp57151 Maize car |
| 59 | 202.5 | 71.8 | 411  | 12 | ADP57152 | Adp57152 Maize car |
| 60 | 202.5 | 71.8 | 414  | 12 | ADP57144 | Adp57144 Maize car |
| 61 | 202.5 | 71.8 | 433  | 12 | ADP57142 | Adp57142 Maize car |
| 62 | 202.5 | 71.8 | 434  | 12 | ADP57154 | Adp57154 Maize car |
| 63 | 202.5 | 71.8 | 434  | 12 | ADP57155 | Adp57155 Maize car |
| 64 | 199.5 | 70.7 | 283  | 12 | ADP56970 | Adp56970 Maize car |
| 65 | 198.5 | 70.4 | 226  | 12 | ADP57028 | Adp57028 Maize car |
| 66 | 198.5 | 70.4 | 428  | 12 | ADP57148 | Adp57148 Maize car |
| 67 | 198.5 | 70.4 | 453  | 12 | ADP57161 | Adp57161 Maize car |
| 68 | 197.5 | 70.0 | 199  | 12 | ADP57036 | Adp57036 Maize car |
| 69 | 197.5 | 70.0 | 312  | 12 | ADP56973 | Adp56973 Maize car |
| 70 | 197.5 | 70.0 | 382  | 12 | ADP57166 | Adp57166 Maize car |
| 71 | 196.5 | 69.7 | 285  | 12 | ADP57006 | Adp57006 Maize car |
| 72 | 196.5 | 69.7 | 415  | 3  | AAQ01002 | Aaq01002 Maize chl |
| 73 | 196.5 | 69.7 | 415  | 3  | AAH15557 | Aah15557 ZnSSU pla |
| 74 | 196.5 | 69.7 | 415  | 6  | AAH37659 | Aad37659 Maize mss |
| 75 | 196.5 | 69.7 | 415  | 8  | ACD29599 | Adc29599 Maize RUB |
| 76 | 196.5 | 69.7 | 416  | 3  | AAZ51647 | Aaz51647 Maize RUB |
| 77 | 196.5 | 69.7 | 416  | 3  | AAZ51649 | Aaz51649 Cauliflow |



|     |       |      |      |    |                     |                     |
|-----|-------|------|------|----|---------------------|---------------------|
| 78  | 196.5 | 69.7 | 416  | 10 | AAD61797 Modified   | Aad61797 Modified   |
| 79  | 196.5 | 69.7 | 416  | 10 | AAD61795 Zea mays   | Ad61795 Zea mays    |
| 80  | 196.5 | 69.7 | 416  | 12 | ADJ62838 CanV35S A  | Adj62838 CanV35S A  |
| 81  | 196.5 | 69.7 | 3450 | 3  | AAZ51643 Bacillus   | Aaz51643 Bacillus   |
| 82  | 196.5 | 69.7 | 3450 | 10 | AAD61791 Bt.cry3Bb  | Ad61791 Bt.cry3Bb   |
| 83  | 196.5 | 69.7 | 3450 | 10 | ABX95187 B. thuring | Abx95187 B. thuring |
| 84  | 196.5 | 69.7 | 3455 | 3  | AAZ51655 Bacillus   | Aaz51655 Bacillus   |
| 85  | 196.5 | 69.7 | 3455 | 10 | AAD61803 Bt.cry3Bb  | Ad61803 Bt.cry3Bb   |
| 86  | 196.5 | 69.7 | 3455 | 10 | ABX95199 B. thuring | Abx95199 B. thuring |
| 87  | 196.5 | 69.7 | 4149 | 3  | AAZ51641 Bacillus   | Aaz51641 Bacillus   |
| 88  | 196.5 | 69.7 | 4149 | 10 | AAD61789 Bt.cry3Bb  | Ad61789 Bt.cry3Bb   |
| 89  | 196.5 | 69.7 | 4149 | 10 | ABX95185 B. thuring | Abx95185 B. thuring |
| 90  | 196.5 | 69.7 | 5600 | 12 | ADK98490 B thuring  | Adk98490 B thuring  |
| 91  | 196.5 | 69.7 | 7000 | 12 | ADK98485 B thuring  | Adk98485 B thuring  |
| 92  | 196.5 | 69.7 | 8349 | 3  | AAJ15565 pMON10464  | Aaj15565 pMON10464  |
| 93  | 195.5 | 69.3 | 212  | 12 | ADP57021 Maize car  | Adp57021 Maize car  |
| 94  | 195.5 | 69.3 | 232  | 12 | ADP57013 Maize car  | Adp57013 Maize car  |
| 95  | 195.5 | 69.3 | 241  | 12 | ADP57003 Maize car  | Adp57003 Maize car  |
| 96  | 195.5 | 69.3 | 242  | 12 | ADP57012 Maize car  | Adp57012 Maize car  |
| 97  | 195.5 | 69.3 | 242  | 12 | ADP57032 Maize car  | Adp57032 Maize car  |
| 98  | 195.5 | 69.3 | 244  | 12 | ADP57019 Maize car  | Adp57019 Maize car  |
| 99  | 195.5 | 69.3 | 250  | 12 | ADP57197 Maize car  | Adp57197 Maize car  |
| 100 | 195.5 | 69.3 | 259  | 12 | ADP57034 Maize car  | Adp57034 Maize car  |
| 101 | 195.5 | 69.3 | 265  | 12 | ADP57029 Maize car  | Adp57029 Maize car  |
| 102 | 195.5 | 69.3 | 266  | 12 | ADP57023 Maize car  | Adp57023 Maize car  |
| 103 | 195.5 | 69.3 | 269  | 12 | ADP57026 Maize car  | Adp57026 Maize car  |
| 104 | 195.5 | 69.3 | 270  | 12 | ADP57025 Maize car  | Adp57025 Maize car  |
| 105 | 195.5 | 69.3 | 273  | 12 | ADP57020 Maize car  | Adp57020 Maize car  |
| 106 | 195.5 | 69.3 | 275  | 12 | ADP57200 Maize car  | Adp57200 Maize car  |
| 107 | 195.5 | 69.3 | 275  | 12 | ADP56990 Maize car  | Adp56990 Maize car  |
| 108 | 195.5 | 69.3 | 276  | 12 | ADP57022 Maize car  | Adp57022 Maize car  |
| 109 | 195.5 | 69.3 | 276  | 12 | ADP57018 Maize car  | Adp57018 Maize car  |
| 110 | 195.5 | 69.3 | 279  | 12 | ADP57014 Maize car  | Adp57014 Maize car  |
| 111 | 195.5 | 69.3 | 286  | 12 | ADP57017 Maize car  | Adp57017 Maize car  |
| 112 | 195.5 | 69.3 | 287  | 12 | ADP57011 Maize car  | Adp57011 Maize car  |
| 113 | 195.5 | 69.3 | 289  | 12 | ADP56981 Maize car  | Adp56981 Maize car  |
| 114 | 195.5 | 69.3 | 291  | 12 | ADP57009 Maize car  | Adp57009 Maize car  |
| 115 | 195.5 | 69.3 | 292  | 12 | ADP57016 Maize car  | Adp57016 Maize car  |
| 116 | 195.5 | 69.3 | 294  | 12 | ADP57008 Maize car  | Adp57008 Maize car  |
| 117 | 195.5 | 69.3 | 298  | 12 | ADP56992 Maize car  | Adp56992 Maize car  |
| 118 | 195.5 | 69.3 | 302  | 12 | ADP56943 Maize car  | Adp56943 Maize car  |
| 119 | 195.5 | 69.3 | 307  | 12 | ADP57007 Maize car  | Adp57007 Maize car  |
| 120 | 195.5 | 69.3 | 310  | 12 | ADP56938 Maize car  | Adp56938 Maize car  |
| 121 | 195.5 | 69.3 | 312  | 12 | ADP56967 Maize car  | Adp56967 Maize car  |
| 122 | 195.5 | 69.3 | 312  | 12 | ADP56948 Maize car  | Adp56948 Maize car  |
| 123 | 195.5 | 69.3 | 315  | 12 | ADP56955 Maize car  | Adp56955 Maize car  |
| 124 | 195.5 | 69.3 | 316  | 12 | ADP57189 Maize car  | Adp57189 Maize car  |
| 125 | 195.5 | 69.3 | 322  | 12 | ADP56949 Maize car  | Adp56949 Maize car  |
| 126 | 195.5 | 69.3 | 326  | 12 | ADP56974 Maize car  | Adp56974 Maize car  |
| 127 | 195.5 | 69.3 | 330  | 12 | ADP56937 Maize car  | Adp56937 Maize car  |
| 128 | 195.5 | 69.3 | 364  | 12 | ADP57185 Maize car  | Adp57185 Maize car  |
| 129 | 195.5 | 69.3 | 364  | 12 | ADP57183 Maize car  | Adp57183 Maize car  |
| 130 | 195.5 | 69.3 | 381  | 12 | ADP57174 Maize car  | Adp57174 Maize car  |
| 131 | 195.5 | 69.3 | 399  | 12 | ADP57170 Maize car  | Adp57170 Maize car  |
| 132 | 195.5 | 69.3 | 399  | 12 | ADP57176 Maize car  | Adp57176 Maize car  |
| 133 | 195.5 | 69.3 | 415  | 12 | ADP57173 Maize car  | Adp57173 Maize car  |
| 134 | 195.5 | 69.3 | 421  | 12 | ADP57191 Maize car  | Adp57191 Maize car  |
| 135 | 195.5 | 69.3 | 425  | 12 | ADP57168 Maize car  | Adp57168 Maize car  |
| 136 | 195.5 | 69.3 | 428  | 12 | ADP57194 Maize car  | Adp57194 Maize car  |
| 137 | 195.5 | 69.3 | 446  | 12 | ADP57172 Maize car  | Adp57172 Maize car  |
| 138 | 195.5 | 69.3 | 455  | 12 | ADP57163 Maize car  | Adp57163 Maize car  |
| 139 | 195.5 | 69.3 | 510  | 12 | ADJ44718 Plant cDN  | Adj44718 Plant cDN  |
| 140 | 194.5 | 69.0 | 261  | 12 | ADP57024 Maize car  | Adp57024 Maize car  |
| 141 | 194.5 | 69.0 | 269  | 12 | ADP56994 Maize car  | Adp56994 Maize car  |
| 142 | 194.5 | 69.0 | 458  | 12 | ADP57147 Maize car  | Adp57147 Maize car  |
| 143 | 192.5 | 68.3 | 265  | 12 | ADP56996 Maize car  | Adp56996 Maize car  |
| 144 | 192.5 | 68.3 | 360  | 12 | ADP57171 Maize car  | Adp57171 Maize car  |
| 145 | 191.5 | 67.9 | 271  | 12 | ADP57031 Maize car  | Adp57031 Maize car  |
| 146 | 191.5 | 67.9 | 325  | 12 | ADP56977 Maize car  | Adp56977 Maize car  |
| 147 | 191.5 | 67.9 | 368  | 12 | ADP57178 Maize car  | Adp57178 Maize car  |
| 148 | 191.5 | 67.9 | 418  | 12 | ADP57180 Maize car  | Adp57180 Maize car  |
| 149 | 190.5 | 67.6 | 303  | 12 | ADP56959 Maize car  | Adp56959 Maize car  |
| 150 | 189.5 | 67.2 | 179  | 12 | ADP57040 Maize car  | Adp57040 Maize car  |

ALIGNMENTS

RESULT 1

AAH27499

ID AAH27499 standard; DNA; 183 BP.

XX

AC AAH27499;

XX

DT 21-AUG-2001 (first entry)

XX

DE Small subunit Rubisco chloroplast transit signal partial DNA sequence.

XX

KW Small subunit RuBP-carboxylase chloroplast transit signal; maize;

KW Rubisco; fructo-oligosaccharide; FOS; ds.

OS Zea mays.

XX

FH Key

FT CDS

FT

FT Location/Qualifiers

FT 1..141

FT /\*tag= a

FT /product= "Maize small subunit RuBP-carboxylase

FT chloroplast transit signal"

FT /transl\_except= (pos:52..54,aa=Trp)

FT /note= "No stop codon given"

XX

PN WO200136622-A2.

XX

XX 25-MAY-2001.

PD

XX 20-NOV-2000; 2000WO-US031788.

PF

XX 18-NOV-1999; 99US-0166268P.

PR

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX

PI Caiimi PG, Lightner J;

XX

XX WPI; 2001-355631/37.

DR P-PSDB; AAB98694.

XX

XX Increasing fructo-oligosaccharide levels in monocots by inserting

XX recombinant DNA construct having tissue specific promoter linked to

XX plastid targeting sequence and fructosyltransferase coding sequence, into

XX monocot cell.

XX

XX Example 1; Page 35; 35pp; English.

PS

XX The present invention relates to a method for increasing fructo-

XX oligosaccharide (FOS) levels in a monocot. The method comprises inserting

XX into a monocot cell, a recombinant DNA construct comprising a tissue

XX specific promoter, operably linked to a plastid targeting sequence,

XX operably linked to a coding sequence for a fructosyltransferase gene, so

XX that the construct can transform a monocot cell and the transformed

XX monocot synthesises and accumulates FOS. The present sequence is a

XX partial coding sequence for the maize small subunit RuBP-carboxylase

XX (Rubisco) chloroplast transit signal, which was used in an example from

XX the present invention

XX

SQ Sequence 183 BP; 31 A; 65 C; 58 G; 29 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:

4.6e-14 Length: 183

203.50 Matches: 47

Score:

81.0% Conservative: 0

Percent Similarity:

81.0% Mismatches: 0

Best Local Similarity:

72.2% Indels: 11

Query Match:

4 Gaps: 2

DB:

US-10-628-525A-34 (1-58) x AAH27499 (1-183)

Qy 1 MetAlaProThrValMetMetAlaSerAlaThrAlaThrArgThrAsnProAlaGln 20

```

Db      1 ATGGCGGCCACCGTGTATGATGGCTCTGTCGGCCACC----- 36
Qy      21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db      37 -----GCCGTGGCTCGGTCCAGGGGCTTAAGTCCACCGCCAGCCTCCCGTCCCGCCGC 90
Qy      41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyArgIleArgCys 58
Db      91 CGCTCTCTAGAACCTCGGCACGTC---AGCAACGGCGGAGAAATCCGGTGC 141

RESULT 2
ADD79096
ID      ADD79096 standard; DNA; 183 BP.
XX
AC      ADD79096;
XX
DT      29-JAN-2004 (first entry)
XX
DE      Corn RUBISCO gene chloroplast transit signal DNA.
XX
KW      Corn; ds; RUBISCO; chloroplast transit signal;
KW      RuBP carboxylase small subunit; PTF; fructosyl transferase; SacB; plant;
KW      Corn; fructo-oligosaccharide; monocotyledon; plastid targeting sequence;
KW      starch-fructo-oligosaccharide blend; food; fructose syrup; plastic;
KW      zein promoter.
XX
OS      Zea mays.
XX
FH      Key      Location/Qualifiers
FT      CDS      1..141
FT              /*tag= a
FT              /partial
FT              /notes= "No stop codon shown"
FT              /product= "RUBISCO chloroplast transit signal"
FT              /transl_except= (pos:52..54,aa:Trp)

US2003213013-A1.
XX
PD      13-NOV-2003.
XX
PF      07-MAY-2002; 2002US-00140410.
XX
PR      07-MAY-2002; 2002US-00140410.
XX
PA      (CAIM/) CAIMI P G.
PA      (LIGH/) LIGHTNER J E.
XX
PI      Caimi PG, Lightner JE;
XX
DR      WPI; 2003-864895/80.
DR      P-PSDB; ADD79097.
XX
XX
PT      Increasing fructo-oligosaccharide levels in monocotyledon by transforming
PT      monocotyledon cell with DNA construct comprising tissue specific
PT      promoter, operably linked to plastid targeting sequence and
PT      fructosyltransferase gene.
XX
XX
PS      Example 1; SEQ ID NO 1; 21pp; English.
XX
CC      The invention relates to increasing the fructo-oligosaccharide levels in
CC      a monocotyledon, comprising inserting into a monocotyledon cell a
CC      recombinant DNA construct having a tissue specific promoter, operably
CC      linked to a plastid targeting sequence, operably linked to a coding
CC      sequence for a fructosyltransferase (PTF) gene, so that the construct can
CC      transform a monocotyledon cell and the transformed monocotyledon
CC      synthesizes and accumulates fructo-oligosaccharides. Also included are
CC      following a recombinant DNA construct (comprising a tissue specific
CC      promoter, operably linked to a plastid targeting sequence, operably
CC      linked to a coding sequence for a fructosyltransferase gene so that the
CC      construct can transform a monocotyledon cell to obtain the production of
CC      fructo-oligosaccharides in the plastid of the monocotyledon cell), a
CC      monocotyledon transformed with the construct (producing fructo-

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CC      oligosaccharides which accumulate in the plastid within cells of the
CC      monocotyledon), a seed produced from the transformed monocotyledon and an
CC      isolated starch-fructo-oligosaccharide blend (where the rheological
CC      properties of pasting temperature and final viscosity are independently
CC      altered related to the pasting temperature and final viscosity of a
CC      starch solution substantially free of fructo-oligosaccharides, provided
CC      that the starch solution comprises substantially the same amount of
CC      starch as in the blend). The construct is useful for making a starch
CC      fructo-oligosaccharide blend. The construct and the method are useful for
CC      increasing fructo-oligosaccharide levels in a monocotyledon such as corn,
CC      wheat, rice barley, sorghum, triticale and rye. The transformed plant is
CC      useful for producing fructo-oligosaccharides. The method allows for
CC      extraction of fructo-oligosaccharide from the transgenic for the purpose
CC      of fructo-oligosaccharide production. The fructo-oligosaccharides and
CC      fructo-oligosaccharide/starch mixture may be used in food and non-food
CC      applications such as human and animal food products, production of
CC      fructose syrups and the production of chemicals and plastics either as
CC      such or in modified form. A construct of the invention was produced
CC      comprising the Bacillus amyloliquefaciens SacB (FTF) gene under the
CC      control of the zein promoter as a fusion protein with the corn RUBISCO
CC      (RuBP carboxylase small subunit) chloroplast transit peptide. The present
CC      sequence encodes the RUBISCO chloroplast transit peptide.
XX
SQ      Sequence 183 BP; 31 A; 65 C; 58 G; 29 T; 0 U; 0 Other;

```

```

Alignment Scores:
Pred. No.:      4.6e-14      Length:      183
Score:          203.50      Matches:    47
Percent Similarity: 81.0%      Conservative: 0
Best Local Similarity: 81.0%      Mismatches: 0
Query Match:    72.2%      Indels:    11
DB:             10        Gaps:      2

```

US-10-628-525A-34 (1-58) x ADD79096 (1-183)

```

Qy      1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db      1 ATGGCGGCCACCGTGTATGATGGCTCTGTCGGCCACC----- 36
Qy      21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db      37 -----GCCGTGGCTCGGTCCAGGGGCTTAAGTCCACCGCCAGCCTCCCGTCCCGCCGC 90
Qy      41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyArgIleArgCys 58
Db      91 CGCTCTCTAGAACCTCGGCACGTC---AGCAACGGCGGAGAAATCCGGTGC 141

```

#### RESULT 3

```

AAQ82917
ID      AAQ82917 standard; DNA; 185 BP.
XX
AC      AAQ82917;
XX
DT      25-MAR-2003 (revised)
DT      01-NOV-1995 (first entry)
XX
DE      Maize chloroplast transit peptide synthetic gene fragment.
XX
KW      Bacillus thuringiensis HD1; Bt gene; endotoxin; transgenic maize;
KW      insect resistance; maize chloroplast transit peptide; ds.
XX
OS      Synthetic.
XX
PN      WO9506128-A2.
XX
PD      02-MAR-1995.
XX
PF      24-AUG-1994; 94WO-US009699.
XX
PR      25-AUG-1993; 93US-00113561.
XX
PA      (DEKA-) DEKALB GENETICS CORP.
XX

```

PI Dams TR, Anderson PC, Daines RJ, Gordon-Kamm WJ, Kausch AP;  
 PI Mackey CJ, Orozco EM, Orr PM, Stephens MA;  
 XX WPI; 1995-106857/14.  
 DR Fertile, transgenic maize plants and their production - useful for crop  
 XX improvements e.g. improved resistance to insect pests and improved  
 PT productivity.  
 PT Example 6; Page 123; 351pp; English.  
 XX  
 XX AAQ82917 is a maize chloroplast transit peptide synthetic gene fragment.  
 CC It was used in the construction of an expression vector for the Bacillus  
 CC thuringiensis strain HD1 Bt gene endotoxin (AAR65297). The vector was  
 CC used to transform maize plants, the progeny of which could express the B.  
 CC thuringiensis endotoxin. This conferred upon the transgenic maize plants  
 CC the advantage of increased insect resistance, compared to wild type  
 CC plants. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 185 BP; 34 A; 70 C; 54 G; 27 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 4.66e-14 Length: 185  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 2 Gaps: 2

US-10-628-525A-34 (1-58) x AAQ82917 (1-185)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 DB 42 ATGGCGCCACCGTGTATGGCTCTCGGCCACC----- 77

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 DB 78 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTGGCCGC 131

QY 41 ArgSerSerArgSerLeuGlyAlaValAlaSerAsnGlyGlyArgIleArgCys 58  
 DB 132 CGGTCTCCAGAGCGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 182

RESULT 4  
 ADP57000  
 ID ADP57000 standard; cDNA; 228 BP.  
 XX  
 AC ADP57000;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Maize carbon assimilation pathway enzyme cDNA #69.  
 XX  
 KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphate; transketolase;  
 KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxylase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.  
 XX  
 OS Zea mays.  
 XX  
 XX US2004116682-A1.  
 XX  
 XX 17-JUN-2004.  
 PD  
 PF 16-NOV-2001; 2001US-00987899.  
 XX

PR 06-MAR-1998; 98US-0076912P.  
 PR 04-MAR-1999; 99US-00262979.  
 XX  
 PA (CHEI/) CHEIKH N.  
 PA (MILL/) MILLER P W.  
 PA (OCON/) O'CONNELL K M.  
 PA (LIU/) LIU J.  
 XX  
 PI Cheikh N, Miller PW, O'connell KM, Liu J;  
 XX WPI; 2004-498291/47.  
 DR  
 XX New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.  
 XX  
 XX Claim 2; SEQ ID NO 69; 196pp; English.  
 XX  
 CC The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase,  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphate,  
 CC transketolase, sedoheptulose-1,7-bisphosphate, D-ribulose-5-phosphate-3-  
 CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxylase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 228 BP; 44 A; 83 C; 68 G; 33 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 6.01e-14 Length: 228  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP57000 (1-228)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 DB 37 ATGGCGCCACCGTGTATGGCTCTCGGCCACC----- 72

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 DB 73 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTGGCCGC 126

QY 41 ArgSerSerArgSerLeuGlyAlaValAlaSerAsnGlyGlyArgIleArgCys 58  
 DB 127 CGTCTCTCCAGAGCGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 177

RESULT 5  
 ADP57015  
 ID ADP57015 standard; cDNA; 229 BP.

ADP57015;  
 09-SEP-2004 (first entry)  
 Maize carbon assimilation pathway enzyme cDNA #84.  
 Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 aldolase; fructose-1,6-bisphosphate; transketolase;  
 sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
 ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 aspartate aminotransferase; alanine aminotransferase;  
 NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 plant metabolic pathway; plant breeding.  
 Zea mays.  
 US2004116682-A1.  
 17-JUN-2004.  
 16-NOV-2001; 2001US-00987899.  
 06-MAR-1998; 98US-0076912P.  
 04-MAR-1999; 99US-00262979.  
 (CHEI/) CHEIKH N.  
 (MILL/) MILLER P W.  
 (OCON/) O'CONNELL K M.  
 (LIUJ/) LIU J.  
 Cheikh N, Miller PW, O'connell KM, Liu J;  
 WPI; 2004-498291/47.  
 New substantially purified nucleic acid molecule encoding a maize or  
 soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 identification and analysis, plant breeding, and preparation of  
 constructs.  
 Claim 2; SEQ ID NO 84; 196pp; English.  
 The invention relates to a substantially purified nucleic acid molecule  
 that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 fragment is selected from ribulose-bisphosphate carboxylase,  
 phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 phosphate isomerase, aldolase, fructose-1,6-bisphosphatase, D-ribulose-5-phosphate-3-  
 epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 phosphate dikinase and pyrophosphatase. The invention also relates to a  
 substantially purified antibody or its fragment which is capable of  
 specifically binding to a specific maize or soybean carbon assimilation  
 pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 molecule comprising an exogenous promoter region which functions in a  
 plant cell to cause the production of an mRNA molecule, and a method of  
 determining a level or pattern in a plant cell of a carbon assimilation  
 pathway enzyme in a plant metabolic pathway. The methods and compositions  
 of the invention are useful for gene mapping, gene identification and  
 analysis, plant breeding and preparation of constructs for use in plant  
 gene expression and transgenic plants. This sequence represents cDNA  
 encoding a maize carbon assimilation pathway enzyme of the invention.  
 Note: The sequence data for this patent did not form part of the printed  
 specification but was obtained in electronic format from USPTO at  
 seqdata.uspto.gov/sequence.html.

SQ Sequence 229 BP; 49 A; 83 C; 67 G; 30 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 6.04e-14 Length: 229  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2  
 US-10-628-525A-34 (1-58) x ADP57015 (1-229)  
 Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 Db 52 ATGGCGCCACCGTGTATGATGGCTCGTCGCCACC----- 87  
 Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuIysSerThrAlaSerLeuProValAlaArg 40  
 Db 88 -----GCCGTGCTCGTTCCAGGGGCTCAAGTCCACCCGACCTCCCGTCGCCGC 141  
 Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGileArgCys 58  
 Db 142 CGTCTCTCCAGAGCCTCGGCACGTC---AGCACGGCGGAGAGATCCGGTGC 192  
 RESULT 6  
 ADP57195  
 ID ADP57195 standard; cDNA; 230 BP.  
 AC ADP57195;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Maize carbon assimilation pathway enzyme cDNA #264.  
 XX  
 KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphate; transketolase;  
 KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.  
 XX  
 OS Zea mays.  
 XX  
 XX US2004116682-A1.  
 XX  
 PD 17-JUN-2004.  
 XX  
 PD 16-NOV-2001; 2001US-00987899.  
 XX  
 PD 06-MAR-1998; 98US-0076912P.  
 PR  
 PR 04-MAR-1999; 99US-00262979.  
 XX  
 PA (CHEI/) CHEIKH N.  
 PA (MILL/) MILLER P W.  
 PA (OCON/) O'CONNELL K M.  
 PA (LIUJ/) LIU J.  
 XX  
 PI Cheikh N, Miller PW, O'connell KM, Liu J;  
 XX  
 DR WPI; 2004-498291/47.  
 XX  
 PT New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.  
 XX  
 PS Claim 2; SEQ ID NO 264; 196pp; English.  
 XX  
 XX



QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58  
 DB 137 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGATCCGGTGC 187

RESULT 8  
 ADP57001  
 ID ADP57001 standard; cDNA; 236 BP.  
 AC ADP57001;  
 XX  
 XX  
 XX 09-SEP-2004 (first entry)  
 XX  
 XX Maize carbon assimilation pathway enzyme cDNA #70.  
 XX  
 XX Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphate; transketolase;  
 KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.  
 XX Zea mays.  
 XX US2004116682-A1.  
 XX 17-JUN-2004.  
 XX 16-NOV-2001; 2001US-00987899.  
 XX 06-MAR-1998; 98US-0076912P.  
 XX 04-MAR-1999; 99US-00262979.  
 XX (CHEI/) CHEIKH N.  
 PA (MILL/) MILLER P W.  
 PA (OCON/) O'CONNELL K M.  
 PA (LIUJ/) LIU J.  
 XX  
 XX Cheikh N, Miller PW, O'connell KM, Liu J;  
 XX WPI; 2004-498291/47.  
 XX  
 XX New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.  
 XX  
 XX Claim 2; SEQ ID NO 70; 196pp; English.  
 XX  
 XX The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase,  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphate, transketolase,  
 CC transketolase, sedoheptulose-1,7-bisphosphate, D-ribulose-5-phosphate-3-  
 CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions

CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 XX seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 236 BP; 40 A; 90 C; 72 G; 34 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 6.27e-14 Length: 236  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP57001 (1-236)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 DB 13 ATGGCCGCCACCGTGATGAGTGGCTGTGCGCCACCC----- 48  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 DB 49 -----GCGGTGCTCGCTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCCGCCGC 102  
 QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58  
 DB 103 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGATCCGGTGC 153

RESULT 9  
 ADP56997  
 ID ADP56997 standard; cDNA; 238 BP.  
 XX  
 AC ADP56997;  
 XX  
 XX 09-SEP-2004 (first entry)  
 XX  
 XX Maize carbon assimilation pathway enzyme cDNA #66.  
 XX  
 KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphate; transketolase;  
 KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.  
 XX Zea mays.  
 XX US2004116682-A1.  
 XX 17-JUN-2004.  
 XX 16-NOV-2001; 2001US-00987899.  
 XX 06-MAR-1998; 98US-0076912P.  
 XX 04-MAR-1999; 99US-00262979.  
 XX (CHEI/) CHEIKH N.  
 PA (MILL/) MILLER P W.  
 PA (OCON/) O'CONNELL K M.  
 PA (LIUJ/) LIU J.  
 XX  
 XX Cheikh N, Miller PW, O'connell KM, Liu J;  
 XX WPI; 2004-498291/47.



XX New substantially purified nucleic acid molecule encoding a maize or  
PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
PT identification and analysis, plant breeding, and preparation of  
PT constructs.  
XX Claim 2; SEQ ID NO 66; 196pp; English.  
PS  
XX  
CC The invention relates to a substantially purified nucleic acid molecule  
CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
CC fragment is selected from ribulose-bisphosphate carboxylase,  
CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,  
CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3  
CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
CC substantially purified antibody or its fragment which is capable of  
CC specifically binding to a specific maize or soybean carbon assimilation  
CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
CC molecule comprising an exogenous promoter region which functions in a  
CC plant cell to cause the production of an mRNA molecule, and a method of  
CC determining a level or pattern in a plant cell of a carbon assimilation  
CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
CC of the invention are useful for gene mapping, gene identification and  
CC analysis, plant breeding and preparation of constructs for use in plant  
CC gene expression and transgenic plants. This sequence represents cDNA  
CC encoding a maize carbon assimilation pathway enzyme of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 238 BP; 41 A; 90 C; 73 G; 34 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 6,34e-14 Length: 238  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56997 (1-238)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 14 ATGGGCGCCACCGTGATGATGGCTCGTGGCCACC----- 49  
QY 21 AlaSerAlaValAlaProPhcGInGlyLeuYsSerThrAlaSerIeuProValAlaArg 40  
Db 50 -----GCCGTGCGTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCCCGCC 103  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 104 CGCTCTCCAGAGGCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 154

RESULT 10  
ADP57002  
ID ADP57002 standard; cDNA; 249 BP.  
XX  
AC ADP57002;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Maize carbon assimilation pathway enzyme cDNA #71.  
XX  
KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
KW aldolase; fructose-1,6-bisphosphatase; transketolase;

KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
KW aspartate aminotransferase; alanine aminotransferase;  
KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
KW plant metabolic pathway; plant breeding.  
XX  
XX Zea mays.  
OS  
XX US2004116682-A1.  
PN  
XX 17-JUN-2004.  
PD  
XX 16-NOV-2001; 2001US-00987899.  
PP  
XX 06-MAR-1998; 98US-0076912P.  
PR  
XX 04-MAR-1999; 99US-00262979.  
PR  
XX (CHEI/) CHEIKH N.  
PA (MILL/) MILLER P W.  
PA (OCON/) O'CONNELL K M.  
PA (LIU/) LIU J.  
XX  
XX Cheikh N, Miller PW, O'connell KM, Liu J;  
PI WPI; 2004-498291/47.  
DR  
XX New substantially purified nucleic acid molecule encoding a maize or  
XX soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
XX identification and analysis, plant breeding, and preparation of  
XX constructs.  
XX Claim 2; SEQ ID NO 71; 196pp; English.  
XX  
CC The invention relates to a substantially purified nucleic acid molecule  
CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
CC fragment is selected from ribulose-bisphosphate carboxylase,  
CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,  
CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3  
CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
CC substantially purified antibody or its fragment which is capable of  
CC specifically binding to a specific maize or soybean carbon assimilation  
CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
CC molecule comprising an exogenous promoter region which functions in a  
CC plant cell to cause the production of an mRNA molecule, and a method of  
CC determining a level or pattern in a plant cell of a carbon assimilation  
CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
CC of the invention are useful for gene mapping, gene identification and  
CC analysis, plant breeding and preparation of constructs for use in plant  
CC gene expression and transgenic plants. This sequence represents cDNA  
CC encoding a maize carbon assimilation pathway enzyme of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 249 BP; 51 A; 91 C; 73 G; 34 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 6.69e-14 Length: 249  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP57002 (1-249)



QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 Db 50 ATGGCGCCACCGTGATGCGCTCGTGGCCACC----- 85  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
 Db 86 -----GCCGTGCGTCCGTTCCAGGGGCTCAAGTCCACCGCAGCTCCCGTGGCCGC 139  
 QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGileArgCys 58  
 Db 140 CGTCTCTCCAGAGCTTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 190  
 RESULT 11  
 ADP56984 standard; cDNA; 264 BP.  
 XX AC ADP56984;  
 XX DT 09-SEP-2004 (first entry)  
 XX DE Maize carbon assimilation pathway enzyme cDNA #53.  
 XX KW Carbon assimilation pathway enzyme; Gene: ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphate; transketolase;  
 KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxylase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.  
 XX OS Zea mays.  
 XX PN US2004116682-A1.  
 XX PD 17-JUN-2004.  
 XX PF 16-NOV-2001; 2001US-00987899.  
 XX PR 06-MAR-1998; 98US-0076912P.  
 XX PR 04-MAR-1999; 99US-00262979.  
 XX PA (CHEI/) CHEIKH N.  
 XX PA (MILL/) MILLER P W.  
 XX PA (OCON/) O'CONNELL K M.  
 XX PA (LIU/) LIU J.  
 XX PI Cheikh N, Miller PW, O'Connell KM, Liu J;  
 XX WI; 2004-498291/47.  
 XX PT New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.  
 XX PS Claim 2; SEQ ID NO 53; 196pp; English.  
 XX CC The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase, triose  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphate, transketolase,  
 CC sedoheptulose-1,7-bisphosphate, D-ribulose-5-phosphate-3-epimerase,  
 CC ribose-5-phosphate isomerase, ribose-5-phosphate kinase, NADP-dependent  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxylase, pyruvate,

CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX SQ Sequence 264 BP; 52 A; 96 C; 79 G; 37 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 7.19e-14 Length: 264  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2  
 US-10-628-525A-34 (1-58) x ADP56984 (1-264)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 Db 46 ATGGCGCCACCGTGATGCGCTCGTGGCCACC----- 81  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
 Db 82 -----GCCGTGCGTCCGTTCCAGGGGCTCAAGTCCACCGCAGCTCCCGTGGCCGC 135  
 QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGileArgCys 58  
 Db 136 CGTCTCTCCAGAGCTTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 186  
 RESULT 12  
 ADP56971 standard; cDNA; 265 BP.  
 XX AC ADP56971;  
 XX DT 09-SEP-2004 (first entry)  
 XX DE Maize carbon assimilation pathway enzyme cDNA #40.  
 XX KW Carbon assimilation pathway enzyme; Gene: ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphate; transketolase;  
 KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxylase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.  
 XX OS Zea mays.  
 XX PN US2004116682-A1.  
 XX PD 17-JUN-2004.  
 XX PF 16-NOV-2001; 2001US-00987899.  
 XX PR 06-MAR-1998; 98US-0076912P.  
 XX PR 04-MAR-1999; 99US-00262979.  
 XX

PA (CHEI/) CHEIKH N.  
 PA (MILL/) MILLER P W.  
 PA (OCON/) O'CONNELL K M.  
 PA (LIU/) LIU J.  
 XX  
 PI Cheikh N, Miller PW, O'connell KM, Liu J;  
 XX WPI; 2004-498291/47.  
 DR  
 XX New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.  
 PS Claim 2; SEQ ID NO 40; 196pp; English.  
 XX  
 CC The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase,  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase, D-ribulose-5-phosphate-3-  
 CC transketolase, sedoheptulose-1,7-bisphosphatase, fructose-1,6-bisphosphatase,  
 CC -epimerase, ribulose-5-phosphate isomerase, ribulose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 265 BP; 46 A; 96 C; 83 G; 40 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 7.22e-14 Length: 265  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2  
 US-10-628-525A-34 (1-58) x ADP56971 (1-265)  
 Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 Db 21 ATGGGCGCCACCGTGTATGTATGGCTCTCGTGGCCACC----- 56  
 Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 Db 57 -----GCCCTGCTCGTCTCCAGGGGCTCAAGTCCAGCCAGCTCCCGTCCGCGC 110  
 Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 Db 111 CGCTCTCTCAGAAGCCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 161  
 RESULT 13  
 ADP56976  
 ID ADP56976 standard; cDNA; 272 BP.  
 XX  
 AC ADP56976;  
 XX

DT 09-SEP-2004 (first entry)  
 XX Maize carbon assimilation pathway enzyme cDNA #45.  
 XX  
 KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphatase; transketolase;  
 KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
 KW ribulose-5-phosphate isomerase; ribulose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.  
 XX  
 OS Zea mays.  
 XX  
 XX US2004116682-A1.  
 PN  
 XX 17-JUN-2004.  
 PD  
 XX 16-NOV-2001; 2001US-00987899.  
 PF  
 XX 06-MAR-1998; 98US-0076912P.  
 PR  
 XX 04-MAR-1999; 99US-00262979.  
 PR  
 XX (CHEI/) CHEIKH N.  
 PA (MILL/) MILLER P W.  
 PA (OCON/) O'CONNELL K M.  
 PA (LIU/) LIU J.  
 XX  
 PI Cheikh N, Miller PW, O'connell KM, Liu J;  
 XX WPI; 2004-498291/47.  
 DR  
 XX New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.  
 PS Claim 2; SEQ ID NO 45; 196pp; English.  
 XX  
 CC The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase,  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,  
 CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3-  
 CC -epimerase, ribulose-5-phosphate isomerase, ribulose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 272 BP; 54 A; 97 C; 82 G; 39 T; 0 U; 0 Other;  
 Alignment Scores:

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Pred. No.: 7 46e-14 Length: 272
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56976 (1-272)

Qy 1 MetaAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 43 ATGGCGCCACCGTGATGATGGCTCGTCCGCCACC----- 78

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 79 -----GCCGTGCTCGTTCAGGGGCTCAGTCCACCGCCAGCTCCCGCTCGGCCGC 132

Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58
Db 133 CGTCTCTCCAGAGCTTCGCCAACGTC---AGCACGGCGGAGGATCCGGTGC 183

RESULT 14
ADP56957
ID ADP56957 standard; cDNA; 276 BP.
XX
AC ADP56957;
XX
DT 09-SEP-2004 (first entry)
XX
DE Maize carbon assimilation pathway enzyme cDNA #26.
XX
KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;
KW ribulose-bisphosphate carboxylase; gene; ss; maize; corn;
KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;
KW aldolase; fructose-1,6-bisphosphate; transketolase;
KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;
KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;
KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;
KW aspartate aminotransferase; alanine aminotransferase;
KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;
KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;
KW plant metabolic pathway; plant breeding.
OS Zea mays.
XX
XX US2004116682-A1.
XX
PD 17-JUN-2004.
XX
PF 16-NOV-2001; 2001US-00987899.
XX
PR 06-MAR-1998; 98US-0076912P.
PR 04-MAR-1999; 99US-00262979.
XX
PA (CHEI/) CHEIKH N.
PA (MILL/) MILLER P W.
PA (OCON/) O'CONNELL K M.
PA (LIU/) LIU J.
XX
XX Cheikh N, Miller PW, O'Connell KM, Liu J;
XX WPI; 2004-498291/47.
XX
XX New substantially purified nucleic acid molecule encoding a maize or
PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene
PT identification and analysis, plant breeding, and preparation of
PT constructs.
XX
XX Claim 2; SEQ ID NO 26; 196pp; English.
XX
XX The invention relates to a substantially purified nucleic acid molecule
CC that encodes a maize or soybean carbon assimilation pathway enzyme or its
CC fragment. The maize or soybean carbon assimilation pathway enzyme or its

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CC fragment is selected from ribulose-bisphosphate carboxylase,
CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose
CC phosphate isomerase, aldolase, fructose-1,6-bisphosphate,
CC transketolase, sedoheptulose-1,7-bisphosphate, D-ribulose-5-phosphate-3-
CC epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,
CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,
CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent
CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,
CC phosphate dikinase and pyrophosphatase. The invention also relates to a
CC substantially purified antibody or its fragment which is capable of
CC specifically binding to a specific maize or soybean carbon assimilation
CC pathway enzyme or its fragment, a transformed plant having a nucleic acid
CC molecule comprising an exogenous promoter region which functions in a
CC plant cell to cause the production of an mRNA molecule, and a method of
CC determining a level or pattern in a plant cell of a carbon assimilation
CC pathway enzyme in a plant metabolic pathway. The methods and compositions
CC of the invention are useful for gene mapping, gene identification and
CC analysis, plant breeding and preparation of constructs for use in plant
CC gene expression and transgenic plants. This sequence represents cDNA
CC encoding a maize carbon assimilation pathway enzyme of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 276 BP; 54 A; 98 C; 84 G; 40 T; 0 U; 0 Other;

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Alignment Scores:
Pred. No.: 7 59e-14 Length: 276
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 12 Gaps: 2

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US-10-628-525A-34 (1-58) x ADP56957 (1-276)

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Qy 1 MetaAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 41 ATGGCGCCACCGTGATGATGGCTCGTCCGCCACC----- 76

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 77 -----GCCGTGCTCGTTCAGGGGCTCAGTCCACCGCCAGCTCCCGCTCGGCCGC 130

Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58
Db 131 CGTCTCTCCAGAGCTTCGCCAACGTC---AGCACGGCGGAGGATCCGGTGC 181

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RESULT 15

ADP56982

ID ADP56982 standard; cDNA; 276 BP.

XX

AC ADP56982;

XX

DT 09-SEP-2004 (first entry)

XX

DE Maize carbon assimilation pathway enzyme cDNA #51.

XX

```

KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;
KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;
KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;
KW aldolase; fructose-1,6-bisphosphate; transketolase;
KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;
KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;
KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;
KW aspartate aminotransferase; alanine aminotransferase;
KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;
KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;
KW plant metabolic pathway; plant breeding.

```

OS Zea mays.

XX

XX US2004116682-A1.

PN



CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.

XX  
 SQ Sequence 284 BP; 58 A; 100 C; 86 G; 40 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 7.86e-14 Length: 284  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56968 (1-284)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 Db 50 ATGGCGCCACCGTGATGGCTCTCGGCCACC----- 85

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 86 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCAGCTCCCGTCCCGCGC 139

Qy 41 ArgSerArgSerLeuGlyAenValAlaSerAenGlyArgGlyArgCys 58  
 |||||  
 Db 140 CGCTCTCTCCAGAGCCCTCGGCAAGTC---AGCAACGCGGAGGATCCGGTGC 190

RESULT 17

ADP56968  
 ID ADP56968 standard; cDNA; 286 BP.

XX AC ADP56968;

XX DT 09-SEP-2004 (first entry)

XX DE Maize carbon assimilation pathway enzyme cDNA #37.

XX KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphate; transketolase;  
 KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.

XX OS Zea mays.

XX PN US2004116682-A1.

XX PD 17-JUN-2004.

XX PF 16-NOV-2001; 2001US-00987899.

XX PR 06-MAR-1998; 98US-0076912P.

XX PR 04-MAR-1999; 99US-00262979.

XX PA (CHEI/) CHEIKH N.

XX PA (MILL/) MILLER P W.

XX PA (OCON/) O'CONNELL K M.

XX PA (LIUJ/) LIU J.

XX PI Cheikh N, Miller PW, O'connell KM, Liu J;

XX DR WPI; 2004-498291/47.

XX PT New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene

PT identification and analysis, plant breeding, and preparation of  
 PT constructs.

PS Claim 2; SEQ ID NO 37; 196pp; English.

XX  
 CC The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase,  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase, transketolase,  
 CC sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3-  
 CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.

XX SQ Sequence 286 BP; 58 A; 102 C; 85 G; 41 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7.93e-14 Length: 286  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56968 (1-286)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20

Db 48 ATGGCGCCACCGTGATGGCTCTCGGCCACC----- 83

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40

Db 84 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCAGCTCCCGTCCCGCGC 137

Qy 41 ArgSerArgSerLeuGlyAenValAlaSerAenGlyArgGlyArgCys 58

Db 138 CGCTCTCTCAGAGCCCTCGGCAAGTC---AGCAACGCGGAGGATCCGGTGC 188

RESULT 18

ADP56978

ID ADP56978 standard; cDNA; 291 BP.

XX AC ADP56978;

XX DT 09-SEP-2004 (first entry)

XX DE Maize carbon assimilation pathway enzyme cDNA #47.

XX KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphate; transketolase;  
 KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;

KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.  
 XX  
 OS Zea mays.  
 XX US2004116682-A1.  
 XX 17-JUN-2004.  
 XX PF 16-NOV-2001; 2001US-00987899.  
 XX PR 06-MAR-1998; 98US-0076912P.  
 XX PR 04-MAR-1999; 99US-00262979.  
 XX PA (CHEI/) CHEIKH N.  
 XX PA (MILL/) MILLER P W.  
 XX PA (OCON/) O'CONNELL K M.  
 XX PA (LIU/) LIU J.  
 XX PI Cheikh N, Miller PW, O'connell KM, Liu J;  
 XX WPI; 2004-498291/47.  
 XX DR New substantially purified nucleic acid molecule encoding a maize or  
 XX soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.  
 PT  
 XX Claim 2; SEQ ID NO 47; 196pp; English.  
 XX  
 CC The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase,  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase, D-ribulose-5-phosphate-3  
 CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate kinase,  
 CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 291 BP; 57 A; 105 C; 88 G; 41 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: Length: 291  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2  
 US-10-628-525a-34 (1-58) x ADP56978 (1-291)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 57 ATGGGGCCACCGTGATGATGCTCGTGGCCACC----- 92  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuIysSerThrAlaSerLeuProValAlaArg 40  
 Db 93 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 146  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 Db 147 CGCTCTCTCCAGGAGCTCGGCAACGTC----AGCAACGGCGGAGGATCCGGTGC 197  
 RESULT 19  
 ADP56945  
 ID ADP56945 standard; cDNA; 297 BP.  
 XX  
 AC ADP56945;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Maize carbon assimilation pathway enzyme cDNA #14.  
 XX  
 KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphate; transketolase;  
 KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.  
 XX  
 OS Zea mays.  
 XX US2004116682-A1.  
 XX 17-JUN-2004.  
 XX PF 16-NOV-2001; 2001US-00987899.  
 XX PR 06-MAR-1998; 98US-0076912P.  
 XX PR 04-MAR-1999; 99US-00262979.  
 XX PA (CHEI/) CHEIKH N.  
 XX PA (MILL/) MILLER P W.  
 XX PA (OCON/) O'CONNELL K M.  
 XX PA (LIU/) LIU J.  
 XX PI Cheikh N, Miller PW, O'connell KM, Liu J;  
 XX WPI; 2004-498291/47.  
 XX  
 CC New substantially purified nucleic acid molecule encoding a maize or  
 CC soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.  
 PT  
 XX Claim 2; SEQ ID NO 14; 196pp; English.  
 XX  
 CC The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase,  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase, D-ribulose-5-phosphate-3  
 CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate kinase,  
 CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation



CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.

SQ Sequence 297 BP; 51 A; 108 C; 92 G; 46 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.3e-14 Length: 297  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56945 (1-297)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 DB 12 ATGGGCCCCACCGTGATGATGGCTCGTCGCCACCC----- 47  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 DB 48 -----GCCGTCGCTCGTTCAGGGGCTCAGTCCACCCGAGCTCCCGTCGCCCGC 101  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58  
 DB 102 CGCTCTCTCCAGAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 152

RESULT 20

ADP56952

ID ADP56952 standard; cDNA; 298 BP.

AC ADP56952;

XX 09-SEP-2004 (first entry)

DE Maize carbon assimilation pathway enzyme cDNA #21.

XX Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphate; transketolase;  
 KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate kinase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate-3-epimerase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxylase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.

XX Zea mays.

XX US200411682-A1.

XX 17-JUN-2004.

XX 16-NOV-2001; 2001US-00987899.

XX 06-MAR-1998; 98US-0076912P.

XX 04-MAR-1999; 99US-00262979.

XX (CHEI/) CHEIKH N.

XX (MILL/) MILLER P W.

XX (OCON/) O'CONNELL K M.

PA (LIU/) LIU J.

XX Cheikh N, Miller PW, O'Connell KM, Liu J;

XX WPI; 2004-498291/47.

XX New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.

XX Claim 2; SEQ ID NO 21; 196pp; English.

XX The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase, triose  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,  
 CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate kinase,  
 CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxylase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.

SQ Sequence 298 BP; 60 A; 106 C; 90 G; 42 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.33e-14 Length: 298  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56952 (1-298)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20

DB 48 ATGGGCCCCACCGTGATGATGGCTCGTCGCCACCC----- 83

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40

DB 84 -----GCCGTCGCTCGTTCAGGGGCTCAGTCCACCCGAGCTCCCGTCGCCCGC 137

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58

DB 138 CGCTCTCTCCAGAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 188

RESULT 21

ADP56947

ID ADP56947 standard; cDNA; 305 BP.

XX ADP56947;

XX 09-SEP-2004 (first entry)

XX Maize carbon assimilation pathway enzyme cDNA #16.



XX Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphatase; transketolase;  
 KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.  
 XX Zea mays.  
 XX US2004116682-A1.  
 XX 17-JUN-2004.  
 XX 16-NOV-2001; 2001US-00987899.  
 XX 06-MAR-1998; 98US-0076912P.  
 XX 04-MAR-1999; 99US-00262979.  
 XX (CHEI/) CHEIKH N.  
 XX (MILL/) MILLER P W.  
 XX (OCON/) O'CONNELL K M.  
 XX (LIU/) LIU J.  
 XX Cheikh N, Miller PW, O'connell KM, Liu J;  
 XX WPI; 2004-498291/47.  
 XX New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.  
 PS Claim 2; SEQ ID NO 16; 196pp; English.  
 XX The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase, triose  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase, D-ribulose-5-phosphate-3-  
 CC epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: the sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX Sequence 305 BP; 59 A; 109 C; 92 G; 45 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 8,57e-14 Length: 305  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0

Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2  
 US-10-628-525A-34 (1-58) x ADP56947 (1-305)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAenProAlaGln 20  
 DB 42 ATGGGGCCACCGTGATGATGCGCTCGTCGGCCACC----- 77  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 DB 78 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 131  
 QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58  
 DB 132 CGCTCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 182  
 RESULT 22  
 ADP56960  
 ID ADP56960 standard; cDNA; 307 BP.  
 XX AC ADP56960;  
 XX 09-SEP-2004 (first entry)  
 XX Maize carbon assimilation pathway enzyme cDNA #29.  
 KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphatase; transketolase;  
 KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.  
 XX Zea mays.  
 XX US2004116682-A1.  
 XX 17-JUN-2004.  
 XX 16-NOV-2001; 2001US-00987899.  
 XX 06-MAR-1998; 98US-0076912P.  
 XX 04-MAR-1999; 99US-00262979.  
 XX (CHEI/) CHEIKH N.  
 XX (MILL/) MILLER P W.  
 XX (OCON/) O'CONNELL K M.  
 XX (LIU/) LIU J.  
 XX Cheikh N, Miller PW, O'connell KM, Liu J;  
 XX WPI; 2004-498291/47.  
 XX New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.  
 PS Claim 2; SEQ ID NO 29; 196pp; English.  
 XX The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase, triose  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase, D-ribulose-5-phosphate-3-  
 CC epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: the sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX Sequence 305 BP; 59 A; 109 C; 92 G; 45 T; 0 U; 0 Other;

transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3-epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase, phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase, aspartate aminotransferase, alanine aminotransferase, NADP-dependent malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate, phosphate dikinase and pyrophosphatase. The invention also relates to a substantially purified antibody or its fragment which is capable of specifically binding to a specific maize or soybean carbon assimilation pathway enzyme or its fragment, a transformed plant having a nucleic acid molecule comprising an exogenous promoter region which functions in a plant cell to cause the production of an mRNA molecule, and a method of determining a level or pattern in a plant cell of a carbon assimilation pathway enzyme in a plant metabolic pathway. The methods and compositions of the invention are useful for gene mapping, gene identification and analysis, plant breeding and preparation of constructs for use in plant gene expression and transgenic plants. This sequence represents cDNA encoding a maize carbon assimilation pathway enzyme of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 307 BP; 63 A; 107 C; 93 G; 44 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.64e-14 Length: 307  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56946 (1-307)

QY 1 MetaAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 DB 50 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 85  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40  
 DB 86 -----GCCGTGCTCGTCTCCAGGGGGCTCAAGTCCACCGCCAGCTCCCGTGGCCGC 139  
 QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 DB 140 CGCTCTCTCAGAGCCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 190

RESULT 23

ID ADP56946 standard; cDNA; 309 BP.

AC ADP56946;

XX 09-SEP-2004 (first entry)  
 DT  
 XX  
 DE Maize carbon assimilation pathway enzyme cDNA #15.  
 DE  
 XX

Carbon assimilation pathway enzyme; Gene; ss; maize; corn;  
 ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 aldolase; fructose-1,6-bisphosphatase; transketolase;  
 sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
 ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 aspartate aminotransferase; alanine aminotransferase;  
 NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 plant metabolic pathway; plant breeding.

XX Zea mays.

XX US2004116682-A1.

XX 17-JUN-2004.

XX

PF 16-NOV-2001; 2001US-00987899.  
 XX  
 PR 06-MAR-1998; 98US-0076912P.  
 PR 04-MAR-1999; 99US-00262979.  
 XX  
 PA (CHEI/) CHEIKH N.  
 PA (MILL/) MILLER P W.  
 PA (OCON/) O'CONNELL K M.  
 PA (LIUJ/) LIU J.

PI Cheikh N, Miller PW, O'Connell KM, Liu J;  
 XX WPI; 2004-498291/47.  
 DR

XX New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.

XX Claim 2; SEQ ID NO 15; 196pp; English.

XX The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase,  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,  
 CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3-  
 CC epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.

XX SQ Sequence 309 BP; 62 A; 110 C; 92 G; 45 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.71e-14 Length: 309  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56946 (1-309)

QY 1 MetaAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 DB 48 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 83  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40  
 DB 84 -----GCCGTGCTCGTCTCCAGGGGGCTCAAGTCCACCGCCAGCTCCCGTGGCCGC 137  
 QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 DB 138 CGCTCTCTCAGAGCCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 188

RESULT 24

ADP56961  
ID ADP56961 standard; cDNA; 311 BP.  
AC ADP56961;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Maize carbon assimilation pathway enzyme cDNA #30.  
XX  
KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
KW aldolase; fructose-1,6-bisphosphate; transketolase;  
KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;  
KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
KW aspartate aminotransferase; alanine aminotransferase;  
KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
KW plant metabolic pathway; plant breeding.  
XX  
OS Zea mays.  
XX  
XX US2004116682-A1.  
XX  
XX 17-JUN-2004.  
XX  
XX 16-NOV-2001; 2001US-00987899.  
XX  
XX 06-MAR-1998; 98US-0076912P.  
XX  
XX 04-MAR-1999; 99US-00262979.  
XX  
XX (CHEI/) CHEIKH N.  
XX (MILL/) MILLER P W.  
XX (OCON/) O'CONNELL K M.  
XX (LIUJ/) LIU J.  
XX  
XX Cheikh N, Miller PW, O'connell KM, Liu J;  
XX WPI; 2004-498291/47.  
XX  
XX New substantially purified nucleic acid molecule encoding a maize or  
XX soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
XX identification and analysis, plant breeding, and preparation of  
XX constructs.  
XX  
XX Claim 2; SEQ ID NO 30; 196pp; English.  
XX  
XX The invention relates to a substantially purified nucleic acid molecule  
XX that encodes a maize or soybean carbon assimilation pathway enzyme or its  
XX fragment. The maize or soybean carbon assimilation pathway enzyme or its  
XX fragment is selected from ribulose-bisphosphate carboxylase,  
XX phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
XX phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,  
XX transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3  
XX -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
XX phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
XX aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
XX malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
XX phosphate dikinase and pyrophosphatase. The invention also relates to a  
XX substantially purified antibody or its fragment which is capable of  
XX specifically binding to a specific maize or soybean carbon assimilation  
XX pathway enzyme or its fragment, a transformed plant having a nucleic acid  
XX molecule comprising an exogenous promoter region which functions in a  
XX plant cell to cause the production of an mRNA molecule, and a method of  
XX determining a level or pattern in a plant cell of a carbon assimilation  
XX pathway enzyme in a plant metabolic pathway. The methods and compositions  
XX of the invention are useful for gene mapping, gene identification and  
XX analysis, plant breeding and preparation of constructs for use in plant  
XX gene expression and transgenic plants. This sequence represents cDNA  
XX encoding a maize carbon assimilation pathway enzyme of the invention.  
XX Note: The sequence data for this patent did not form part of the printed  
XX specification but was obtained in electronic format from USPTO at

CC seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 311 BP; 60 A; 113 C; 93 G; 45 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 8.78e-14 Length: 311  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 12 Gaps: 2  
XX  
US-10-628-525A-34 (1-58) x ADP56961 (1-311)  
QY 1 MetaAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
DB 42 ATGGCGCCACCGTGTATGATGCGCTCGTGGCCACC----- 77  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
DB 78 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGGCTCCCGTGGCCGC 131  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
DB 132 CGCTCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 182  
RESULT 25  
ADP56999  
ID ADP56999 standard; cDNA; 312 BP.  
XX  
AC ADP56999;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Maize carbon assimilation pathway enzyme cDNA #68.  
XX  
KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
KW aldolase; fructose-1,6-bisphosphate; transketolase;  
KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
KW aspartate aminotransferase; alanine aminotransferase;  
KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
KW plant metabolic pathway; plant breeding.  
XX  
XX Zea mays.  
XX  
XX US2004116682-A1.  
XX  
XX 17-JUN-2004.  
XX  
XX 16-NOV-2001; 2001US-00987899.  
XX  
XX 06-MAR-1998; 98US-0076912P.  
XX  
XX 04-MAR-1999; 99US-00262979.  
XX  
XX (CHEI/) CHEIKH N.  
XX (MILL/) MILLER P W.  
XX (OCON/) O'CONNELL K M.  
XX (LIUJ/) LIU J.  
XX  
XX Cheikh N, Miller PW, O'connell KM, Liu J;  
XX WPI; 2004-498291/47.  
XX  
XX New substantially purified nucleic acid molecule encoding a maize or  
XX soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
XX identification and analysis, plant breeding, and preparation of  
XX constructs.

PS Claim 2; SEQ ID NO 68; 196pp; English.

XX The invention relates to a substantially purified nucleic acid molecule

CC that encodes a maize or soybean carbon assimilation pathway enzyme or its

CC fragment. The maize or soybean carbon assimilation pathway enzyme or its

CC fragment is selected from ribulose-bisphosphate carboxylase,

CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose

CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,

CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3

CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,

CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,

CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent

CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,

CC phosphate dikinase and pyrophosphatase. The invention also relates to a

CC substantially purified antibody or its fragment which is capable of

CC specifically binding to a specific maize or soybean carbon assimilation

CC pathway enzyme or its fragment, a transformed plant having a nucleic acid

CC molecule comprising an exogenous promoter region which functions in a

CC plant cell to cause the production of an mRNA molecule, and a method of

CC determining a level or pattern in a plant cell of a carbon assimilation

CC pathway enzyme in a plant metabolic pathway. The methods and compositions

CC of the invention are useful for gene mapping, gene identification and

CC analysis, plant breeding and preparation of constructs for use in plant

CC gene expression and transgenic plants. This sequence represents cDNA

CC encoding a maize carbon assimilation pathway enzyme of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification but was obtained in electronic format from USPTO at

CC seqdata.uspto.gov/sequence.html.

XX

SQ Sequence 312 BP; 63 A; 105 C; 92 G; 49 T; 0 U; 3 Other;

Alignment Scores:

|                        |          |               |     |
|------------------------|----------|---------------|-----|
| Pred. No.:             | 8.91e-14 | Length:       | 312 |
| Score:                 | 203.50   | Matches:      | 47  |
| Percent Similarity:    | 81.0%    | Conservative: | 0   |
| Best Local Similarity: | 81.0%    | Mismatches:   | 0   |
| Query Match:           | 72.2%    | Indels:       | 11  |
| DB:                    | 12       | Gaps:         | 2   |

US-10-628-525A-34 (1-58) x ADP56999 (1-312)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20

DB 43 ATGGCGCCACCGTGATGATGGCTCGTCGGCACC----- 78

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40

DB 79 -----GCCGTGCTCGTTTCAGGGGCTCAATCCACCGCCAGCTCCCGTCGCCCGC 132

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyCys 58

DB 133 CGCTCTCCAGAGCCTCGGCACACGTC---AGCAACGGCGGAGGATCCGGTGC 183

RESULT 26

ADP56942

ID ADP56942 standard; cDNA; 315 BP.

XX

AC ADP56942;

XX

DT 09-SEP-2004 (first entry)

XX

DE Maize carbon assimilation pathway enzyme cDNA #11.

XX

XX Carbon assimilation pathway enzyme; gene; ss; maize; corn;

KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;

KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;

KW aldolase; fructose-1,6-bisphosphatase; transketolase;

KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;

KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;

KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;

KW aspartate aminotransferase; alanine aminotransferase;

KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;

KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;

KW

plant metabolic pathway; plant breeding.

Zea mays.

US2004116682-A1.

17-JUN-2004.

16-NOV-2001; 2001US-00987899.

06-MAR-1998; 98US-0076912P.

04-MAR-1999; 99US-00262979.

(CHEI/) CHEIKH N.

(MILL/) MILLER P W.

(OCON/) O'CONNELL K M.

(LIUJ/) LIU J.

Cheikh N, Miller PW, O'connell KM, Liu J;

WPI; 2004-498291/47.

New substantially purified nucleic acid molecule encoding a maize or

soybean carbon assimilation pathway enzyme, useful for gene mapping, gene

identification and analysis, plant breeding, and preparation of

constructs.

Claim 2; SEQ ID NO 11; 196pp; English.

The invention relates to a substantially purified nucleic acid molecule

that encodes a maize or soybean carbon assimilation pathway enzyme or its

fragment. The maize or soybean carbon assimilation pathway enzyme or its

fragment is selected from ribulose-bisphosphate carboxylase,

phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose

phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,

transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3

-epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,

phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,

aspartate aminotransferase, alanine aminotransferase, NADP-dependent

malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,

phosphate dikinase and pyrophosphatase. The invention also relates to a

substantially purified antibody or its fragment which is capable of

specifically binding to a specific maize or soybean carbon assimilation

pathway enzyme or its fragment, a transformed plant having a nucleic acid

molecule comprising an exogenous promoter region which functions in a

plant cell to cause the production of an mRNA molecule, and a method of

determining a level or pattern in a plant cell of a carbon assimilation

pathway enzyme in a plant metabolic pathway. The methods and compositions

of the invention are useful for gene mapping, gene identification and

analysis, plant breeding and preparation of constructs for use in plant

gene expression and transgenic plants. This sequence represents cDNA

encoding a maize carbon assimilation pathway enzyme of the invention.

Note: The sequence data for this patent did not form part of the printed

specification but was obtained in electronic format from USPTO at

seqdata.uspto.gov/sequence.html.

XX

SQ Sequence 315 BP; 62 A; 113 C; 94 G; 46 T; 0 U; 0 Other;

Alignment Scores:

|                        |          |               |     |
|------------------------|----------|---------------|-----|
| Pred. No.:             | 8.92e-14 | Length:       | 315 |
| Score:                 | 203.50   | Matches:      | 47  |
| Percent Similarity:    | 81.0%    | Conservative: | 0   |
| Best Local Similarity: | 81.0%    | Mismatches:   | 0   |
| Query Match:           | 72.2%    | Indels:       | 11  |
| DB:                    | 12       | Gaps:         | 2   |

US-10-628-525A-34 (1-58) x ADP56942 (1-315)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20

DB 48 ATGGCGCCACCGTGATGATGGCTCGTCGGCACC----- 83

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40

Db 84 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTGGCCGC 137  
QY 41 ArgSerSerArgSerLeuGlyValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 138 CGCTCTCTCAGAGCCTCGGCAACGTC---AGCAACGGCGAAGGATCCGGTGC 188  
RESULT 27  
ADP56941  
ID ADP56941 standard; cDNA; 317 BP.  
XX ADP56941;  
AC ADP56941;  
DT 09-SEP-2004 (first entry)  
DE Maize carbon assimilation pathway enzyme cDNA #10.  
XX  
KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
KW aldolase; fructose-1,6-bisphosphate; transketolase;  
KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;  
KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
KW aspartate aminotransferase; alanine aminotransferase;  
KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
KW plant metabolic pathway; plant breeding.  
XX  
OS Zea mays.  
XX  
XX US2004116682-A1.  
XX  
PD 17-JUN-2004.  
XX  
PF 16-NOV-2001; 2001US-00987899.  
XX  
PR 06-MAR-1998; 98US-0076912P.  
PR 04-MAR-1999; 99US-00262979.  
XX  
XX (CHEI/) CHEIKH N.  
PA (MILL/) MILLER P W.  
PA (OCON/) O'CONNELL K M.  
PA (LIUJ/) LIU J.  
XX  
PI Cheikh N, Miller PW, O'connell KM, Liu J;  
XX  
XX WPI; 2004-498291/47.  
XX  
PT New substantially purified nucleic acid molecule encoding a maize or  
PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
PT identification and analysis, plant breeding, and preparation of  
PT constructs.  
XX  
PS Claim 2; SEQ ID NO 10; 196pp; English.  
XX  
CC The invention relates to a substantially purified nucleic acid molecule  
CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
CC fragment is selected from ribulose-bisphosphate carboxylase,  
CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
CC phosphate isomerase, aldolase, fructose-1,6-bisphosphate,  
CC transketolase, sedoheptulose-1,7-bisphosphate, D-ribulose-5-phosphate-3-  
CC epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
CC substantially purified antibody or its fragment which is capable of  
CC specifically binding to a specific maize or soybean carbon assimilation  
CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
CC molecule comprising an exogenous promoter region which functions in a  
CC plant cell to cause the production of an mRNA molecule, and a method of

CC determining a level or pattern in a plant cell of a carbon assimilation  
CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
CC of the invention are useful for gene mapping, gene identification and  
CC analysis, plant breeding and preparation of constructs for use in plant  
CC gene expression and transgenic plants. This sequence represents cDNA  
CC encoding a maize carbon assimilation pathway enzyme of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX

SQ Sequence 317 BP; 63 A; 113 C; 95 G; 46 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 8,99e-14 Length: 317  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56941 (1-317)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 50 ATGGCGCCACCGTATGATGGCTCGTGGCCACC----- 85  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuIleValSerThrAlaSerLeuProValAlaArg 40  
Db 86 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTGGCCGC 139  
QY 41 ArgSerSerArgSerLeuGlyValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 140 CGCTCTCTCAGAGCCTCGGCAACGTC---AGCAACGGCGAAGGATCCGGTGC 190

## RESULT 28

ADP56935

ID ADP56935 standard; cDNA; 319 BP.

AC ADP56935;

DT 09-SEP-2004 (first entry)

DE Maize carbon assimilation pathway enzyme cDNA #4.

KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
KW aldolase; fructose-1,6-bisphosphate; transketolase;  
KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;  
KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
KW aspartate aminotransferase; alanine aminotransferase;  
KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
KW plant metabolic pathway; plant breeding.

XX Zea mays.

XX US2004116682-A1.

PD 17-JUN-2004.

PF 16-NOV-2001; 2001US-00987899.

PR 06-MAR-1998; 98US-0076912P.

PR 04-MAR-1999; 99US-00262979.

XX (CHEI/) CHEIKH N.

PA (MILL/) MILLER P W.

PA (OCON/) O'CONNELL K M.

PA (LIUJ/) LIU J.

PI Cheikh N, Miller PW, O'connell KM, Liu J;

XX WPI; 2004-498291/47.  
 XX  
 XX New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.  
 XX  
 XX Claim 2; SEQ ID NO 4; 196pp; English.  
 PS  
 XX The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase,  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,  
 CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3  
 CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 319 BP; 63 A; 112 C; 96 G; 48 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9,05e-14 Length: 319  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservatives: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56935 (1-319)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThrAenProAlaGln 20  
 |||||  
 DB 41 ATGGCGCCACCCTGATGATGGCTCGTGGCCACC----- 76

QY 21 AlaSerAlaValAlaProHeGInGlyLeuLySerThraAlaSerLeuProValAlaArg 40  
 |||||  
 DB 77 -----GCCGTGCTCGTCTCCAGGGGGCTCAAGTCCACGCCAGCTCCCGCGCCGCG 130

QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgGlyArgCys 58  
 |||||  
 DB 131 CGCTCTCCAGAGCTTCGGCAAGTC---AGCACGGCGAGGATCCGGTGC 181

RESULT 29  
 ADP57162  
 ID ADP57162 standard; cDNA; 344 BP.  
 XX  
 AC ADP57162;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Maize carbon assimilation pathway enzyme cDNA #231.  
 DE  
 XX Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;

glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 aldolase; fructose-1,6-bisphosphatase; transketolase;  
 sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
 ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 aspartate aminotransferase; alanine aminotransferase;  
 NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 plant metabolic pathway; plant breeding.

Zea mays.  
 OS  
 XX  
 XX US2004116682-A1.  
 PN  
 XX  
 XX 17-JUN-2004.  
 PD  
 XX  
 XX 16-NOV-2001; 2001US-00987899.  
 PF  
 XX  
 XX 06-MAR-1998; 98US-0076912P.  
 PR  
 XX  
 XX 04-MAR-1999; 99US-00262979.  
 PR  
 XX  
 XX (CHEI/) CHEIKH N.  
 PA  
 XX  
 XX (MILL/) MILLER P. W.  
 PA  
 XX  
 XX (OCON/) O'CONNELL K M.  
 PA  
 XX  
 XX (LIU/) LIU J.

Cheikh N, Miller PW, O'Connell KM, Liu J;

WPI; 2004-498291/47.

New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.

Claim 2; SEQ ID NO 231; 196pp; English.

The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase,  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,  
 CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3  
 CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.

Sequence 344 BP; 67 A; 120 C; 104 G; 53 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9,93e-14 Length: 344  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservatives: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP57162 (1-344)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 46 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC----- 81  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
Db 82 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 135  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 136 CGCTCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 186

RESULT 30  
AAQ88331  
ID AAQ88331 standard; DNA; 405 BP.

XX AAQ88331;  
XX 11-JAN-1996 (first entry)  
XX Optimised transit peptide coding sequence.  
XX Plant promoter; root; meristem; pollen; immature embryo;  
KW upstream regulatory element; alpha tubulin gene; transit peptide; ss.  
XX Synthetic.

XX BP652286-A1.  
XX 10-MAY-1995.  
XX 09-NOV-1994; 94EP-00420306.  
XX 10-NOV-1993; 93FR-00013684.  
XX (RHON ) RHONE POULENC AGROCHIMIE.  
XX Capallades M, De Rose R, Montoliu L, Puigdomenech P, Torres MA;  
PI Rigau J, Uribe J;  
XX WPI; 1995-171922/23.

XX New maize alpha-tubulin promoters - and chimeric genes comprising  
PT promoter and heterologous gene for prodn. of transgenic plants.  
XX Example 4; Page 18; 24pp; French.  
XX Upstream regulatory elements (UREs) from maize alpha-tubulin genes (esp.  
CC the alpha 1, 2 or 3 genes, see AAQ88328-Q88330) can be used for  
CC controlling specific expression of (heterologous) genes in root,  
CC meristem, pollen and/or immature embryos. Transgenic plants able to  
CC express a heterologous gene can be generated using the different promoter  
CC regions, in partic. herbicide-resistant plants. In an example, the maize  
CC tub-alpha-1 regulatory element was incorporated into a plasmid which also  
CC contained an optimised transit peptide coding sequence (AAQ88331), the  
CC aroA gene and the nos terminator. Tobacco leaf discs were transformed  
CC with the plasmid (via A.tumefaciens) and plants regenerated from the  
CC discs showed increased tolerance to glyphosate  
XX Sequence 405 BP; 79 A; 148 C; 106 G; 72 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.21e-13 Length: 405  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 2 Gaps: 2

US-10-628-525A-34 (1-58) x AAQ88331 (1-405)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 262 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC----- 297  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
Db 298 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 351  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 352 CGCTCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 402

Search completed: April 1, 2006, 04:28:44  
Job time : 139.553 secs



GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 15:18:57 ; Search time 935.32 Seconds  
(without alignments)  
2901.306 Million cell updates/sec

Title: US-10-628-525A-34

Perfect score: 282

Sequence: 1 MAPTVWASSATATRNPAQ.....ARRSSRLGNVASNGRIRC 58

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-Q/-abes/ABSWEB spool/US10628525/runat\_31032006\_095118\_16742/app\_query.fasta\_1  
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150  
-DOCALIGN=200 -THR\_SCORE=oct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abes06h  
-USER=US10628525 @CGN\_1\_11098\_orunat\_31032006\_095118\_16742 -NCPV=6 -ICPU=3  
-NO\_WMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hct:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gsal:\*  
10: gb\_gsal2:\*  
11: gb\_gsal3:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query | Match | Length | ID       | Description        |
|------------|-------|-------|-------|--------|----------|--------------------|
| 1          | 203.5 | 72.2  | 171   | 1      | AW438072 | AW438072 707072C09 |
| 2          | 203.5 | 72.2  | 281   | 3      | B1430868 | B1430868 949062B09 |
| 3          | 203.5 | 72.2  | 320   | 6      | CD988795 | CD988795 QAR1a03.y |
| 4          | 203.5 | 72.2  | 369   | 1      | A1372109 | A1372109 am78b09.x |
| 5          | 203.5 | 72.2  | 428   | 9      | BZ647531 | BZ647531 OGCBJ16NC |
| 6          | 203.5 | 72.2  | 476   | 2      | BG458793 | BG458793 947054D04 |
| 7          | 203.5 | 72.2  | 481   | 8      | DR826659 | DR826659 ZM_BFB006 |

|   |    |       |      |      |    |          |                     |
|---|----|-------|------|------|----|----------|---------------------|
| C | 8  | 203.5 | 72.2 | 481  | 9  | CC168222 | CC168222 i183b10.g  |
|   | 9  | 203.5 | 72.2 | 487  | 2  | BG550311 | BG550311 947039E03  |
|   | 10 | 203.5 | 72.2 | 513  | 3  | B1431142 | B1431142 949059C09  |
| C | 11 | 203.5 | 72.2 | 525  | 9  | CC616048 | CC616048 OGUKH26TH  |
|   | 12 | 203.5 | 72.2 | 544  | 2  | BG349334 | BG349334 947028A12  |
|   | 13 | 203.5 | 72.2 | 545  | 6  | CF025689 | CF025689 QCAle07.y  |
|   | 14 | 203.5 | 72.2 | 569  | 6  | CD998700 | CD998700 QBF15C08.  |
|   | 15 | 203.5 | 72.2 | 608  | 6  | CF025518 | CF025518 QCA18a04.  |
|   | 16 | 203.5 | 72.2 | 619  | 6  | CD990730 | CD990730 QAY3f06.y  |
|   | 17 | 203.5 | 72.2 | 622  | 2  | BG458523 | BG458523 947045B08  |
|   | 18 | 203.5 | 72.2 | 652  | 1  | AW352495 | AW352495 707050B11  |
|   | 19 | 203.5 | 72.2 | 657  | 7  | CO523152 | CO523152 3530_1_15  |
| C | 20 | 203.5 | 72.2 | 660  | 2  | BG320791 | BG320791 Zm04_10c0  |
|   | 21 | 203.5 | 72.2 | 660  | 7  | CO532595 | CO532595 3530_1_21  |
|   | 22 | 203.5 | 72.2 | 671  | 6  | CD990623 | CD990623 QAY2D03.y  |
|   | 23 | 203.5 | 72.2 | 711  | 7  | CO533682 | CO533682 3530_1_22  |
|   | 24 | 203.5 | 72.2 | 712  | 6  | CD991089 | CD991089 QAZ4B01.y  |
|   | 25 | 203.5 | 72.2 | 769  | 8  | DR822461 | DR822461 ZM_BFB006  |
|   | 26 | 203.5 | 72.2 | 773  | 8  | DR824125 | DR824125 ZM_BFB006  |
|   | 27 | 203.5 | 72.2 | 777  | 10 | CG094731 | CG094731 FUKDK52TD  |
|   | 28 | 203.5 | 72.2 | 779  | 8  | DR829152 | DR829152 ZM_BFB007  |
|   | 29 | 203.5 | 72.2 | 800  | 9  | CC641056 | CC641056 OGIC030TV  |
|   | 30 | 203.5 | 72.2 | 802  | 8  | DR797511 | DR797511 ZM_BFB001  |
|   | 31 | 203.5 | 72.2 | 808  | 10 | CG447685 | CG447685 OGATAT65TV |
|   | 32 | 203.5 | 72.2 | 817  | 1  | AA979879 | AA979879 MEST2-G2.  |
|   | 33 | 203.5 | 72.2 | 821  | 8  | DR826660 | DR826660 ZM_BFB006  |
|   | 34 | 203.5 | 72.2 | 825  | 8  | DR798785 | DR798785 ZM_BFB002  |
| C | 35 | 203.5 | 72.2 | 831  | 2  | BG319747 | BG319747 Zm03_05b0  |
|   | 36 | 203.5 | 72.2 | 853  | 8  | DR802699 | DR802699 ZM_BFB002  |
| C | 37 | 203.5 | 72.2 | 870  | 10 | CG094728 | CG094728 FUKDK52TB  |
|   | 38 | 203.5 | 72.2 | 885  | 8  | DR819095 | DR819095 ZM_BFB005  |
|   | 39 | 203.5 | 72.2 | 890  | 10 | CG262745 | CG262745 OG0FY03TH  |
| C | 40 | 203.5 | 72.2 | 918  | 8  | CG262755 | CG262755 OG0FY03TV  |
|   | 41 | 203.5 | 72.2 | 929  | 8  | DR820791 | DR820791 ZM_BFB005  |
| C | 42 | 203.5 | 72.2 | 939  | 10 | CG461924 | CG461924 FUFIC04TD  |
|   | 43 | 203.5 | 72.2 | 1041 | 10 | CG461884 | CG461884 FUFIC04TB  |
|   | 44 | 200.5 | 71.1 | 318  | 8  | DR820790 | DR820790 ZM_BFB005  |
| C | 45 | 198.5 | 70.4 | 670  | 6  | CD990729 | CD990729 QAY3f05.y  |
|   | 46 | 197.5 | 70.0 | 320  | 6  | CD988611 | CD988611 QAY2d11.y  |
|   | 47 | 196.5 | 69.7 | 574  | 2  | BG517358 | BG517358 947061E01  |
| C | 48 | 195.5 | 69.3 | 289  | 1  | A1967090 | A1967090 496021F11  |
|   | 49 | 195.5 | 69.3 | 325  | 6  | CD989002 | CD989002 QAR3f11.y  |
|   | 50 | 195.5 | 69.3 | 379  | 1  | AW600621 | AW600621 707104A10  |
|   | 51 | 195.5 | 69.3 | 411  | 1  | AW331399 | AW331399 707012E03  |
|   | 52 | 195.5 | 69.3 | 412  | 2  | BG462689 | BG462689 947059C04  |
|   | 53 | 195.5 | 69.3 | 438  | 2  | BG317226 | BG317226 947026G02  |
|   | 54 | 195.5 | 69.3 | 445  | 3  | B1325424 | B1325424 949038G09  |
|   | 55 | 195.5 | 69.3 | 485  | 6  | CD998181 | CD998181 QBF10a04.  |
|   | 56 | 195.5 | 69.3 | 486  | 3  | B1430769 | B1430769 949060G06  |
|   | 57 | 195.5 | 69.3 | 486  | 6  | CD998218 | CD998218 QBF10d10.  |
|   | 58 | 195.5 | 69.3 | 487  | 6  | CF005221 | CF005221 OBH9B04.x  |
|   | 59 | 195.5 | 69.3 | 507  | 6  | CF003569 | CF003569 OBH21b06.  |
|   | 60 | 195.5 | 69.3 | 558  | 3  | B164315  | B164315 949077G05   |
|   | 61 | 195.5 | 69.3 | 565  | 3  | B1644173 | B1644173 949022F06  |
|   | 62 | 195.5 | 69.3 | 586  | 6  | CD999602 | CD999602 QAY2B04.y  |
|   | 63 | 195.5 | 69.3 | 591  | 6  | CD999712 | CD999712 QBF8B11.x  |
|   | 64 | 195.5 | 69.3 | 717  | 8  | CO530543 | CO530543 3530_1_20  |
|   | 65 | 195.5 | 69.3 | 728  | 7  | DR969955 | DR969955 ZM_BFB009  |
|   | 66 | 195.5 | 69.3 | 732  | 3  | BW080707 | BW080707 MEST112-C  |
| C | 67 | 195.5 | 69.3 | 745  | 2  | BG842572 | BG842572 MEST13-80  |
|   | 68 | 195.5 | 69.3 | 858  | 8  | DR823021 | DR823021 ZM_BFB006  |
|   | 69 | 195.5 | 69.3 | 866  | 8  | DR788406 | DR788406 ZM_BFB000  |
| C | 70 | 195.5 | 69.3 | 880  | 2  | BG837797 | BG837797 Zm10_0400  |
|   | 71 | 195.5 | 69.3 | 1004 | 10 | CG242767 | CG242767 OG0Q81TV   |
|   | 72 | 195.5 | 69.3 | 1172 | 4  | AY103730 | AY103730 Zea_mays   |
| C | 73 | 194.5 | 69.0 | 262  | 2  | BG316752 | BG316752 947026E07  |
|   | 74 | 194.5 | 69.0 | 619  | 3  | B1430981 | B1430981 949063F09  |
| C | 75 | 194.5 | 69.0 | 705  | 2  | BG320451 | BG320451 Zm03_10f0  |
| C | 76 | 191.5 | 67.9 | 320  | 6  | CD988645 | CD988645 QAO2f07.y  |
|   | 77 | 191.5 | 67.9 | 563  | 6  | CF021885 | CF021885 QBP6f11.x  |
|   | 78 | 190.5 | 67.6 | 587  | 2  | BG320894 | BG320894 Zm04_09g0  |
|   | 79 | 188.5 | 66.8 | 723  | 6  | CF014053 | CF014053 QBL12g12.  |
|   | 80 | 185.5 | 65.8 | 529  | 6  | CD998557 | CD998557 QBF13f09.  |

|     |       |      |     |   |          |                     |
|-----|-------|------|-----|---|----------|---------------------|
| 81  | 183.5 | 65.1 | 467 | 2 | BG517862 | BG517862 947071H03  |
| 82  | 183   | 64.9 | 351 | 2 | BG549043 | BG549043 947072E03  |
| 83  | 182.5 | 64.7 | 214 | 2 | BG549870 | BG549870 947076D05  |
| 84  | 180.5 | 64.0 | 147 | 3 | BI325456 | BI325456 949039C04  |
| 85  | 178.5 | 63.3 | 234 | 3 | BI430730 | BI430730 949060C01  |
| 86  | 178.5 | 63.3 | 505 | 6 | CF005283 | CF005283 QBH9F03.X  |
| 87  | 178.5 | 63.3 | 565 | 6 | CF021641 | CF021641 QBP3C05.X  |
| 88  | 177.5 | 62.9 | 509 | 2 | BG462181 | BG462181 947047G02  |
| 89  | 176.5 | 62.6 | 426 | 2 | BG517870 | BG517870 947071H10  |
| 90  | 175.5 | 62.2 | 580 | 3 | BI674933 | BI674933 949076E10  |
| 91  | 175.5 | 62.2 | 915 | 2 | BG837761 | BG837761 Zm10_05R0  |
| 92  | 174.5 | 61.9 | 271 | 2 | BG317210 | BG317210 947026E07  |
| 93  | 172   | 61.0 | 549 | 1 | AW398998 | AW398998 EST309498  |
| 94  | 171.5 | 60.8 | 441 | 3 | BI434512 | BI434512 EST37273   |
| 95  | 171.5 | 60.8 | 478 | 1 | AW618854 | AW618854 EST32084   |
| 96  | 171.5 | 60.8 | 526 | 1 | AW399256 | AW399256 EST309756  |
| 97  | 171.5 | 60.8 | 557 | 2 | BG097016 | BG097016 EST461535  |
| 98  | 171.5 | 60.8 | 559 | 2 | AW618743 | AW618743 EST320729  |
| 99  | 171.5 | 60.8 | 611 | 1 | AW398171 | AW398171 EST397934  |
| 100 | 171.5 | 60.8 | 641 | 1 | AW160224 | AW160224 EST290082  |
| 101 | 171.5 | 60.8 | 674 | 7 | CK863768 | CK863768 35047_In   |
| 102 | 171.5 | 60.8 | 703 | 3 | BI432231 | BI432231 EST534992  |
| 103 | 170   | 60.3 | 341 | 3 | BI433582 | BI433582 EST536343  |
| 104 | 170   | 60.3 | 595 | 1 | AW618741 | AW618741 EST320727  |
| 105 | 170   | 60.3 | 634 | 2 | BG589314 | BG589314 EST497156  |
| 106 | 170   | 60.3 | 667 | 3 | BQ113678 | BQ113678 EST599254  |
| 107 | 170   | 60.3 | 693 | 3 | BI432899 | BI432899 EST535660  |
| 108 | 170   | 60.3 | 697 | 2 | BG590013 | BG590013 EST497855  |
| 109 | 170   | 60.3 | 699 | 3 | BM404597 | BM404597 EST579334  |
| 110 | 170   | 60.3 | 834 | 3 | BI434599 | BI434599 EST537360  |
| 111 | 169.5 | 60.1 | 140 | 3 | BI325462 | BI325462 949039D04  |
| 112 | 169.5 | 60.1 | 414 | 3 | BI434313 | BI434313 EST537074  |
| 113 | 169.5 | 60.1 | 515 | 1 | AI483371 | AI483371 EST243348  |
| 114 | 169   | 59.9 | 407 | 2 | BG097139 | BG097139 EST461658  |
| 115 | 169   | 59.9 | 409 | 3 | BP745218 | BP745218 BP745218   |
| 116 | 169   | 59.9 | 563 | 7 | CN599952 | CN599952 EG-A11_00  |
| 117 | 169   | 59.9 | 629 | 3 | BM407356 | BM407356 EST581683  |
| 118 | 169   | 59.9 | 634 | 3 | BM113573 | BM113573 EST561109  |
| 119 | 169   | 59.9 | 687 | 3 | BM405149 | BM405149 EST579476  |
| 120 | 169   | 59.9 | 743 | 7 | CV504514 | CV504514 71064.1_M  |
| 121 | 168.5 | 59.8 | 521 | 3 | BI595975 | BI595975 949075C03  |
| 122 | 168.5 | 59.8 | 528 | 1 | AW039394 | AW039394 EST281651  |
| 123 | 168.5 | 59.8 | 578 | 3 | BI396085 | BI396085 949048B04  |
| 124 | 168.5 | 59.8 | 614 | 1 | AW443539 | AW443539 EST408469  |
| 125 | 168   | 59.6 | 461 | 6 | CA117824 | CA117824 SCBGLR104  |
| 126 | 168   | 59.6 | 461 | 6 | CA273397 | CA273397 SCBPSD100  |
| 127 | 168   | 59.6 | 556 | 6 | CA281255 | CA281255 SCBPSD102  |
| 128 | 168   | 59.6 | 665 | 6 | CA282404 | CA282404 SCCCLV100  |
| 129 | 168   | 59.6 | 671 | 6 | CA297496 | CA297496 SCCSD100   |
| 130 | 168   | 59.6 | 712 | 8 | DN238298 | DN238298 MUC41H100  |
| 131 | 168   | 59.6 | 715 | 6 | CF574544 | CF574544 MUC41L1600 |
| 132 | 168   | 59.6 | 744 | 8 | DN240065 | DN240065 MUC41C101  |
| 133 | 168   | 59.6 | 756 | 8 | DN239801 | DN239801 MUC41C101  |
| 134 | 168   | 59.6 | 764 | 6 | CA208714 | CA208714 SCACSB111  |
| 135 | 168   | 59.6 | 767 | 6 | CA208645 | CA208645 SCACSB111  |
| 136 | 168   | 59.6 | 771 | 6 | CA282815 | CA282815 SCOGSD104  |
| 137 | 168   | 59.6 | 951 | 6 | CA275516 | CA275516 SCBPSD103  |
| 138 | 167.5 | 59.4 | 200 | 2 | BE924621 | BE924621 EST428390  |
| 139 | 167.5 | 59.4 | 555 | 1 | AW443028 | AW443028 EST307958  |
| 140 | 167.5 | 59.4 | 560 | 1 | AI772337 | AI772337 EST253437  |
| 141 | 167   | 59.2 | 522 | 6 | CA276409 | CA276409 SCBPSD100  |
| 142 | 167   | 59.2 | 532 | 6 | CA169255 | CA169255 SCJFSB101  |
| 143 | 167   | 59.2 | 538 | 1 | AI484172 | AI484172 EST249325  |
| 144 | 167   | 59.2 | 571 | 1 | AW399318 | AW399318 EST309818  |
| 145 | 167   | 59.2 | 572 | 6 | CA274801 | CA274801 SCBPSD103  |
| 146 | 167   | 59.2 | 580 | 1 | AW443497 | AW443497 EST308427  |
| 147 | 167   | 59.2 | 598 | 1 | AW399017 | AW399017 EST309517  |
| 148 | 167   | 59.2 | 599 | 6 | CA210512 | CA210512 SCBPSB112  |
| 149 | 167   | 59.2 | 604 | 6 | CA110175 | CA110175 SCVPHR108  |
| 150 | 167   | 59.2 | 608 | 6 | CA295185 | CA295185 SCACLV102  |

RESULT 1

LOCUS

DEFINITION

AW438072

707072C09.x1 707 - Mixed adult tissues from Walbot lab (SK) Zea

mayes cDNA, mRNA sequence.

AW438072

AW438072.1 GI:6973378

EST.

KEYWORDS

SOURCE

Zeas mayes

ORGANISM

Zeas mayes

REFERENCE

1 (bases 1 to 171)

Walbot.V.

AUTHORS

Walbot.V.

TITLE

Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL

Unpublished (1999)

COMMENT

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 707072 row: C column: 09.

location/Qualifiers

1..171

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="W23"

/db\_xref="taxon:4577"

/tissue\_type="tassel, kernel, silk, husk, root, leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="707 - Mixed adult tissues from Walbot lab (SK)"

/note="Organ: tassel, kernel, silk, husk, root, leaf; Vector: pGAD10; Site: 1: EcoRI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned."

ORIGIN

Alignment Scores:

Pred. No.: 1.27e-13 Length: 171

Score: 203.50 Matches: 47

Percent Similarity: 81.0% Conservative: 0

Best Local Similarity: 81.0% Mismatches: 0

Query Match: 72.2% Indels: 11

DB: 1 Gaps: 2

US-10-628-525A-34 (1-58) x AW438072 (1-171)

Qy 1 MetalProThrValMetAlaSerSerAlaThrAlaThrArgThrAsmProAlaGln 20

Db 18 ATGGGCCCCACCGTGATGATGGCTCTGTCGCCACC-----53

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40

Db 54 -----GCCGTCGCTCCGTCAGGGGGTCAAGTCCACGCCGCGCTCCCGTCGCCGC 107

Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58

Db 108 CGCTCTCCAGAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 158

RESULT 2

LOCUS

DEFINITION

BI430868

949062B09.y1 949 - Juvenile leaf and shoot cDNA from Steve Moose

Zeas mayes cDNA, mRNA sequence.

ACCESSION

BI430868

VERSION BI430868.1 GI:15208984  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 281)  
 Walbot, V.  
 Maize ESTs from various cDNA libraries sequenced at Stanford  
 University  
 Unpublished (1999)  
 Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 949062 row: B column: 09.  
 Location/Qualifiers  
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 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="W64A"  
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 meristem"  
 /dev\_stage="4 stages from 3-13 days after imbibing"  
 /lab\_host="E. coli XL0LR"  
 /clone\_lib="949 - Juvenile leaf and shoot cDNA from Steve  
 Moose"  
 /notes="Organ: juvenile vegetative shoots; Vector:  
 pAD-GAL4-2.1; Site 1: EcoRI; Site 2: XhoI; Equal amounts  
 of total RNA by weight from 4 tissue sources (see below)  
 were pooled, polyA+ RNA isolated, and cDNA synthesized for  
 EcoRI (5') and XhoI (3') directional cloning into lambda  
 Hybrizap vector from Stratagene. Tissue Sources: 1. Whole  
 shoots 3 days after sowing/imbibing in wet soil. 2. Basal  
 1.5 cm shoots 6 days after sowing - includes yellow  
 portions of developing leaves 1-5, primordia from 6-8, and  
 the vegetative apex. 3. Non-green portions of developing  
 leaves 4-5 and the vegetative apex, including adult leaf  
 primordia, 9 days after sowing. 4. Partially expanded and  
 greening leaves 4-5 at 13 days after sowing."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2,3e-13 Length: 281  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 3 Gaps: 2  
 US-10-628-525A-34 (1-58) x BI430868 (1-281)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 DB 15 ATGGCGCCACCGGTGATGCTCGTGGCCACC-----50  
 QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 DB 51 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTGGCCGC 104  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 DB 105 CGCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 155  
 RESULT 3  
 CD988795 320 bp mRNA linear EST 16-JUL-2003  
 LOCUS QAR1a03.yg QAR Zea mays cDNA clone QAR1a03, mRNA sequence.  
 DEFINITION

CD988795  
 CD988795.1 GI:32849114  
 EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 320)  
 Genoplante.  
 Genoplante, a major partnership french program in plant genomics  
 Unpublished (2003)  
 Contact: Genoplante  
 Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
 and <http://genoplante-info.infobiogen.fr>).  
 Location/Qualifiers  
 1..320  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="F2"  
 /db\_xref="taxon:4577"  
 /clone="QAR1a03"  
 /tissue\_type="aerial, root, whole plant"  
 /clone\_lib="QAR"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.68e-13 Length: 320  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 6 Gaps: 2  
 US-10-628-525A-34 (1-58) x CD988795 (1-320)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 DB 29 ATGGCGCCACCGGTGATGCTCGTGGCCACC-----64  
 QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 DB 65 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTGGCCGC 118  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 DB 119 CGCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 169  
 RESULT 4  
 AI372109 369 bp mRNA linear EST 12-JAN-1999  
 LOCUS am78b09.xl maize ear glume library Zea mays cDNA clone am78b09 5',  
 mRNA sequence.  
 DEFINITION  
 AI372109  
 AI372109.1 GI:4151975  
 EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 369)  
 Norris, A., Parnell, L.D., Schutz, K., de la Bastide, M.,  
 Nasciminto, L., Shah, R., Swaby, I., Shekher, M., Vil, M.D., Preston, R.,  
 Huang, E.N., Habermann, K., Dedhia, N., Martienssen, R. and  
 McCombie, W.R.  
 Expressed sequence tags from Zea mays (1999)  
 Unpublished (1999)  
 TITLE  
 JOURNAL

## COMMENT

Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mcombie@cshl.org  
Plate: am78 row: b column: 09  
Seq primer: M13 reverse universal  
High quality sequence stop: 369.

FEATURES  
source

1..369  
/organism="Zea mays"  
/mol\_type="mRNA"  
/db\_xref="taxon:4577"  
/clone="am78b03"  
/tissue\_type="glume ear 2 weeks post-pollination"  
/cell\_line="W22-TGA"  
/clone\_lib="maize ear glume library"  
/note="Vector: pBLUESCRIPT SK+ (X52325); Site 1: XhoI;  
Site 2: EcoRI; This library was supplied by John Doebley  
(Univ. of Minnesota). cDNAs are directionally cloned into  
the XhoI and EcoRI sites; XhoI is near the polyA tail.  
Most reads from this library are made with the reverse  
universal M13 primer and are 5' in direction. Additional  
information on this library as well as ftp access to all  
sequences can be found at  
<http://www.cshl.org/maizegenome>"

## ORIGIN

Alignment Scores:  
Pred. No.: 3,18e-13 Length: 369  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 1 Gaps: 2

US-10-628-525A-34 (1-58) x AJ1372109 (1-369)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
|||||  
DB 54 ATGGCGCCACCGTGATGATGCGCTCGTGGCCACC----- 89  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
|||||  
DB 90 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 143  
QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
|||||  
DB 144 CGCTCTCCAGAGCTCGGCAACGTC---AGCAACGGTGAAGGATCCGGTGC 194

RESULT 5  
BZ647531  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BZ647531  
OGCBJ16TC ZM 0.7 1.5 KB Zea mays genomic clone ZMWBMa0133D08,  
genomic survey sequence.  
BZ647531  
BZ647531.1 GI:28110542  
GSS.  
Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 428)  
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other\_GSSs: OGCBJ16TM  
Contact: Cathy Whitelaw

## TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TF  
Classes: methylation filtered.

FEATURES  
source

1..428  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMWBMa0133D08"  
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

## ORIGIN

Alignment Scores:  
Pred. No.: 3,79e-13 Length: 428  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 9 Gaps: 2

US-10-628-525A-34 (1-58) x BZ647531 (1-428)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
|||||  
DB 84 ATGGCGCCACCGTGATGATGCGCTCGTGGCCACC----- 119  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
|||||  
DB 120 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 173  
QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
|||||  
DB 174 CGCTCTCCAGAGCTCGGCAACGTC---AGCAACGGGGAAGGATCCGGTGC 224

RESULT 6  
BG458793  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BG458793  
947054D04.y1 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA  
sequence.  
BG458793  
BG458793.1 GI:13382118  
EST.  
Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 476)  
Walbot, V.  
Maize ESTs from various cDNA libraries sequenced at Stanford  
University  
Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 947054 row: D column: 04.

FEATURES  
source

1..476  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"

/tissue type="leaf and stem, including leaf base"  
/dev\_stage="2 week old seedling (3 leaves)"  
/lab\_host="XLI-Blue"  
/clone\_lib="947 - 2 week shoot from Barkan lab"  
/notes="Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-);  
Site 1: EcoRI; Site 2: XhoI; Directionally cloned using  
Stratagene's Unizap XR cDNA cloning kit with the 5' end  
at the EcoRI site. The library represents 8 x 10<sup>5</sup>  
independent recombinant phage. The plants were greenhouse  
grown."

## ORIGIN

Alignment Scores:  
Pred. No.: 4,31e-13 Length: 476  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 2 Gaps: 2

US-10-628-525A-34 (1-58) x BG458793 (1-476)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
|||||  
DB 9 ATGGGCGCCACCGTGTGATGGCTCTCGTGGCCACC----- 44  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
|||||  
DB 45 -----GCCGTCGCTCGTGTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTGGCCGC 98  
QY 41 ArgSerSerArgSerLeuGlyAnValAlaSerAsnGlyGlyArgGlyArgCys 58  
|||||  
DB 99 CGCTCTCTCCAGAGCCCTCGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 149

## RESULT 7

DR826659 481 bp mRNA linear EST 28-JUL-2005  
LOCUS ZM\_BFB0069110.f ZM\_BFB Zea mays cDNA 3', mRNA sequence.  
DEFINITION DR826659

ACCESSION DR826659.1 GI:71445609  
VERSION  
KEYWORDS EST.

SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 481)  
Kim H., Collura K., Wissotski M., Smart D., Kudrna D., Muller C.,  
Rao K., Haller K., Wing R., Soderlund C., Walbot V. and Yu Y.  
Maize Full-length cDNA Project

Unpublished (2005)  
Contact: Yeisoo Yu

Arizona Genomics Institute  
The University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plate: 0069 row: I column: 10.

Location/Qualifiers

## FEATURES

1. .481

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/tissue\_type="mixed (silks, husks, ears, pollen, shoot

tips, leaf, root tips, whole seed, embryo)"

/dev\_stage="varies by tissue"

/lab\_host="DH10B T1 phage resistant"

/clone\_lib="ZM BFB"

/notes="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:

NotI; Zea Full length cDNA library (3530 library)

created by Invitrogen from multiple tissues; Organ: silks,

## ORIGIN

Alignment Scores:  
Pred. No.: 4,36e-13 Length: 481  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x DR826659 (1-481)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
|||||  
DB 42 ATGGGCGCCACCGTGTGATGGCTCTCGTGGCCACC----- 77

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
|||||  
DB 78 -----GCCGTCGCTCGTGTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTGGCCGC 131

QY 41 ArgSerSerArgSerLeuGlyAnValAlaSerAsnGlyGlyArgGlyArgCys 58  
|||||  
DB 132 CGCTCTCTCCAGAGCCCTCGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 182

## RESULT 8

CC168222/c

LOCUS

DEFINITION

iJ83b10.g1 WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone

CC168222

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Ze mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 481)

Rabinowicz P.D., O'Shaughnessy A.L., Balija V., Dedhia N.,

Katzenburger F., King L., Miller B., Muller S., Nascimeto L.,

Zutavern T., McCombie W.R. and Martienssen R.A.

Genomic shotgun sequences from Zea mays (methyl-filtered)

Unpublished (2002)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

husks, ears, pollen, shoot tips, leaf, root tips, whole  
seed, embryo. This is a Gateway compatible vector,  
permitting clone movement to new vector backbones for  
expression in diverse host cells using recombination  
rather than restriction enzymes. poly(A)+ mRNA was  
prepared by invitrogen, and equimolar amounts of RNA from  
each of the 12 tissue samples were mixed together for  
a selection of mRNA with a 5' cap. After synthesis of cDNA,  
a normalization step was conducted against the mixture of  
RNA sources. Tissues prepared: 1. just emerging silks; 2.  
inner husks from ears of sample #1; 3. 20 dap aleurone; 4.  
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to  
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from  
15 day old seedlings; all leaves with an expanded or  
partially expanded sheath were removed; 8. mature leaf  
tissue; 9. 0.5 cm long root tips from 15 day old  
seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and  
embryo; 12. 17 dap endosperm and embryo. All of the  
sequenced clones in Maize Full-length cDNA Project will be  
archived at the University of Arizona. Clones, high  
density filters and amplified library can be ordered from  
the University of Arizona  
(http://www.genome.arizona.edu/orders/).

Plate: ij83 row: b column: 10  
Seq primer: -21M13UnivRev  
Class: shotgun  
High quality sequence stop: 481.

## FEATURES

```
1. .%01
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="j183b10"
/lab_host="DH5a"
/clone_lib="WGS-2maysF
```

"/clone\_1lb=wGS-ZmaysP (DH5a methyl filtered)"  
/notes=Organ: immature ears; Site1: Xba 1; Site2: Xba 1;  
The vector was digested with XbaI and one nucleotide was  
added by fill in the recessive '3' end. The genomic DNA  
was nebulized, end repaired, adaptor ligated and size  
fractionated using sephadex. The resulting fragments were  
between 0.8 and 3 kb and were cloned into the vector (x/y  
reads in M13mp19, b/g reads in pUC19). The same ligation  
was transformed into DH5a."

## ORIGIN

|                        |          |                 |
|------------------------|----------|-----------------|
| Alignment Scores:      |          |                 |
| Pred. No.:             | 4,36e-13 | 481             |
| Score:                 | 203.50   | 47              |
| Percent Similarity:    | 81.0%    | Conservative: 0 |
| Best Local Similarity: | 81.0%    | Mismatches: 11  |
| Query Match:           | 72.2%    | Indels: 2       |
| DB:                    | 9        | Gaps: 2         |

US-10-628-525A-34 (1-58) x CC168222 (1-481)

|    |     |       |      |      |      |     |     |     |     |      |         |      |       |       |       |       |       |       |       |       |     |    |
|----|-----|-------|------|------|------|-----|-----|-----|-----|------|---------|------|-------|-------|-------|-------|-------|-------|-------|-------|-----|----|
| Qy | 1   | Meta  | Pro  | Thr  | Val  | Met | Met | Ala | Ser | Ser  | Ala     | Thr  | Ala   | Thr   | Arg   | Thr   | Asn   | Pro   | Ala   | Gln   | 20  |    |
| Db | 245 | ATGG  | CGCC | CAC  | CGT  | GAT | GAT | GGC | CTC | GT   | CGG     | CACC | ----- | ----- | ----- | ----- | ----- | ----- | ----- | ----- | 210 |    |
| Qy | 21  | Ala   | Ser  | Ala  | Val  | Ala | Pro | Phe | Gln | Gly  | Leu     | Val  | Ser   | Thr   | Ala   | Ser   | Leu   | Pro   | Val   | Ala   | Arg | 40 |
| Db | 209 | ----- | GGCG | TGCT | CGCT | TTC | CAG | GGG | CTC | AA   | GTCC    | ACC  | CGCC  | AGC   | CTC   | CC    | CGT   | CGCC  | CGC   | CGC   | 156 |    |
| Qy | 41  | Arg   | Ser  | Ser  | Arg  | Ser | Leu | Gly | Asn | Val  | Ala     | Ser  | Asn   | Gly   | Gly   | Arg   | Ile   | Arg   | Cys   | 58    |     |    |
| Db | 155 | CGCT  | CCT  | CTC  | CAG  | AAG | CCT | CGG | CAA | GGTC | ---AGCA | ACGG | CGG   | AGG   | ATC   | CGG   | TGC   | 105   |       |       |     |    |

RESULT 9  
BG550311

|                                                           |
|-----------------------------------------------------------|
| DG96J11                                                   |
| LOCUS                                                     |
| BG550311          487 bp       EST 05-APR - 2001          |
| DEFINITION        mRNA         linear                     |
| Y1 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA |
| sequence.                                                 |

|           |                                                                                                                                                                                    |
|-----------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ACCESSION | sequence.                                                                                                                                                                          |
| VERSION   | BG550311                                                                                                                                                                           |
| KEYWORDS  | BG550311.1 GI:13558956                                                                                                                                                             |
| ORGANISM  | EST.                                                                                                                                                                               |
| SOURCE    | Zea mays                                                                                                                                                                           |
| ORGANISM  | Zea mays                                                                                                                                                                           |
| SOURCE    | Zea mays                                                                                                                                                                           |
| ORGANISM  | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;<br>Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD<br>clade; Panicoideae; Andropogoneae; Zea. |
| REFERENCE | 1 (bases 1 to 487)                                                                                                                                                                 |

REFERENCES  
AUTHORS

Maize ESTs from various cDNA libraries sequence  
University  
Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 947039 row: E column: 03.  
Location/Qualifiers  
1. 487

## FEATURES

```

/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="leaf and stem, including leaf base"
/dev_stage="2 week old seedling (3 leaves)"
/lab_host="X11-Blue"
/clone_lib="947 - 2 week shoot from Barkan lab"
/notes="Organ: shoot; Vector: Lambda ZAP (pBluescript SK-); Site 1: EcoRI; Site 2: XhoI; Directionally cloned using Stratagene's Unizap XR cDNA cloning kit with the 5' end at the EcoRI site. The library represents 8 x 10e5 independent recombinant phage. The plants were greenhouse grown."

```

| GROWN.                 |          |
|------------------------|----------|
| ORIGIN                 |          |
| Alignment Scores:      |          |
| Pred. No.:             | 4.43e-13 |
| Score:                 | 203.50   |
| Percent Similarity:    | 81.0%    |
| Best Local Similarity: | 81.0%    |
| Query Match:           | 72.2%    |
| DB:                    | 2        |
|                        | 2        |
| Length:                | 487      |
| Matches:               | 47       |
| Conservative:          | 0        |
| Mismatches:            | 0        |
| Indels:                | 11       |
| Gaps:                  | 2        |

US-10-628-525A-34 (1-58) x BG550311 (1-487)

|    |     |                                                              |     |
|----|-----|--------------------------------------------------------------|-----|
| QY | 1   | MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln | 20  |
| Db | 18  | ATGGGCGCCACCGTGATGCTCGTCGGCCACC-----                         | 53  |
| QY | 21  | AlaSerAlaValAlaProPheGlnGlyLeuIysSerThrAlaSerLeuProValAlaArg | 40  |
| Db | 54  | -----GCCGTCGTCGCTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC      | 107 |
| QY | 41  | ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys       | 58  |
| Db | 108 | CGCTCTCTCAGAAGCTTCGGCAAGTC---AGCAACGCGCGGAAGATTCGGGTGC       | 158 |

RESULT 10  
BT431142

| EST        | EST 20-AUG-2001               |
|------------|-------------------------------|
| BI4311142  | linear                        |
| LOCUS      | 513 bp                        |
| DEFINITION | mRNA                          |
|            | Juvenile leaf and shoot       |
|            | CDNA from Steve Moose         |
|            | Zea mays CDNA, mRNA sequence. |

|           |                                                                                                                                                                                                    |             |
|-----------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------|
| ACCESSION | BI431142                                                                                                                                                                                           | GI:15215043 |
| VERSION   | BI431142.1                                                                                                                                                                                         |             |
| KEYWORDS  | EST.                                                                                                                                                                                               |             |
| SOURCE    | Zea mays                                                                                                                                                                                           |             |
| ORGANISM  | Zea mays                                                                                                                                                                                           |             |
| REFERENCE | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.<br>1 (bases 1 to 513) |             |

## REFERENCE AUTHORS

|         |                                                                         |
|---------|-------------------------------------------------------------------------|
| TITLE   | Maize ESTs from various cDNA libraries sequenced at Stanford University |
| JOURNAL | Unpublished (1999)                                                      |
| COMMENT | Contact: Walbot V                                                       |

COMMENT

Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 949059 row: C column: 09.  
Location/Qualifiers  
1..513  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="W64A"  
/db\_xref="taxon:4577"  
/tissue\_type="immature leaf primordium meristem"  
/dev\_stage="4 stages from 3-13 days"

/lab\_host="E. coli XL0LR"  
 /clone\_lib="949 - juvenile leaf and shoot cDNA from Steve  
 Moose"  
 /notes="Organ: juvenile vegetative shoots; Vector:  
 pAD-GAL4-2.1; Site 1: EcoRI; Site 2: XhoI; Equal amounts  
 of total RNA by weight from 4 tissue sources (see below)  
 were pooled, polyA+ RNA isolated, and cDNA synthesized for  
 EcoRI (5') and XhoI (3') directional cloning into lambda  
 HybriZap vector from Stratagene. Tissue Sources: 1. Whole  
 shoots 3 days after sowing/imbibing in wet soil. 2. Basal  
 1.5 cm shoots 6 days after sowing - includes yellow  
 portions of developing leaves 1-5, primordia from 6-8, and  
 the vegetative apex. 3. Non-green portions of developing  
 leaves 4-5 and the vegetative apex, including adult leaf  
 primordia, 9 days after sowing. 4. Partially expanded and  
 greening leaves 4-5 at 13 days after sowing."

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,71e-13 Length: 513  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x BI431142 (1-513)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThrAanProAlaGln 20  
 |||||||  
 Db 2 ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 37  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
 |||||||  
 Db 38 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCAGCCAGCTCCCGTCGCCCGC 91  
 QY 41 ArgSerSerArgSerLeuGlyAanValAlaSerAanGlyGlyArgileArgCys 58  
 |||||||  
 Db 92 CGCTCTCCAGAAAGCTCGGCAAGTC---AGCAACGGCGGAAGGATCCGGTGC 142

RESULT 11  
 CC616048/c 525 bp DNA linear GSS 18-JUN-2003  
 LOCUS  
 DEFINITION  
 genomic survey sequence.

ACCESSION  
 CC616048  
 VERSION  
 CC616048.1 GI:31977469  
 GSS.  
 SOURCE  
 Zea mays  
 ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 525)

REFERENCE  
 AUTHORS  
 Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,  
 Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,  
 Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.  
 Consortium for Maize Genomics  
 Unpublished (2002)

TITLE  
 JOURNAL  
 COMMENT  
 Other GSSs: OGIUKH26TV  
 Contact: Cathy Whitelaw

TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitelaw@tigr.org  
 Seq primer: TR

Class: methylation filtered.  
 Location/Qualifiers

## FEATURES

source  
 1..525  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"

/db\_xref="taxon:4577"  
 /clone\_lib="ZM04060P04"  
 /clone\_lib="ZM\_0.7\_1.5 KB"  
 /notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,84e-13 Length: 525  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 9 Gaps: 2

US-10-628-525A-34 (1-58) x CC616048 (1-525)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThrAanProAlaGln 20  
 |||||||  
 Db 306 ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 271  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
 |||||||  
 Db 270 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCAGCCAGCTCCCGTCGCCCGC 217  
 QY 41 ArgSerSerArgSerLeuGlyAanValAlaSerAanGlyGlyArgileArgCys 58  
 |||||||  
 Db 216 CGCTCTCCAGAAAGCTCGGCAAGTC---AGCAACGGCGGAAGGATCCGGTGC 166

## RESULT 12

BG349334

LOCUS

DEFINITION

sequence.

ACCESSION

BG349334

VERSION

BG349334.1 GI:13178076

KEYWORDS

EST.

SOURCE

Zea mays

ORGANISM

Zea mays

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 947028 row: A column: 12.

Location/Qualifiers

1..544

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/tissue\_type="leaf and stem, including leaf base"

/dev\_stage="2 week old seedling (3 leaves)"

/lab\_host="XLI-Blue"

/clone\_lib="947 - 2 week shoot from Barkan lab"

/note="Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-);

Site 1: EcoRI; Site 2: XhoI; Directionally cloned using

Stratagene's Unizap XR cDNA cloning kit with the 5' end

at the EcoRI site. The library represents 8 x 10<sup>5</sup>

independent recombinant phage. The plants were greenhouse

grown."

## ORIGIN



```

Alignment Scores:
Pred. No.: 5.05e-13 Length: 544
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 2 Gaps: 2

US-10-628-525A-34 (1-58) x BG349334 (1-544)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 44 ATGGGCCCCACCGTGATGGCTCGTCCGCCACC----- 79
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLeuSerThrAlaSerLeuProValAlaArg 40
Db 80 -----GCCGTGCTCGTTCAGGGGGCTCAAGTCCACCGCAGCTCCCGTCGCCCGC 133
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 134 CGCTCTCTCCAGAGCTTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 184

RESULT 13
CF025689
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 545)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
1..545
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="f334"
/db_xref="taxon:4577"
/clone="QCA1e07"
/tissue_type="3rd adult leaf"
/clone_lib="QCA"

ORIGIN
Alignment Scores:
Pred. No.: 5.06e-13 Length: 545
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x CF025689 (1-545)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 29 ATGGGCCCCACCGTGATGGCTCGTCCGCCACC----- 64
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLeuSerThrAlaSerLeuProValAlaArg 40

```

---

```

Db 65 -----GCCGTGCTCGTTCAGGGGGCTCAAGTCCACCGCAGCTCCCGTCGCCCGC 118
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 119 CGCTCTCTCCAGAGCTTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 169

RESULT 14
CD998700
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 569)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
1..569
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="QBF15c08"
/tissue_type="ear leaf"
/clone_lib="QBF"

ORIGIN
Alignment Scores:
Pred. No.: 5.33e-13 Length: 569
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x CD998700 (1-569)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 57 ATGGGCCCCACCGTGATGGCTCGTCCGCCACC----- 92
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLeuSerThrAlaSerLeuProValAlaArg 40
Db 93 -----GCCGTGCTCGTTCAGGGGGCTCAAGTCCACCGCAGCTCCCGTCGCCCGC 146
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 147 CGCTCTCTCCAGAGCTTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 197

RESULT 15
CF025518
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 608)  
Genoplante.  
Genoplante, a major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).

FEATURES  
source

Location/Qualifiers  
1..608  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="F334"  
/db\_xref="taxon:4577"  
/clone="QCA18e04"  
/tissue\_type="3rd adult leaf"  
/clone\_lib="QCA"

ORIGIN

Alignment Scores:  
Pred. No.: 5,76e-13 Length: 608  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x CF025518 (1-608)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
DB 29 ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 64  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
DB 65 -----GCCGTGCTCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 118  
QY 41 ArgSerSerArgSerLeuGlyAnValAlaSerAsnGlyGlyArgIleArgCys 58  
DB 119 CGCTCTCCAGAAGCCTCGGCACGTC---AGCACGGCGGAAGGATCGGTGC 169

RESULT 16  
CD990730

LOCUS CD990730 619 bp mRNA linear EST 16-JUL-2003  
DEFINITION QAY3f06.Yg QAY Zea mays cDNA clone QAY3f06, mRNA sequence.  
ACCESSION CD990730  
VERSION CD990730.1 GI:32851049  
KEYWORDS EST.  
SOURCE Zea mays

ORGANISM

Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Genoplante.  
Genoplante, a major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).

FEATURES  
source

Location/Qualifiers  
1..619

/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="F2"  
/db\_xref="taxon:4577"  
/clone="QAY3f06"  
/tissue\_type="aerial, root, whole plant"  
/clone\_lib="QAY"

ORIGIN

Alignment Scores:  
Pred. No.: 5,89e-13 Length: 619  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x CD990730 (1-619)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
DB 62 ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 97  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
DB 98 -----GCCGTGCTCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 151  
QY 41 ArgSerSerArgSerLeuGlyAnValAlaSerAsnGlyGlyArgIleArgCys 58  
DB 152 CGCTCTCCAGAAGCCTCGGCACGTC---AGCACGGCGGAAGGATCGGTGC 202

RESULT 17  
BG458523

LOCUS BG458523 622 bp mRNA linear EST 19-MAR-2001  
DEFINITION 947045808.y1 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA  
sequence.

ACCESSION BG458523  
VERSION BG458523.1 GI:13381848  
KEYWORDS EST.  
SOURCE Zea mays

ORGANISM

Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
AUTHORS  
TITLE

1 (bases 1 to 622)  
Walbot V.  
Maize ESTs from various cDNA libraries sequenced at Stanford  
University  
Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 947045 row: B column: 08.

LOCATION/Qualifiers

1..622  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf and stem, including leaf base"  
/dev\_stage="2 week old seedling (3 leaves)"  
/lab\_host="XLI-Blue"  
/clone\_lib="947 - 2 week shoot from Barkan lab"  
/note="Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-);  
Site 1: EcoRI; Site 2: XhoI; Directionally cloned using  
Stratagene's Unizap-XR cDNA cloning kit with the 5' end  
at the EcoRI site. The library represents 8 x 10e5  
independent recombinant phage. The plants were greenhouse  
grown."

FEATURES  
source

```

ORIGIN
Alignment Scores:
Pred. No.: 5,92e-13 Length: 622
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 2 Gaps: 2

US-10-628-525A-34 (1-58) x BG458523 (1-622)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAenProAlaGln 20
Db 31 ATGGCGCCACCGTGATGATGCGCTCGTCGGCCACC----- 66
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerIeuProValAlaArg 40
Db 67 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGTCGCCGCG 120
QY 41 ArgSerSerArgSerIeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58
Db 121 CGCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGT 171

RESULT 18
LOCUS AW352495 652 bp mRNA linear EST 02-FEB-2000
DEFINITION 707050811.y1 707 - Mixed adult tissues from Walbot lab (SK) Zea
ACCESSION AW352495
VERSION AW352495.1 GI:6851485
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 652)
AUTHORS Walbot V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
UNIVERSITY
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 707050 row: B column: 11.
FEATURES
source
1..652
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W23"
/db_xref="taxon:4577"
/tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DH10B"
(clone_lib="707 - Mixed adult tissues from Walbot lab
(SK)")
/notes="Organ: tassel, kernel, silk, husk, root, leaf;
Vector: pGAD10; Site 1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator
plant. tissue ratio is 4/2/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned."

ORIGIN
Alignment Scores:
Pred. No.: 6,27e-13 Length: 652
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0

```

```

Query Match: 72.2% Indels: 11
DB: 1 Gaps: 2

US-10-628-525A-34 (1-58) x AW352495 (1-652)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAenProAlaGln 20
Db 74 ATGGCGCCACCGTGATGATGCGCTCGTCGGCCACC----- 109
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerIeuProValAlaArg 40
Db 110 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGTCGCCGCG 163
QY 41 ArgSerSerArgSerIeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58
Db 164 CGCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGT 214

RESULT 19
LOCUS COS23152 657 bp mRNA linear EST 15-JUL-2004
DEFINITION 3530.1_153.1_B03.y.1 3530 - Full length cDNA library created by
Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
ACCESSION COS23152
VERSION COS23152.1 GI:50328026
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 657)
AUTHORS Walbot V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
UNIVERSITY
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3530.1_153.1 row: B column: 03.
FEATURES
source
1..657
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="multiple"
/dev_stage="varies by tissue"
/lab_host="DH10B"
(clone_lib="3530 - Full length cDNA library created by
Invitrogen from multiple tissues")
/notes="Organ: silks, husks, ears, pollen, shoot tips,
leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery
Project contracted with Invitrogen to produce a
normalized, full length library in a pSPORT vector. This
is a Gateway compatible vector, permitting clone movement
to new vector backbones for expression in diverse host
cells using recombination rather than restriction enzymes.
Details of the vector and sequencing primers are available
at ZmDB in the EST library description tables. poly(A)+
mRNA was prepared by Invitrogen, and equimolar amounts of
RNA from each of the 12 tissue samples were mixed together
for selection of mRNA with a 5' cap. After synthesis of
cDNA, a normalization step was conducted against the
mixture of RNA sources. This step effected a 20X to 80X
reduction in common transcript types. Tissues prepared: 1.
just emerging silks; 2. inner husks from ears of sample
#1; 3. 20 dap aleurone; 4. immature tassels, stages from
1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm

```

vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 day whole seed; 11. 12 day endosperm and embryo; 12. 17 day endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the Unigene clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

## ORIGIN

Alignment Scores:  
Pred. No.: 6.32e-13 Length: 657  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 7 Gaps: 2

US-10-628-525A-34 (1-58) x COS23152 (1-657)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThrArgThrAsnProAlaGln 20  
|||||  
Db 54 ATGGCGCCCAACCGTGATGATGGCTCGTCGCCACC----- 89  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
|||||  
Db 90 -----GCCGTCTCTCGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGCGCGCC 143  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyCys 58  
|||||  
Db 144 CGCTCTCCAGAGCTCGGCAAGTC---AGCACGGCGGAGGATCCGGTGC 194

## RESULT 20

BG320791/c  
LOCUS BG320791 660 bp mRNA linear EST 27-FEB-2001  
DEFINITION Zm04\_10c04\_R Zm04\_AAPC\_ECORC cold stressed\_maize\_seedlings Zea mays  
cDNA clone Zm04\_10c04, mRNA sequence.

ACCESSION BG320791.1 GI:13150469  
VERSION EST.  
KEYWORDS Zea mays

## SOURCE

ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 660)  
Singh, J.A., Wakui, K., Couroux, P., De Moors, A., Harris, L.J., Hattori, J.I., Ouellet, T., Robert, L.S., Spott, D. and Tinker, N.A.  
Expressed Sequence Tags from Cold-Stressed Maize Seedlings  
Unpublished (2001)  
Contact: Singh, J.A.

## JOURNAL

COMMENT Eastern Cereal and Oilseed Research Centre  
Agriculture and Agri-food Canada  
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A 0C6, Canada  
Tel: (613) 759-1662  
Fax: (613) 759-1701  
Email: singhja@agr.gc.ca.  
Location/Qualifiers  
1. .660  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="CO328"  
/db\_xref="taxon:CO328"  
/clone="Zm04\_10c04"  
/issue\_type="Leaf\_crown"  
/clone\_lib="Zm04\_AAPC\_ECORC cold stressed\_maize\_seedlings"  
/note="Vector: Bluescript SK-/XhoI-EcoRI; Site\_1: Eco RI;

## FEATURES

source

Site 2: Xho I; Lower temperature 50 C / hour from 22 to 120C; bring to 50 in 1 hour from 120C. Leave at 50C 2 days, photoperiod 16 hours. Light intensity was 125 uE-1. Library prepared by in vivo mass excision from amplified library."

## ORIGIN

Alignment Scores:  
Pred. No.: 6.36e-13 Length: 660  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 2 Gaps: 2

US-10-628-525A-34 (1-58) x BG320791 (1-660)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThrArgThrAsnProAlaGln 20  
|||||  
Db 623 ATGGCGCCCAACCGTGATGATGGCTCGTCGCCACC----- 588  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
|||||  
Db 587 -----GCCGTCTCTCGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGCGCGCC 534  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyCys 58  
|||||  
Db 533 CGCTCTCCAGAGCTCGGCAAGTC---AGCACGGCGGAGGATCCGGTGC 483

## RESULT 21

COS32595  
LOCUS COS32595 660 bp mRNA linear EST 15-JUL-2004  
DEFINITION 3530.1.214.1.E03.Y.1.3530 - Full length cDNA library created by  
Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.

ACCESSION COS32595  
VERSION COS32595.1 GI:50337469  
KEYWORDS EST.  
SOURCE Zea mays

## ORGANISM

Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 660)  
Walbot, V.

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 3530.1.214.1 row: E column: 03.  
Location/Qualifiers  
1. .660  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/tissue\_type="multiple"  
/dev\_stage="varies by tissue"  
/lab\_host="DH10B"  
/clone\_lib="3530 - Full length cDNA library created by  
Invitrogen from multiple tissues"  
/note="Organ: silks, husks, ears, pollen, shoot tips,  
leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT  
6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery  
Project contracted with Invitrogen to produce a  
normalized, full length library in a psort vector. This  
is a Gateway compatible vector, permitting clone movement  
to new vector backbones for expression in diverse host

## FEATURES

source

cells using recombination rather than restriction enzymes. Details of the vector and sequencing primers are available at ZmDB in the EST library description tables. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the Unigene clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

## ORIGIN

Alignment Scores:  
 Pred. No.: 6,36e-13 Length: 660  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 7 Gaps: 2

US-10-628-525A-34 (1-58) x C0532595 (1-660)

QY 1 MetaLaProThrValMetAlaSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 Db 47 ATGGGCCCCACCGTATGATGCTCGTCGGCCACC----- 82  
 |||||  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 83 -----GCCGTCGCTCCGTTCCAGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 136  
 |||||  
 QY 41 ArgSerSerArgSerLeuGlyValAlaSerAsnGlyGlyVArgIleArgCys 58  
 |||||  
 Db 137 CGCTCTCCAGAGGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 187  
 |||||

RESULT 22  
 CD990623  
 LOCUS CD990623 671 bp mRNA linear EST 16-JUL-2003  
 DEFINITION QAY2d03.Y9 QAY Zea mays cDNA clone QAY2d03, mRNA sequence.  
 ACCESSION CD990623  
 VERSION CD990623.1 GI:32850942  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 671)  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
 /tissue\_type="multiple"  
 /dev\_stages="varies by tissue"  
 /lab\_host="DH10B"  
 /clone\_lib="3530 - Full length cDNA library created by Invitrogen from multiple tissues"  
 /note="Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT 6.1; Site\_1: EcoRV; Site\_2: NotI; Maize Gene Discovery

FEATURES  
 Source

Location/Qualifiers  
 1..671  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
 /clone="QAY2d03"  
 /tissue\_type="aerial, root, whole plant"  
 /clone\_lib="QAY"

## ORIGIN

Alignment Scores:  
 Pred. No.: 6,48e-13 Length: 671  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x CD990623 (1-671)

QY 1 MetaLaProThrValMetAlaSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 Db 114 ATGGGCCCCACCGTATGATGCTCGTCGGCCACC----- 149  
 |||||  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 150 -----GCCGTCGCTCCGTTCCAGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 203  
 |||||  
 QY 41 ArgSerSerArgSerLeuGlyValAlaSerAsnGlyGlyVArgIleArgCys 58  
 |||||  
 Db 204 CGCTCTCCAGAGGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 254  
 |||||

## RESULT 23

C0533682  
 LOCUS C0533682 711 bp mRNA linear EST 15-JUL-2004  
 DEFINITION 3530.1.221.1.H01.Y.1 3530 - Full length cDNA library created by Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.  
 ACCESSION C0533682  
 VERSION C0533682.1 GI:50338556  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 711)  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
 /tissue\_type="multiple"  
 /dev\_stages="varies by tissue"  
 /lab\_host="DH10B"  
 /clone\_lib="3530 - Full length cDNA library created by Invitrogen from multiple tissues"  
 /note="Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT 6.1; Site\_1: EcoRV; Site\_2: NotI; Maize Gene Discovery

## JOURNAL

COMMENT  
 Unpublished (1999)  
 Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 3530.1.221.1 row: H column: 01.  
 Location/Qualifiers  
 1..711

## FEATURES

## Source

Location/Qualifiers  
 1..711  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
 /tissue\_type="multiple"  
 /dev\_stages="varies by tissue"  
 /lab\_host="DH10B"  
 /clone\_lib="3530 - Full length cDNA library created by Invitrogen from multiple tissues"  
 /note="Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT 6.1; Site\_1: EcoRV; Site\_2: NotI; Maize Gene Discovery

Project contracted with Invitrogen to produce a normalized, full length library in a pSport vector. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. Details of the vector and sequencing primers are available at ZmDB in the EST library description tables. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 day aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 day whole seed; 11. 12 day endosperm and embryo; 12. 17 day endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the Unigene clones from the Maize Gene Discovery RST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

## ORIGIN

Alignment Scores:  
 Pred. No.: 6,95e-13 Length: 711  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 7 Gaps: 2

US-10-628-525A-34 (1-58) x COS33682 (1-711)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 DB 54 ATGGCCGCCACCGTGATGCGCTCGTCGCCACCC----- 89  
 QY 21 AlaSerAlaValalaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
 |||||  
 DB 90 -----GCCGTCCGTCGGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 143  
 QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgIleArgCys 58  
 |||||  
 DB 144 CGCTCCTCCAGAGCCCTCGGCAACGTC---AGCACGGCGGAAGGATCCGGTGC 194

## RESULT 24

CD991089  
 LOCUS Zm BFB0062L05.r ZM\_BFB Zea mays cDNA clone QAZ4b01, mRNA linear EST 16-JUL-2003  
 DEFINITION QAZ4b01.yg QAZ Zea mays cDNA clone QAZ4b01, mRNA sequence.  
 ACCESSION CD991089  
 VERSION CD991089.1 GI:32851408  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 712)  
 Genoplate.  
 Genoplate, a major partnership french program in plant genomics  
 Unpublished (2003)  
 CONTACT: Genoplate  
 Genoplate  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french plant genomics programme 'Genoplate' (<http://www.genoplate.com>) and <http://genoplate-info.infobiogen.fr>.

FEATURES  
 source

Location/Qualifiers  
 1..712  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
 /clone="QAZ4b01"  
 /tissue\_type="aerial, root, whole plant"  
 /clone\_lib="QAZ"

## ORIGIN

Alignment Scores:  
 Pred. No.: 6,96e-13 Length: 712  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x CD991089 (1-712)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 DB 64 ATGGCCGCCACCGTGATGCGCTCGTCGCCACCC----- 99  
 QY 21 AlaSerAlaValalaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
 |||||  
 DB 100 -----GCCGTCCGTCGGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 153  
 QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgIleArgCys 58  
 |||||  
 DB 154 CGCTCCTCCAGAGCCCTCGGCAACGTC---AGCACGGCGGAAGGATCCGGTGC 204

## RESULT 25

DR822461  
 LOCUS ZM BFB0062L05.r ZM\_BFB Zea mays cDNA 5', mRNA linear EST 28-JUL-2005  
 DEFINITION DR822461  
 ACCESSION DR822461.1 GI:71441411  
 VERSION DR822461.1  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 769)  
 Kim H., Collura, K., Wissesteki, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.  
 Maize Full-length cDNA Project  
 Unpublished (2005)  
 CONTACT: Yeisoo Yu  
 Arizona Genomics Institute  
 The University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9585  
 Fax: 520 621 1259  
 Email: yeisoo@genome.arizona.edu  
 Plate: 0062 row: L column: 05.

FEATURES  
 source

Location/Qualifiers  
 1..769  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
 /tissue\_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"  
 /dev\_stage="varies by tissue"  
 /lab\_host="DH10B T1 phage resistant"  
 /clone\_lib="ZM\_BFB"

/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona  
(http://www.genome.arizona.edu/orders/)."

## ORIGIN

Alignment Scores:  
Pred. No.: 7,63e-13 Length: 769  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x DR822461 (1-769)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
DB 54 ATGGGCGCCACCGTGATGATGCGCTCGTGGCCACC----- 89  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
DB 90 -----GCCGTGCTCCGTTCCAGGGCTCAAGTCCACGCCAGCTCCCGTCCGCCGC 143  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
DB 144 CGCTCCTCCAGAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 194

## RESULT 26

DR824125  
LOCUS ZM\_BFB0065M08.r\_ZM\_BFB Zea mays cDNA 5', mRNA linear EST 28-JUL-2005

DEFINITION DR824125

ACCESSION DR824125

VERSION DR824125.1 GI:71443075

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 773)

Kim, H., Collura, K., Wisotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.

Maize Full-length cDNA Project

Unpublished (2005)

Contact: Yeisoo Yu

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu  
Plate: 0065 row: M column: 08.

## FEATURES

## source

1..773  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/tissue\_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"  
/dev\_stage="varies by tissue"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="ZM BFB"  
/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona  
(http://www.genome.arizona.edu/orders/)."

## ORIGIN

Alignment Scores:  
Pred. No.: 7,67e-13 Length: 773  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x DR824125 (1-773)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
DB 54 ATGGGCGCCACCGTGATGATGCGCTCGTGGCCACC----- 89

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
DB 90 -----GCCGTGCTCCGTTCCAGGGCTCAAGTCCACGCCAGCTCCCGTCCGCCGC 143

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58

DB 144 CGCTCCTCCAGAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 194

## RESULT 27

CG094731

LOCUS

DEFINITION

CG094731

ACCESSION

CG094731.1

KEYWORDS

SOURCE

ORGANISM

CG094731  
PUDK52TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTA079A107,  
genomic survey sequence.

CG094731

CG094731.1

KEYWORDS

SOURCE

ORGANISM

CG094731  
PUDK52TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTA079A107,  
genomic survey sequence.

CG094731

CG094731.1

KEYWORDS

SOURCE

ORGANISM



Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade; Panicoideae; Andropogoneae; Zea.

#### REFERENCE AUTHORS

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Reenick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennett, J.

Maize Genomics Consortium  
Unpublished (2003)  
Other GSSs: PURDKS2TB

#### JOURNAL COMMENT

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TF

Class: sheared ends.

#### FEATURES

source

1. 777  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZM8P0794107"  
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high  
CoT selected genomic DNA library"

Alignment Scores:  
Pred. No.: 7,72e-13 Length: 777  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 10 Gaps: 2

#### ORIGIN

US-10-628-525A-34 (1-58) x CG094731 (1-777)  
Alignment Scores:  
Pred. No.: 7,72e-13 Length: 777  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 10 Gaps: 2

US-10-628-525A-34 (1-58) x CG094731 (1-777)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraAlaThraArgThrAsnProAlaGln 20  
DB 610 ATGGCGCCACCGTGATGATGGCTCTGTCGCCACCC----- 645

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
DB 646 -----GCCGTCGCTCGTTCCAGGGGCTCAAGTCCACCGCAGCTCCCGTCGCCCGC 699

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
DB 700 CGCTCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 750

#### RESULT 28

DR829152 ZM\_BFB0074M16.r ZM\_BFB Zea mays cDNA 5', mRNA linear EST 28-JUL-2005  
LOCUS DR829152  
DEFINITION DR829152  
VERSION DR829152.1 GI:71448102  
KEYWORDS EST.

ORGANISM Zea mays

Zeae

Zeae

Zeae

Zeae

Zeae

Zeae

Zeae

Zeae

Zeae

Zeae

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Zeae

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Zeae

Zeae

Zeae

Zeae

Zeae

Zeae

Tel: 520 626 9585

Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plate: 0074 row: M column: 16.

#### FEATURES

source

1. 779  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/tissue\_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"  
/dev\_stage="varies by tissue"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="ZM BFB"

/notes="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for a selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 day aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 day whole seed; 11. 12 day endosperm and embryo; 12. 17 day endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (http://www.genome.arizona.edu/orders/)."

#### ORIGIN

Alignment Scores:  
Pred. No.: 7,74e-13 Length: 779  
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DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x DR829152 (1-779)

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DB 85 -----GCCGTCGCTCGTTCCAGGGGCTCAAGTCCACCGCAGCTCCCGTCGCCCGC 138

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
DB 139 CGCTCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 189

#### RESULT 29

CC641056

LOCUS CC641056

DEFINITION OGLCD30TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0320F12,

genomic survey sequence.

ACCESSION CC641056

VERSION CC641056.1

KEYWORDS GI:32024778

GSS.

CC641056 OGLCD30TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0320F12,

genomic survey sequence.

ACCESSION CC641056

VERSION CC641056.1

KEYWORDS GI:32024778

GSS.



GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 31, 2006, 22:47:42 ; Search time 77.568 Seconds  
(without alignments)  
1329.139 Million cell updates/sec

Title: US-10-628-525A-34

Perfect score: 282

Sequence: 1 MATVWMASSATATRNPAQ.....ARRSSRLGNVASNGRIIRC 58

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Database :

Issued Patents NA:\*

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- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:\*
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- 6: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq:\*
- 7: /cgn2\_6/ptodata/1/ina/PP COMB.seq:\*
- 8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 2          | 203.5 | 72.2        | 185    | 3  | US-08-852-340-14  |
| 3          | 203.5 | 72.2        | 405    | 2  | US-08-336-778-4   |
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| 5          | 203.5 | 72.2        | 5909   | 3  | US-09-921-263-2   |
| 6          | 196.5 | 69.7        | 415    | 3  | US-09-063-733A-49 |
| 7          | 196.5 | 69.7        | 415    | 3  | US-09-441-340-13  |
| 8          | 196.5 | 69.7        | 415    | 3  | US-09-186-002-3   |
| 9          | 196.5 | 69.7        | 415    | 3  | US-09-377-466B-25 |

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|----|-------|------|-------|---|-------------------|-------------------|
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| 11 | 196.5 | 69.7 | 416   | 3 | US-10-232-665-25  | Sequence 25, Appl |
| 12 | 196.5 | 69.7 | 416   | 3 | US-10-232-665-30  | Sequence 30, Appl |
| 13 | 196.5 | 69.7 | 3450  | 3 | US-09-377-466B-17 | Sequence 17, Appl |
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| 15 | 196.5 | 69.7 | 3455  | 3 | US-09-377-466B-36 | Sequence 36, Appl |
| 16 | 196.5 | 69.7 | 3455  | 3 | US-10-232-665-36  | Sequence 36, Appl |
| 17 | 196.5 | 69.7 | 4149  | 3 | US-09-377-466B-13 | Sequence 13, Appl |
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| 22 | 187.5 | 66.5 | 195   | 3 | US-09-122-399-9   | Sequence 9, Appl  |
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| 24 | 159.5 | 56.6 | 177   | 2 | US-08-095-726-12  | Sequence 12, Appl |
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| 33 | 150.5 | 53.4 | 2109  | 2 | US-09-155-989A-2  | Sequence 2, Appl  |
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136 70 24.8 4767 3 US-09-231-899-76 Sequence 76, Appl  
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## ALIGNMENTS

US-08-447-985-14  
; Sequence 14, Application US/08447985  
; Patent No. 6399861  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Thomas R. et al.  
; TITLE OF INVENTION: Methods and Compositions for the  
; Production of Stably Transformed, Fertile Monocot Plants  
; and Cells Thereof  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/447,985  
; FILING DATE: 23-May-1995  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/113,561  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: DEKM:055/PAR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 713/789-2679  
; TELEX: 79-0924  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 185 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-08-447-985-14  
Alignment Scores:  
Pred. No.: 2,25e-15 Length: 185  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 3 Gaps: 2  
US-10-628-525A-34 (1-58) x US-08-447-985-14 (1-185)  
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Db 42 ATGGGGCCACCGTATGATGGCTTCGTCGGCCACC----- 77  
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerIleuProValAlaArg 40  
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RESULT 2  
US-08-852-340-14  
; Sequence 14, Application US/08852340  
; Patent No. 6803499  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Thomas R., et al.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PRODUCTION OF STABLY TRANSFORMED, FERTILE MONOCOT PLANTS  
TITLE OF INVENTION: AND CELLS THEREOF  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/852,340  
FILING DATE: 07-MAY-1997  
CLASSIFICATION: 504  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/113,561  
FILING DATE: 25-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Wilson, Mark B.  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: DEKM:146/WIM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 185 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-852-340-14

Alignment Scores:  
Pred. No.: 2,25e-15 Length: 185  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-08-852-340-14 (1-185)

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Db 42 ATGGCGCCACCGTGATGGCTCGTCGGCCACC----- 77

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
Db 78 -----GCCGTCGCTCGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCGC 131

QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyArgIleArgCys 58  
Db 132 CGGTCCTCCAGAGCTCGGCAAGTC---AGCAACGGCGGAGGATCGGTGC 182

RESULT 3  
US-08-336-778-4  
Sequence 4, Application US/08336778  
Patent No. 5635618  
GENERAL INFORMATION:  
APPLICANT: Capellades, Montserrat  
APPLICANT: Derose, Richard  
APPLICANT: Montoliu, Lluís  
APPLICANT: Puigdomenech, Pedro  
APPLICANT: Torres, Miguel  
APPLICANT: Uribe, Javier  
APPLICANT: Rigau, Juan  
TITLE OF INVENTION: PROMOTER ELEMENTS OF CHIMERIC GENES

TITLE OF INVENTION: OF ALPHA-TUBULIN  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Preseer  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/336,778  
FILING DATE: 09-NOV-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: DiGiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9487  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 405 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-336-778-4

Alignment Scores:  
Pred. No.: 6.08e-15 Length: 405  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 82.2% Indels: 11  
DB: 2 Gaps: 2

US-10-628-525A-34 (1-58) x US-08-336-778-4 (1-405)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAenProAlaGln 20  
Db 262 ATGGCGCCACCGTGATGGCTCGTCGGCCACC----- 297

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
Db 298 -----GCCGTCGCTCGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCGC 351

QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyArgIleArgCys 58  
Db 352 CGGTCCTCCAGAGCTCGGCAAGTC---AGCAACGGCGGAGGATCGGTGC 402

RESULT 4  
US-09-921-263-1/c  
Sequence 1, Application US/09921263  
Patent No. 6791014  
GENERAL INFORMATION:  
APPLICANT: Aventis CropScience S.A.  
TITLE OF INVENTION: Use of HPPD inhibitors as selection agents in the transformation of plants  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/921,263  
CURRENT FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 1  
LENGTH: 5281  
TYPE: DNA  
ORGANISM: Artificial sequence



```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: N region
; LOCATION: (15)..(163)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (164)..(322)
; FEATURE:
; NAME/KEY: C region
; LOCATION: (323)..(411)
US-09-441-340-13

Alignment Scores:
Pred. No.: 4.02e-14 Length: 415
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-441-340-13 (1-415)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 15 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 50
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 51 -----GCCGTGCTCGTTCCTGGGGCTCAAGTCCACCGCCAGCTCCCGTGGCCGC 104
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 105 CGTCTCTCCAGAGCTCGGCAAGTC---AGCAACGGCGGAGGATCCGGTGC 155

RESULT 8
US-09-186-002-3
; Sequence 3, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; FILE REFERENCE: delta-Endotoxins
; CURRENT APPLICATION NUMBER: US Pat No. 6489542 09/186,002
; CURRENT FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Zea mays
US-09-186-002-3

Alignment Scores:
Pred. No.: 4.02e-14 Length: 415
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-186-002-3 (1-415)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 15 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 50
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 51 -----GCCGTGCTCGTTCCTGGGGCTCAAGTCCACCGCCAGCTCCCGTGGCCGC 104
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 105 CGTCTCTCCAGAGCTCGGCAAGTC---AGCAACGGCGGAGGATCCGGTGC 155
```

```
Db 51 -----GCCGTGCTCGTTCCTGGGGCTCAAGTCCACCGCCAGCTCCCGTGGCCGC 104
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 105 CGTCTCTCCAGAGCTCGGCAAGTC---AGCAACGGCGGAGGATCCGGTGC 155

RESULT 9
US-09-377-466B-25
; Sequence 25, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: non-naturally
; OTHER INFORMATION: occurring nucleotide sequence encoding Zea mays
; OTHER INFORMATION: ribulose bis-phosphate carboxylase chloroplast
; OTHER INFORMATION: targeting peptide
; NAME/KEY: CDS
; LOCATION: (16)..(162)
; NAME/KEY: CDS
; LOCATION: (326)..(415)
; NAME/KEY: intron
; LOCATION: (163)..(325)
; OTHER INFORMATION: I-Zm.rbcS
US-09-377-466B-25

Alignment Scores:
Pred. No.: 4.03e-14 Length: 416
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-377-466B-25 (1-416)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 16 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 51
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 52 -----GCCGTGCTCGTTCCTGGGGCTCAAGTCCACCGCCAGCTCCCGTGGCCGC 105
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 106 CGTCTCTCCAGAGCTCGGCAAGTC---AGCAACGGCGGAGGATCCGGTGC 156

RESULT 10
US-09-377-466B-30
; Sequence 30, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry2Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 416
```



; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: modified  
; OTHER INFORMATION: cauliflower mosaic virus promoter AS4  
US-09-377-466B-30

Alignment Scores:  
Pred. No.: 4,03e-14 Length: 416  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservative: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-377-466B-30 (1-416)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 16 ATGGCGCCACCGTGATGGCTCGTCGGCCACC----- 51  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 52 -----GCCGTGCTCCGTTCTTGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 105  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 106 CGCTCTCTCAGAAAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 156

#### RESULT 11

US-10-232-665-25  
; Sequence 25, Application US/10232665  
; Patent No. 6943281  
; GENERAL INFORMATION:  
; APPLICANT: Romano, Charles P.  
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
; CURRENT APPLICATION NUMBER: US/10/232,665  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US/09/377,466  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 416

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: non-naturally  
; OTHER INFORMATION: occurring nucleotide sequence encoding Zea mays  
; OTHER INFORMATION: ribulose bis-phosphate carboxylase chloroplast  
; OTHER INFORMATION: targeting peptide  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (16)..(162)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (326)..(415)  
; FEATURE:  
; NAME/KEY: Intron  
; LOCATION: (163)..(325)  
; OTHER INFORMATION: I-Zm.rbcS

US-10-232-665-25  
Alignment Scores:  
Pred. No.: 4.03e-14 Length: 416  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservative: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-10-232-665-25 (1-416)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 16 ATGGCGCCACCGTGATGGCTCGTCGGCCACC----- 51  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 52 -----GCCGTGCTCCGTTCTTGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 105  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 106 CGCTCTCTCAGAAAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 156

#### RESULT 12

US-10-232-665-30  
; Sequence 30, Application US/10232665  
; Patent No. 6943281  
; GENERAL INFORMATION:  
; APPLICANT: Romano, Charles P.  
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
; CURRENT APPLICATION NUMBER: US/10/232,665  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US/09/377,466  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 416  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: modified  
; OTHER INFORMATION: cauliflower mosaic virus promoter AS4  
US-10-232-665-30

#### Alignment Scores:

Pred. No.: 4.03e-14 Length: 416  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservative: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-10-232-665-30 (1-416)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 16 ATGGCGCCACCGTGATGGCTCGTCGGCCACC----- 51  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 52 -----GCCGTGCTCCGTTCTTGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 105  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 106 CGCTCTCTCAGAAAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 156

#### RESULT 13

US-09-377-466B-17  
; Sequence 17, Application US/09377466B  
; Patent No. 6501009  
; GENERAL INFORMATION:  
; APPLICANT: Romano, Charles P.

; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
; CURRENT APPLICATION NUMBER: US/09/377,466B  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 3450  
; TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: Description of Artificial Sequence: expression  
OTHER INFORMATION: cassette  
NAME/KEY: promoter  
LOCATION: (14)..(235)  
OTHER INFORMATION: P-CaMV.AS4  
NAME/KEY: 5'UTR  
LOCATION: (240)..(304)  
OTHER INFORMATION: L-Ta.hcb1  
NAME/KEY: intron  
LOCATION: (318)..(805)  
OTHER INFORMATION: I-Os.Act1  
NAME/KEY: transit\_peptide  
LOCATION: (825)..(971)  
OTHER INFORMATION: amino terminal TS-Zm.rbcS  
NAME/KEY: intron  
LOCATION: (972)..(1134)  
OTHER INFORMATION: I-Zm.rbcS  
NAME/KEY: transit\_peptide  
LOCATION: (1135)..(1221)  
OTHER INFORMATION: carboxy terminus TS-Zm.rbcS  
NAME/KEY: CDS  
LOCATION: (1222)..(3180)  
OTHER INFORMATION: Cry3Bb1 variant 11231mv1  
NAME/KEY: terminator  
LOCATION: (3198)..(3431)  
OTHER INFORMATION: T-Ta.hsp17  
US-09-377-466B-17

Alignment Scores:  
Pred. No.: 5.89e-13 Length: 3450  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservative: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-377-466B-17 (1-3450)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 825 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 860  
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 861 -----GCCGTCGCTCGTTCTCTGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCGC 914  
Qy 41 ArgSerSerArgSerLeuGlyAnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 915 CGCTCTCCAGAGCCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 965

RESULT 14  
US-10-232-665-17  
Sequence 17, Application US/10232665  
Patent No. 6943281  
GENERAL INFORMATION:  
APPLICANT: Romano, Charles P.  
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
CURRENT APPLICATION NUMBER: US/10232,665  
PRIOR FILING DATE: 2002-08-29  
CURRENT FILING DATE: 2002-08-29  
PRIORITY APPLICATION NUMBER: US/09/377,466  
PRIOR FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 17  
LENGTH: 3450  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: expression  
OTHER INFORMATION: cassette

FEATURE:  
NAME/KEY: promoter  
LOCATION: (14)..(235)  
OTHER INFORMATION: P-CaMV.AS4  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: (240)..(304)  
OTHER INFORMATION: L-Ta.hcb1  
FEATURE:  
NAME/KEY: intron  
LOCATION: (318)..(805)  
OTHER INFORMATION: I-Os.Act1  
FEATURE:  
NAME/KEY: transit\_peptide  
LOCATION: (825)..(971)  
OTHER INFORMATION: amino terminal TS-Zm.rbcS  
FEATURE:  
NAME/KEY: intron  
LOCATION: (972)..(1134)  
OTHER INFORMATION: I-Zm.rbcS  
FEATURE:  
NAME/KEY: transit\_peptide  
LOCATION: (1135)..(1221)  
OTHER INFORMATION: carboxy terminus TS-Zm.rbcS  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1222)..(3180)  
OTHER INFORMATION: Cry3Bb1 variant 11231mv1  
FEATURE:  
NAME/KEY: terminator  
LOCATION: (3198)..(3431)  
OTHER INFORMATION: T-Ta.hsp17  
US-10-232-665-17

Alignment Scores:  
Pred. No.: 5.89e-13 Length: 3450  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservative: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-10-232-665-17 (1-3450)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 825 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 860  
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 861 -----GCCGTCGCTCGTTCTCTGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCGC 914  
Qy 41 ArgSerSerArgSerLeuGlyAnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 915 CGCTCTCCAGAGCCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 965

RESULT 15  
US-09-377-466B-36  
Sequence 36, Application US/09377466B  
Patent No. 6501009  
GENERAL INFORMATION:  
APPLICANT: Romano, Charles P.  
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
CURRENT APPLICATION NUMBER: US/09/377,466B  
CURRENT FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 36  
LENGTH: 3455  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: expression  
OTHER INFORMATION: cassette

```

/ OTHER INFORMATION: Description of Artificial Sequence: expression
/ NAME/KEY: cassette
/ LOCATION: (14)..(235)
/ OTHER INFORMATION: P.CaMV.AS4
/ NAME/KEY: 5'UTR
/ LOCATION: (240)..(304)
/ OTHER INFORMATION: L-Ta.hcb1
/ NAME/KEY: intron
/ LOCATION: (318)..(805)
/ OTHER INFORMATION: I-Os.Act1
/ NAME/KEY: transit_peptide
/ LOCATION: (825)..(971)
/ OTHER INFORMATION: TS-Zm.rbcS amino terminal coding sequence upstream
/ NAME/KEY: intron
/ LOCATION: (972)..(1134)
/ OTHER INFORMATION: I-Zm.rbcS
/ NAME/KEY: transit_peptide
/ LOCATION: (1135)..(1221)
/ OTHER INFORMATION: TS-Zm.rbcS carboxy terminus coding sequence
/ NAME/KEY: CDS
/ LOCATION: (1222)..(3180)
/ OTHER INFORMATION: downstream of Zea mays rbcS intron
/ NAME/KEY: intron
/ LOCATION: (3198)..(3431)
/ OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-36

```

```

Alignment Scores:
Pred. No.: 5,9e-13 Length: 3455
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 3 Gaps: 2

```

US-10-628-525A-34 (1-58) x US-09-377-466B-36 (1-3455)

```

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThAlaThrArgThrAsnProAlaGln 20
Db 825 ATGGCGCCACCGTGATGATGGCTCGTGGCCACC----- 860

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 861 -----GCCGTGCTCCGTTCTTGGGGCTCAAGTCCACCGCAGCCTCCCGTCCCGCC 914

QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyValGlyLeuArgCys 58
Db 915 CGCTCTCCAGAGCTCGGCAACGTC---ACCAACGGGGGAAGGATCCGGTGC 965

```

```

RESULT 16
US-10-232-665-36
; Sequence 36, Application US/10232665
; Patent No. 6943281
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/10/232,665
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 36
; LENGTH: 3455
; TYPE: DNA
; ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: expression

```

```

/ FEATURE:
/ NAME/KEY: promoter
/ LOCATION: (14)..(235)
/ OTHER INFORMATION: P.CaMV.AS4
/ FEATURE:
/ NAME/KEY: 5'UTR
/ LOCATION: (240)..(304)
/ OTHER INFORMATION: L-Ta.hcb1
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: (318)..(805)
/ OTHER INFORMATION: I-Os.Act1
/ FEATURE:
/ NAME/KEY: transit_peptide
/ LOCATION: (825)..(971)
/ OTHER INFORMATION: TS-Zm.rbcS amino terminal coding sequence upstream
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: (972)..(1134)
/ OTHER INFORMATION: I-Zm.rbcS
/ FEATURE:
/ NAME/KEY: transit_peptide
/ LOCATION: (1135)..(1221)
/ OTHER INFORMATION: TS-Zm.rbcS carboxy terminus coding sequence
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1222)..(3180)
/ OTHER INFORMATION: variant Cry3BB1 coding sequence encoding v11231
/ FEATURE:
/ NAME/KEY: terminator
/ LOCATION: (3198)..(3431)
/ OTHER INFORMATION: T-Ta.hsp17
US-10-232-665-36

```

```

Alignment Scores:
Pred. No.: 5,9e-13 Length: 3455
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 3 Gaps: 2

```

US-10-628-525A-34 (1-58) x US-10-232-665-36 (1-3455)

```

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThAlaThrArgThrAsnProAlaGln 20
Db 825 ATGGCGCCACCGTGATGATGGCTCGTGGCCACC----- 860

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 861 -----GCCGTGCTCCGTTCTTGGGGCTCAAGTCCACCGCAGCCTCCCGTCCCGCC 914

QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyValGlyLeuArgCys 58
Db 915 CGCTCTCCAGAGCTCGGCAACGTC---ACCAACGGGGGAAGGATCCGGTGC 965

```

```

RESULT 17
US-09-377-466B-13
; Sequence 13, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 4149
; TYPE: DNA

```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; NAME/KEY: promoter
; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMV.35S
; NAME/KEY: intron
; LOCATION: (669)..(1472)
; OTHER INFORMATION: I-Zm.Hsp70
; NAME/KEY: intron
; LOCATION: (1489)..(1635)
; OTHER INFORMATION: amino terminal TS-Zm.rbcS
; NAME/KEY: intron
; LOCATION: (1636)..(1798)
; OTHER INFORMATION: I-Zm.rbcS
; NAME/KEY: intron
; LOCATION: (1799)..(1885)
; OTHER INFORMATION: carboxy terminus TS-Zm.rbcS
; NAME/KEY: CDS
; LOCATION: (1885)..(3843)
; OTHER INFORMATION: Cry3Bb1 variant v11231
; NAME/KEY: terminator
; LOCATION: (3871)..(4127)
; OTHER INFORMATION: T-AGRTu.nos 3' transcription termination and
; OTHER INFORMATION: polyadenylation sequence
US-09-377-466B-13
```

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Alignment Scores:
Pred. No.: 7.44e-13 Length: 4149
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 3 Gaps: 2
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US-10-628-525A-34 (1-58) x US-09-377-466B-13 (1-4149)

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QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 1488 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC----- 1523
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
DB 1524 -----GCCGTCGCTCGTTCTCGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 1577
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgLeuArgCys 58
DB 1578 CGCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 1628
```

#### RESULT 18

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US-10-232-665-13
; Sequence 13, Application US/10232665
; Patent No. 6943281
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/10/232,665
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 4149
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; NAME/KEY: promoter
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; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMV.35S
; FEATURE:
; NAME/KEY: intron
; LOCATION: (669)..(1472)
; OTHER INFORMATION: I-Zm.Hsp70
; NAME/KEY: intron
; LOCATION: (1489)..(1635)
; OTHER INFORMATION: amino terminal TS-Zm.rbcS
; NAME/KEY: intron
; LOCATION: (1636)..(1798)
; OTHER INFORMATION: I-Zm.rbcS
; NAME/KEY: intron
; LOCATION: (1799)..(1885)
; OTHER INFORMATION: carboxy terminus TS-Zm.rbcS
; NAME/KEY: CDS
; LOCATION: (1885)..(3843)
; OTHER INFORMATION: Cry3Bb1 variant v11231
; NAME/KEY: terminator
; LOCATION: (3871)..(4127)
; OTHER INFORMATION: T-AGRTu.nos 3' transcription termination and
; OTHER INFORMATION: polyadenylation sequence
US-10-232-665-13
```

```
Alignment Scores:
Pred. No.: 7.44e-13 Length: 4149
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 3 Gaps: 2
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US-10-628-525A-34 (1-58) x US-10-232-665-13 (1-4149)

```
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 1488 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC----- 1523
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
DB 1524 -----GCCGTCGCTCGTTCTCGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 1577
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgLeuArgCys 58
DB 1578 CGCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 1628
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#### RESULT 19

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US-09-186-002-16
; Sequence 16, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
; CURRENT APPLICATION NUMBER: US/09/186,002B
; CURRENT FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 8349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (3666)..(5573)
; OTHER INFORMATION: completely synthesized
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## US-09-186-002-16

## Alignment Scores:

Pred. No.: 1.8e-12 Length: 8349  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservatives: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-186-002-16 (1-8349)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20

Db 3269 ATGGGCGCCACCGTGATGCTCGTCCGCCACC----- 3304

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40

Db 3305 -----GCCGTGCTCCGTTCTTGGGGCTCAAGTCCACGCCAGCGCTCCCGTCCGCCGC 3358

QY 41 ArgSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgIleArgCys 58

Db 3359 CGCTCTCCAGAGCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 3409

## RESULT 20

US-08-622-740-9

; Sequence 9, Application US/08622740

; Patent No. 5950390

; GENERAL INFORMATION:

; APPLICANT: Lundquist, Ronald C.

; APPLICANT: Walters, David A.

; APPLICANT: Kirihara, Julie A.

; TITLE OF INVENTION: Methods and Compositions for the

; TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants

; TITLE OF INVENTION: and Cells Thereof

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Schwegman, Lundberg, Woessner &amp; Kluth, P.A.

; STREET: 3500 IDS Center

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/622,740

; FILING DATE: 27-MARCH-1996

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Woessner, Warren D.

; REGISTRATION NUMBER: 30,440

; REFERENCE/DOCKET NUMBER: 950.013US4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-339-0331

; TELEFAX: 612-339-3061

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 195 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-622-740-9

## Alignment Scores:

Pred. No.: 1.68e-13 Length: 195  
Score: 187.50 Matches: 44  
Percent Similarity: 80.0% Conservatives: 0  
Best Local Similarity: 80.0% Mismatches: 1  
Query Match: 66.5% Indels: 11

DB:

2

Gaps:

2

US-10-628-525A-34 (1-58) x US-08-622-740-9 (1-195)

QY 4 ThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAlaSerAla 23

Db 61 ACCGTGATGATGGCTCGTCCGCCACC-----GCC 90

QY 24 ValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArgSerSer 43

Db 91 GTCGCTCGTTCAGGGGCTCAAGTCCACGCCAGCGTCCCGTCCCGCGGCTCTCC 150

QY 44 ArgSerLeuGlyAenValAlaSerAsnGlyGlyArgIleArgCys 58

Db 151 AGAAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 192

## RESULT 21

US-08-440-689-9

; Sequence 9, Application US/08440689

; Patent No. 6025545

; GENERAL INFORMATION:

; APPLICANT: Lundquist, Ronald C.

; APPLICANT: Walters, David A.

; APPLICANT: Kirihara, Julie A.

; TITLE OF INVENTION: Methods and Compositions for the

; TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants

; TITLE OF INVENTION: and Cells Thereof

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Schwegman, Lundberg, Woessner &amp; Kluth, P.A.

; STREET: 3500 IDS Center

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/440,689

; FILING DATE: 15-MAY-1995

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Woessner, Warren D.

; REGISTRATION NUMBER: 30,440

; REFERENCE/DOCKET NUMBER: 950.013US2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-339-0331

; TELEFAX: 612-339-3061

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 195 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-440-689-9

## Alignment Scores:

Pred. No.: 1.68e-13 Length: 195  
Score: 187.50 Matches: 44  
Percent Similarity: 80.0% Conservatives: 0  
Best Local Similarity: 80.0% Mismatches: 0  
Query Match: 66.5% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-08-440-689-9 (1-195)

QY 4 ThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAlaSerAla 23

Db 61 ACCGTGATGATGGCTCGTCCGCCACC-----GCC 90

QY 24 ValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArgSerSer 43  
Db 91 GTGCTCCGTTCCAGGGGCTCAAGTCCACCCAGGCTCCCGTCCGCGCGGTCTCTCC 150

QY 44 ArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 151 AGAAGCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 192

RESULT 22  
US-09-122-399-9  
; Sequence 9, Application US/09122399  
; Patent No. 6329574  
; GENERAL INFORMATION:  
; APPLICANT: Lundquist, Ronald C.  
; APPLICANT: Walters, David A.  
; APPLICANT: Kirihara, Julie A.  
; TITLE OF INVENTION: Methods and Compositions for the  
; TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants  
; TITLE OF INVENTION: and Cells Thereof  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.  
; STREET: 3500 IDS Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09122.399  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/112.245  
; FILING DATE: 25-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Woessner, Warren D.  
; REGISTRATION NUMBER: 30,440  
; REFERENCE/DOCKET NUMBER: 950.13US01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-339-0331  
; TELEFAX: 612-339-3061  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 195 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-122-399-9

Alignment Scores:  
Pred. No.: 1.68e-13 Length: 195  
Score: 187.50 Matches: 44  
Percent Similarity: 80.0% Conservative: 0  
Best Local Similarity: 80.0% Mismatches: 0  
Query Match: 66.5% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-122-399-9 (1-195)

QY 4 ThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAlaSerAla 23  
Db 61 ACCGTGATGATGGCTCGTCGGCCACC-----GCC 90

QY 24 ValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArgSerSer 43  
Db 91 GTGCTCCGTTCCAGGGGCTCAAGTCCACCCAGGCTCCCGTCCGCGCGGTCTCTCC 150

QY 44 ArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58

Db 151 AGAAGCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 192

RESULT 23  
US-08-440-646A-9  
; Sequence 9, Application US/08440646A  
; Patent No. 6775589  
; GENERAL INFORMATION:  
; APPLICANT: Lundquist, Ronald C.  
; APPLICANT: Walters, David A.  
; APPLICANT: Kirihara, Julie A.  
; TITLE OF INVENTION: Methods and Compositions for the  
; TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants  
; TITLE OF INVENTION: and Cells Thereof  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.  
; STREET: 3500 IDS Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440.646A  
; FILING DATE: 15-May-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/112.245  
; FILING DATE: 25-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Woessner, Warren D.  
; REGISTRATION NUMBER: 30,440  
; REFERENCE/DOCKET NUMBER: 950.13US01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-339-0331  
; TELEFAX: 612-339-3061  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 195 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-08-440-646A-9

Alignment Scores:  
Pred. No.: 1.68e-13 Length: 195  
Score: 187.50 Matches: 44  
Percent Similarity: 80.0% Conservative: 0  
Best Local Similarity: 80.0% Mismatches: 0  
Query Match: 66.5% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-08-440-646A-9 (1-195)

QY 4 ThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAlaSerAla 23  
Db 61 ACCGTGATGATGGCTCGTCGGCCACC-----GCC 90

QY 24 ValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArgSerSer 43  
Db 91 GTGCTCCGTTCCAGGGGCTCAAGTCCACCCAGGCTCCCGTCCGCGCGGTCTCTCC 150

QY 44 ArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 151 AGAAGCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 192

RESULT 24









; LENGTH: 204  
; TYPE: DNA  
; ORGANISM: Nicotiana tabacum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(204)  
US-09-839-477-3

Alignment Scores:  
Pred. No.: 3.01e-10 Length: 204  
Score: 159.50 Matches: 32  
Percent Similarity: 79.3% Conservative: 14  
Best Local Similarity: 55.2% Mismatches: 11  
Query Match: 56.6% Indels: 1  
DB: 3 Gaps: 1

US-10-628-525A-34 (1-58) x US-09-839-477-3 (1-204)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 1 ATGGCTTCCTCAGTT---CTTCTCTGCAGCAGTTGCCACCCGACGAATGTTGCTCAA 57  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 58 GCTAACATGGTTCACCTTTCACCTGCGCTTAAGTCAGTCGCTCATTCCTGTTTCAGG 117  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 118 AAGCAAAACCTTGACATCACTTCCTATTCAGCAACCGGGGAAGAGTGCAATGC 171

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GenCore version 5.1.7  
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(without alignments)  
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Perfect score: 282

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Maximum Match 100%

Listing first 150 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result | No.   | Score | Query | Match | Length            | DB | ID | Description       |
|--------|-------|-------|-------|-------|-------------------|----|----|-------------------|
| 1      | 203.5 | 72.2  | 183   | 6     | US-10-140-410-1   |    |    | Sequence 1, Appl  |
| 2      | 203.5 | 72.2  | 228   | 3     | US-09-987-899-69  |    |    | Sequence 69, Appl |
| 3      | 203.5 | 72.2  | 229   | 3     | US-09-987-899-84  |    |    | Sequence 84, Appl |
| 4      | 203.5 | 72.2  | 230   | 3     | US-09-987-899-264 |    |    | Sequence 264, App |
| 5      | 203.5 | 72.2  | 235   | 3     | US-09-987-899-79  |    |    | Sequence 79, Appl |
| 6      | 203.5 | 72.2  | 236   | 3     | US-09-987-899-70  |    |    | Sequence 70, Appl |
| 7      | 203.5 | 72.2  | 238   | 3     | US-09-987-899-66  |    |    | Sequence 66, Appl |

|    |       |      |      |   |                     |  |  |                   |
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| 8  | 203.5 | 72.2 | 249  | 3 | US-09-987-899-71    |  |  | Sequence 71, Appl |
| 9  | 203.5 | 72.2 | 264  | 3 | US-09-987-899-53    |  |  | Sequence 53, Appl |
| 10 | 203.5 | 72.2 | 265  | 3 | US-09-987-899-40    |  |  | Sequence 40, Appl |
| 11 | 203.5 | 72.2 | 272  | 3 | US-09-987-899-45    |  |  | Sequence 45, Appl |
| 12 | 203.5 | 72.2 | 276  | 3 | US-09-987-899-26    |  |  | Sequence 26, Appl |
| 13 | 203.5 | 72.2 | 276  | 3 | US-09-987-899-51    |  |  | Sequence 51, Appl |
| 14 | 203.5 | 72.2 | 284  | 3 | US-09-987-899-32    |  |  | Sequence 32, Appl |
| 15 | 203.5 | 72.2 | 286  | 3 | US-09-987-899-37    |  |  | Sequence 37, Appl |
| 16 | 203.5 | 72.2 | 291  | 3 | US-09-987-899-47    |  |  | Sequence 47, Appl |
| 17 | 203.5 | 72.2 | 297  | 3 | US-09-987-899-14    |  |  | Sequence 14, Appl |
| 18 | 203.5 | 72.2 | 298  | 3 | US-09-987-899-21    |  |  | Sequence 21, Appl |
| 19 | 203.5 | 72.2 | 305  | 3 | US-09-987-899-16    |  |  | Sequence 16, Appl |
| 20 | 203.5 | 72.2 | 307  | 3 | US-09-987-899-29    |  |  | Sequence 29, Appl |
| 21 | 203.5 | 72.2 | 309  | 3 | US-09-987-899-15    |  |  | Sequence 15, Appl |
| 22 | 203.5 | 72.2 | 311  | 3 | US-09-987-899-30    |  |  | Sequence 30, Appl |
| 23 | 203.5 | 72.2 | 312  | 3 | US-09-987-899-68    |  |  | Sequence 68, Appl |
| 24 | 203.5 | 72.2 | 315  | 3 | US-09-987-899-11    |  |  | Sequence 11, Appl |
| 25 | 203.5 | 72.2 | 317  | 3 | US-09-987-899-10    |  |  | Sequence 10, Appl |
| 26 | 203.5 | 72.2 | 319  | 3 | US-09-987-899-4     |  |  | Sequence 4, Appl  |
| 27 | 203.5 | 72.2 | 344  | 3 | US-09-987-899-231   |  |  | Sequence 231, App |
| 28 | 203.5 | 72.2 | 409  | 3 | US-09-987-899-215   |  |  | Sequence 215, App |
| 29 | 203.5 | 72.2 | 415  | 3 | US-09-987-899-244   |  |  | Sequence 244, App |
| 30 | 203.5 | 72.2 | 438  | 3 | US-09-987-899-210   |  |  | Sequence 210, App |
| 31 | 203.5 | 72.2 | 441  | 3 | US-09-987-899-229   |  |  | Sequence 229, App |
| 32 | 203.5 | 72.2 | 443  | 3 | US-09-987-899-225   |  |  | Sequence 225, App |
| 33 | 203.5 | 72.2 | 740  | 8 | US-10-425-115-83321 |  |  | Sequence 83321, A |
| 34 | 203.5 | 72.2 | 1085 | 8 | US-10-425-115-83320 |  |  | Sequence 83320, A |
| 35 | 203.5 | 72.2 | 1945 | 8 | US-10-425-115-83331 |  |  | Sequence 83331, A |
| 36 | 203.5 | 72.2 | 5281 | 3 | US-09-921-263-1     |  |  | Sequence 1, Appl  |
| 37 | 203.5 | 72.2 | 5909 | 3 | US-09-921-263-2     |  |  | Sequence 2, Appl  |
| 38 | 202.5 | 71.8 | 197  | 3 | US-09-987-899-270   |  |  | Sequence 270, App |
| 39 | 202.5 | 71.8 | 198  | 3 | US-09-987-899-99    |  |  | Sequence 99, Appl |
| 40 | 202.5 | 71.8 | 258  | 3 | US-09-987-899-48    |  |  | Sequence 48, Appl |
| 41 | 202.5 | 71.8 | 268  | 3 | US-09-987-899-54    |  |  | Sequence 54, Appl |
| 42 | 202.5 | 71.8 | 269  | 3 | US-09-987-899-62    |  |  | Sequence 62, Appl |
| 43 | 202.5 | 71.8 | 276  | 3 | US-09-987-899-44    |  |  | Sequence 44, Appl |
| 44 | 202.5 | 71.8 | 278  | 3 | US-09-987-899-22    |  |  | Sequence 22, Appl |
| 45 | 202.5 | 71.8 | 283  | 3 | US-09-987-899-31    |  |  | Sequence 31, Appl |
| 46 | 202.5 | 71.8 | 286  | 3 | US-09-987-899-41    |  |  | Sequence 41, Appl |
| 47 | 202.5 | 71.8 | 290  | 3 | US-09-987-899-35    |  |  | Sequence 35, Appl |
| 48 | 202.5 | 71.8 | 291  | 3 | US-09-987-899-25    |  |  | Sequence 25, Appl |
| 49 | 202.5 | 71.8 | 291  | 3 | US-09-987-899-34    |  |  | Sequence 34, Appl |
| 50 | 202.5 | 71.8 | 291  | 3 | US-09-987-899-49    |  |  | Sequence 49, Appl |
| 51 | 202.5 | 71.8 | 296  | 3 | US-09-987-899-38    |  |  | Sequence 38, Appl |
| 52 | 202.5 | 71.8 | 310  | 3 | US-09-987-899-23    |  |  | Sequence 23, Appl |
| 53 | 202.5 | 71.8 | 310  | 3 | US-09-987-899-27    |  |  | Sequence 27, Appl |
| 54 | 202.5 | 71.8 | 316  | 3 | US-09-987-899-9     |  |  | Sequence 9, Appl  |
| 55 | 202.5 | 71.8 | 381  | 3 | US-09-987-899-220   |  |  | Sequence 220, App |
| 56 | 202.5 | 71.8 | 411  | 3 | US-09-987-899-221   |  |  | Sequence 221, App |
| 57 | 202.5 | 71.8 | 414  | 3 | US-09-987-899-213   |  |  | Sequence 213, App |
| 58 | 202.5 | 71.8 | 433  | 3 | US-09-987-899-211   |  |  | Sequence 211, App |
| 59 | 202.5 | 71.8 | 434  | 3 | US-09-987-899-223   |  |  | Sequence 223, App |
| 60 | 202.5 | 71.8 | 434  | 3 | US-09-987-899-224   |  |  | Sequence 224, App |
| 61 | 202.5 | 71.8 | 1271 | 8 | US-10-425-115-83324 |  |  | Sequence 83324, A |
| 62 | 199.5 | 70.7 | 283  | 3 | US-09-987-899-39    |  |  | Sequence 39, Appl |
| 63 | 198.5 | 70.4 | 226  | 3 | US-09-987-899-97    |  |  | Sequence 97, Appl |
| 64 | 198.5 | 70.4 | 428  | 3 | US-09-987-899-217   |  |  | Sequence 217, App |
| 65 | 198.5 | 70.4 | 453  | 3 | US-09-987-899-230   |  |  | Sequence 230, App |
| 66 | 197.5 | 70.0 | 199  | 3 | US-09-987-899-105   |  |  | Sequence 105, App |
| 67 | 197.5 | 70.0 | 312  | 3 | US-09-987-899-42    |  |  | Sequence 42, Appl |
| 68 | 197.5 | 70.0 | 382  | 3 | US-09-987-899-235   |  |  | Sequence 235, App |
| 69 | 196.5 | 69.7 | 285  | 3 | US-09-987-899-75    |  |  | Sequence 75, Appl |
| 70 | 196.5 | 69.7 | 415  | 5 | US-10-005-530-49    |  |  | Sequence 49, Appl |
| 71 | 196.5 | 69.7 | 415  | 5 | US-10-213-791-13    |  |  | Sequence 13, Appl |
| 72 | 196.5 | 69.7 | 415  | 6 | US-10-198-478-3     |  |  | Sequence 3, Appl  |
| 73 | 196.5 | 69.7 | 416  | 5 | US-10-232-665-25    |  |  | Sequence 25, Appl |
| 74 | 196.5 | 69.7 | 416  | 5 | US-10-232-665-30    |  |  | Sequence 30, Appl |
| 75 | 196.5 | 69.7 | 3450 | 5 | US-10-232-665-17    |  |  | Sequence 17, Appl |
| 76 | 196.5 | 69.7 | 3455 | 5 | US-10-232-665-36    |  |  | Sequence 36, Appl |
| 77 | 196.5 | 69.7 | 4149 | 5 | US-10-232-665-13    |  |  | Sequence 13, Appl |
| 78 | 196.5 | 69.7 | 8349 | 6 | US-10-198-478-16    |  |  | Sequence 16, Appl |
| 79 | 195.5 | 69.3 | 212  | 3 | US-09-987-899-90    |  |  | Sequence 90, Appl |
| 80 | 195.5 | 69.3 | 232  | 3 | US-09-987-899-82    |  |  | Sequence 82, Appl |

81 195.5 69.3 241 3 US-09-987-899-72  
82 195.5 69.3 242 3 US-09-987-899-81  
83 195.5 69.3 242 3 US-09-987-899-101  
84 195.5 69.3 244 3 US-09-987-899-88  
85 195.5 69.3 250 3 US-09-987-899-266  
86 195.5 69.3 259 3 US-09-987-899-103  
87 195.5 69.3 265 3 US-09-987-899-98  
88 195.5 69.3 266 3 US-09-987-899-92  
89 195.5 69.3 269 3 US-09-987-899-95  
90 195.5 69.3 270 3 US-09-987-899-94  
91 195.5 69.3 273 3 US-09-987-899-89  
92 195.5 69.3 275 3 US-09-987-899-269  
93 195.5 69.3 275 3 US-09-987-899-59  
94 195.5 69.3 276 3 US-09-987-899-87  
95 195.5 69.3 276 3 US-09-987-899-91  
96 195.5 69.3 279 3 US-09-987-899-83  
97 195.5 69.3 286 3 US-09-987-899-86  
98 195.5 69.3 287 3 US-09-987-899-80  
99 195.5 69.3 289 3 US-09-987-899-50  
100 195.5 69.3 291 3 US-09-987-899-78  
101 195.5 69.3 292 3 US-09-987-899-85  
102 195.5 69.3 294 3 US-09-987-899-77  
103 195.5 69.3 298 3 US-09-987-899-61  
104 195.5 69.3 302 3 US-09-987-899-12  
105 195.5 69.3 307 3 US-09-987-899-76  
106 195.5 69.3 310 3 US-09-987-899-7  
107 195.5 69.3 312 3 US-09-987-899-17  
108 195.5 69.3 312 3 US-09-987-899-36  
109 195.5 69.3 315 3 US-09-987-899-24  
110 195.5 69.3 316 3 US-09-987-899-258  
111 195.5 69.3 322 3 US-09-987-899-18  
112 195.5 69.3 326 3 US-09-987-899-43  
113 195.5 69.3 330 3 US-09-987-899-6  
114 195.5 69.3 364 3 US-09-987-899-252  
115 195.5 69.3 364 3 US-09-987-899-254  
116 195.5 69.3 381 3 US-09-987-899-243  
117 195.5 69.3 399 3 US-09-987-899-239  
118 195.5 69.3 399 3 US-09-987-899-245  
119 195.5 69.3 410 7 US-10-424-598-66587  
120 195.5 69.3 415 3 US-09-987-899-242  
121 195.5 69.3 421 3 US-09-987-899-260  
122 195.5 69.3 425 3 US-09-987-899-237  
123 195.5 69.3 428 3 US-09-987-899-263  
124 195.5 69.3 446 3 US-09-987-899-241  
125 195.5 69.3 455 3 US-09-987-899-232  
126 195.5 69.3 510 7 US-10-260-238-5718  
127 195.5 69.3 1200 8 US-10-425-115-83327  
128 195.5 69.3 2390 8 US-10-425-115-13220  
129 194.5 69.0 261 3 US-09-987-899-93  
130 194.5 69.0 269 3 US-09-987-899-63  
131 194.5 68.0 458 3 US-09-987-899-216  
132 194.5 68.3 265 3 US-09-987-899-65  
133 192.5 68.3 360 3 US-09-987-899-240  
134 191.5 67.9 271 3 US-09-987-899-100  
135 191.5 67.9 325 3 US-09-987-899-46  
136 191.5 67.9 368 3 US-09-987-899-247  
137 191.5 67.9 418 3 US-09-987-899-249  
138 190.5 67.6 303 3 US-09-987-899-28  
139 189.5 67.2 179 3 US-09-987-899-109  
140 189.5 67.2 316 3 US-09-987-899-108  
141 188.5 66.8 316 8 US-10-425-115-158707  
142 187.5 66.5 195 9 US-10-919-228-9  
143 187.5 66.5 379 3 US-09-987-899-267  
144 186.5 66.1 262 3 US-09-987-899-67  
145 185.5 65.8 200 3 US-09-987-899-107  
146 184.5 64.7 384 3 US-09-987-899-265  
147 179.5 63.7 259 3 US-09-987-899-52  
148 179.5 63.7 367 3 US-09-987-899-257  
149 178.5 63.3 281 8 US-10-425-115-142195  
150 178.5 63.3 314 3 US-09-987-899-73

ALIGNMENTS

Sequence 72, Appl  
Sequence 81, Appl  
Sequence 101, Appl  
Sequence 88, Appl  
Sequence 266, Appl  
Sequence 103, Appl  
Sequence 98, Appl  
Sequence 92, Appl  
Sequence 95, Appl  
Sequence 94, Appl  
Sequence 89, Appl  
Sequence 269, Appl  
Sequence 59, Appl  
Sequence 87, Appl  
Sequence 91, Appl  
Sequence 83, Appl  
Sequence 86, Appl  
Sequence 80, Appl  
Sequence 50, Appl  
Sequence 78, Appl  
Sequence 85, Appl  
Sequence 77, Appl  
Sequence 61, Appl  
Sequence 12, Appl  
Sequence 76, Appl  
Sequence 7, Appl  
Sequence 17, Appl  
Sequence 36, Appl  
Sequence 24, Appl  
Sequence 258, Appl  
Sequence 18, Appl  
Sequence 43, Appl  
Sequence 6, Appl  
Sequence 252, Appl  
Sequence 254, Appl  
Sequence 243, Appl  
Sequence 239, Appl  
Sequence 245, Appl  
Sequence 66587, A  
Sequence 242, Appl  
Sequence 260, Appl  
Sequence 237, Appl  
Sequence 263, Appl  
Sequence 241, Appl  
Sequence 232, Appl  
Sequence 5718, Ap  
Sequence 83327, A  
Sequence 13220, A  
Sequence 93, Appl  
Sequence 63, Appl  
Sequence 216, Appl  
Sequence 65, Appl  
Sequence 240, Appl  
Sequence 100, Appl  
Sequence 46, Appl  
Sequence 247, Appl  
Sequence 249, Appl  
Sequence 28, Appl  
Sequence 109, Appl  
Sequence 108, Appl  
Sequence 158707,  
Sequence 9, Appl  
Sequence 267, Appl  
Sequence 67, Appl  
Sequence 107, Appl  
Sequence 265, Appl  
Sequence 52, Appl  
Sequence 257, Appl  
Sequence 142195,  
Sequence 73, Appl

RESULT 1  
US-10-140-410-1  
; Sequence 1, Application US/10140410  
; Publication No. US20030213013A1  
; GENERAL INFORMATION:  
; APPLICANT: Caimi, Perry G.  
; APPLICANT: Lightner, Jonathan E.  
; TITLE OF INVENTION: Fructose Polymer Synthesis in Monocot Plastids  
; FILE REFERENCE: BB1347 US NA  
; CURRENT APPLICATION NUMBER: US/10/140,410  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: PCT/US00/31788  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: 60/166,268  
; PRIOR FILING DATE: 1999-11-18  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 1  
; LENGTH: 183  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-10-140-410-1  
  
Alignment Scores:  
Pred. No.: 1,08e-18 Length: 183  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 6 Gaps: 2  
  
US-10-628-525A-34 (1-58) x US-10-140-410-1 (1-183)  
Qy 1 MetalProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 1 ATGGCGCCACCGTATGATGCTCGTGGCCACC----- 36  
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerIeuProValAlaArg 40  
Db 37 -----GCCGTGCTCCGTTCCAGGGGCTTAAGTCCACGCCAGGCTCCCGTCGCCGCGC 90  
Qy 41 ArgSerSerArgSerLeuGlyValAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 91 CCTCTCTAGAACCTCGCAACGTC---AGCAACGGCGGAAGAATCCGGTGC 141  
  
RESULT 2  
US-09-987-899-69  
; Sequence 69, Application US/09987899  
; Publication No. US20040116682A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 69  
; LENGTH: 228  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700042688H1  
US-09-987-899-69

Alignment Scores:  
 Pred. No.: 1.41e-18 Length: 228  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-69 (1-228)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 Db 37 ATGGCGCCACCGTGATGATGCTCGTCCGCCACC----- 72  
 Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 Db 73 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 126  
 Qy 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 Db 127 CGCTCTCCAGAGCCTCGGCAAGTGC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 3

US-09-987-899-84  
 ; Sequence 84, Application US/09987899  
 ; Publication No. US20040116682A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheikh, Nordine  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Miller, Phillip W.  
 ; APPLICANT: O Connell, Keith M.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
 ; FILE REFERENCE: 16517.258  
 ; CURRENT APPLICATION NUMBER: US/09/987,899  
 ; PRIOR FILING DATE: 2001-11-16  
 ; PRIOR APPLICATION NUMBER: US 09/262,979  
 ; PRIOR FILING DATE: 1999-03-04  
 ; PRIOR APPLICATION NUMBER: US 60/076,712  
 ; PRIOR FILING DATE: 1998-03-06  
 ; NUMBER OF SEQ ID NOS: 7341  
 ; SEQ ID NO 84  
 ; LENGTH: 229  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: 700198026H1  
 US-09-987-899-84

Alignment Scores:  
 Pred. No.: 1.42e-18 Length: 229  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-84 (1-229)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 Db 52 ATGGCGCCACCGTGATGATGCTCGTCCGCCACC----- 87  
 Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 Db 88 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 141  
 Qy 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 Db 142 CGCTCTCCAGAGCCTCGGCAAGTGC---AGCAACGGCGGAAGGATCCGGTGC 192

RESULT 4

US-09-987-899-264

; Sequence 264, Application US/09987899  
 ; Publication No. US20040116682A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheikh, Nordine  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Miller, Phillip W.  
 ; APPLICANT: O Connell, Keith M.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
 ; FILE REFERENCE: 16517.258  
 ; CURRENT APPLICATION NUMBER: US/09/987,899  
 ; PRIOR FILING DATE: 2001-11-16  
 ; PRIOR APPLICATION NUMBER: US 09/262,979  
 ; PRIOR FILING DATE: 1999-03-04  
 ; PRIOR APPLICATION NUMBER: US 60/076,712  
 ; PRIOR FILING DATE: 1998-03-06  
 ; NUMBER OF SEQ ID NOS: 7341  
 ; SEQ ID NO 264  
 ; LENGTH: 230  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: LIB3068-029-Q1-K1-F6  
 US-09-987-899-264

Alignment Scores:  
 Pred. No.: 1.42e-18 Length: 230  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-264 (1-230)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 Db 37 ATGGCGCCACCGTGATGATGCTCGTCCGCCACC----- 72  
 Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 Db 73 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 126  
 Qy 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 Db 127 CGCTCTCCAGAGCCTCGGCAAGTGC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 5

US-09-987-899-79  
 ; Sequence 79, Application US/09987899  
 ; Publication No. US20040116682A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheikh, Nordine  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Miller, Phillip W.  
 ; APPLICANT: O Connell, Keith M.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
 ; FILE REFERENCE: 16517.258  
 ; CURRENT APPLICATION NUMBER: US/09/987,899  
 ; PRIOR FILING DATE: 2001-11-16  
 ; PRIOR APPLICATION NUMBER: US 09/262,979  
 ; PRIOR FILING DATE: 1999-03-04  
 ; PRIOR APPLICATION NUMBER: US 60/076,712  
 ; PRIOR FILING DATE: 1998-03-06  
 ; NUMBER OF SEQ ID NOS: 7341  
 ; SEQ ID NO 79  
 ; LENGTH: 235  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: 700046244H1  
 US-09-987-899-79



```
Alignment Scores:
Pred. No.: 1,46e-18 Length: 235
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-79 (1-235)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 47 ATGGCGCCACCGTGATGCTCGTCGGCCACC----- 82
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 93 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 136
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 137 CGCTCCTCAGAAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 187

RESULT 6
US-09-987-899-70
; Sequence 70, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 70
; LENGTH: 236
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700044947H1
US-09-987-899-70
Alignment Scores:
Pred. No.: 1,47e-18 Length: 236
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-70 (1-236)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 13 ATGGCGCCACCGTGATGCTCGTCGGCCACC----- 48
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 49 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 102
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 103 CGCTCCTCAGAAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 153

RESULT 7
US-09-987-899-66
; Sequence 66, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 66
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700044245H1
US-09-987-899-66
Alignment Scores:
Pred. No.: 1,48e-18 Length: 238
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-66 (1-238)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 14 ATGGCGCCACCGTGATGCTCGTCGGCCACC----- 49
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 50 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 103
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 104 CGCTCCTCAGAAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 154

RESULT 8
US-09-987-899-71
; Sequence 71, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 71
; LENGTH: 249
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700045847H1
```

## US-09-987-899-71

Alignment Scores:  
Pred. No.: 1.56e-18 Length: 249  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-71 (1-249)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
|||||  
DB 50 ATGGGCGCCACCGTGATGGCTCTCGGCCACC----- 85  
QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
|||||  
DB 86 -----GCCGTCGCTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 139  
QY 41 ArgSerArgSerLeuGlyAanValAlaSerAsnGlyGlyArgIleArgCys 58  
|||||  
DB 140 CGCTCTCTCAGAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 190

## RESULT 9

US-09-987-899-53  
; Sequence 53, Application US/09987899  
; Publication No. US20040116682A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 53  
; LENGTH: 264  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700044292H1  
US-09-987-899-53

Alignment Scores:  
Pred. No.: 1.68e-18 Length: 264  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-53 (1-264)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
|||||  
DB 46 ATGGGCGCCACCGTGATGGCTCTCGGCCACC----- 81  
QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
|||||  
DB 82 -----GCCGTCGCTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 135  
QY 41 ArgSerArgSerLeuGlyAanValAlaSerAsnGlyGlyArgIleArgCys 58  
|||||  
DB 136 CGCTCTCTCAGAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 186

## RESULT 10

US-09-987-899-40  
; Sequence 40, Application US/09987899  
; Publication No. US20040116682A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 40  
; LENGTH: 265  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700025653H1  
US-09-987-899-40

Alignment Scores:  
Pred. No.: 1.69e-18 Length: 265  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-40 (1-265)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
|||||  
DB 21 ATGGGCGCCACCGTGATGGCTCTCGGCCACC----- 56  
QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
|||||  
DB 57 -----GCCGTCGCTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 110  
QY 41 ArgSerArgSerLeuGlyAanValAlaSerAsnGlyGlyArgIleArgCys 58  
|||||  
DB 111 CGCTCTCTCAGAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 161

## RESULT 11

US-09-987-899-45  
; Sequence 45, Application US/09987899  
; Publication No. US20040116682A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 45  
; LENGTH: 272  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:

; OTHER INFORMATION: Clone ID: 700042186H1  
US-09-987-899-45

Alignment Scores:  
Pred. No.: 1,77e-18 Length: 272  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-45 (1-272)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 43 ATGGCGCCACCGTATGATGCGCTCGTGGCCACC----- 78  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
Db 79 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGTCGCCCGC 132  
QY 41 ArgSerSerArgSerLeuGlyValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 133 CGCTCTCTCAGAAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 183

RESULT 12

US-09-987-899-26

; Sequence 26, Application US/09987899

; Publication No. US20040116682A1

; GENERAL INFORMATION:

; APPLICANT: Cheikh, Nordine

; APPLICANT: Liu, Jingdong

; APPLICANT: Miller, Phillip W.

; APPLICANT: O Connell, Keith M.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated

; FILE OF INVENTION: With the Carbon Assimilation Pathway

; FILE REFERENCE: 16517.258

; CURRENT APPLICATION NUMBER: US/09/987,899

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: US 09/262,979

; PRIOR FILING DATE: 1999-03-04

; PRIOR APPLICATION NUMBER: US 60/076,712

; PRIOR FILING DATE: 1998-03-06

; NUMBER OF SEQ ID NOS: 7341

; SEQ ID NO 26

; LENGTH: 276

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: 700045728H1

US-09-987-899-26

Alignment Scores:

Pred. No.: 1,77e-18 Length: 276  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-26 (1-276)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 41 ATGGCGCCACCGTATGATGCGCTCGTGGCCACC----- 76  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
Db 77 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGTCGCCCGC 130  
QY 41 ArgSerSerArgSerLeuGlyValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 131 CGCTCTCTCAGAAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 181

RESULT 13

US-09-987-899-51

; Sequence 51, Application US/09987899

; Publication No. US20040116682A1

; GENERAL INFORMATION:

; APPLICANT: Cheikh, Nordine

; APPLICANT: Liu, Jingdong

; APPLICANT: Miller, Phillip W.

; APPLICANT: O Connell, Keith M.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated

; FILE OF INVENTION: With the Carbon Assimilation Pathway

; FILE REFERENCE: 16517.258

; CURRENT APPLICATION NUMBER: US/09/987,899

; CURRENT FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: US 09/262,979

; PRIOR FILING DATE: 1999-03-04

; PRIOR APPLICATION NUMBER: US 60/076,712

; PRIOR FILING DATE: 1998-03-06

; NUMBER OF SEQ ID NOS: 7341

; SEQ ID NO 51

; LENGTH: 276

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: 700433801H1

US-09-987-899-51

Alignment Scores:

Pred. No.: 1,77e-18 Length: 276  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-51 (1-276)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 46 ATGGCGCCACCGTATGATGCGCTCGTGGCCACC----- 81  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
Db 82 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGTCGCCCGC 135  
QY 41 ArgSerSerArgSerLeuGlyValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 136 CGCTCTCTCAGAAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 186

RESULT 14

US-09-987-899-32

; Sequence 32, Application US/09987899

; Publication No. US20040116682A1

; GENERAL INFORMATION:

; APPLICANT: Cheikh, Nordine

; APPLICANT: Liu, Jingdong

; APPLICANT: Miller, Phillip W.

; APPLICANT: O Connell, Keith M.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated

; FILE OF INVENTION: With the Carbon Assimilation Pathway

; FILE REFERENCE: 16517.258

; CURRENT APPLICATION NUMBER: US/09/987,899

; CURRENT FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: US 09/262,979

; PRIOR FILING DATE: 1999-03-04

; PRIOR APPLICATION NUMBER: US 60/076,712

; PRIOR FILING DATE: 1998-03-06

; NUMBER OF SEQ ID NOS: 7341

; SEQ ID NO 32

; LENGTH: 284

; TYPE: DNA

; ORGANISM: Zea mays

```
;
; FEATURE:
; OTHER INFORMATION: Clone ID: 700100637H1
US-09-987-899-32

Alignment Scores:
Pred. No.: 1.83e-18 Length: 284
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-32 (1-284)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 50 ATGGCGCCACCGTGATGGCTCGTGGCCACC-----85
QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
DB 86 -----GCCGTGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 139
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
DB 140 CGTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 190

RESULT 15
US-09-987-899-37
; Sequence 37, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 37
; LENGTH: 286
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700212658H1
US-09-987-899-37

Alignment Scores:
Pred. No.: 1.85e-18 Length: 286
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-37 (1-286)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 48 ATGGCGCCACCGTGATGGCTCGTGGCCACC-----83
QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
DB 84 -----GCCGTGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 137
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
DB 140 CGTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 190
```

```
Db 138 CGTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 188

RESULT 16
US-09-987-899-47
; Sequence 47, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 47
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700097886H1
US-09-987-899-47

Alignment Scores:
Pred. No.: 1.88e-18 Length: 291
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-47 (1-291)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 57 ATGGCGCCACCGTGATGGCTCGTGGCCACC-----92
QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
DB 93 -----GCCGTGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 146
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
DB 147 CGTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 197

RESULT 17
US-09-987-899-14
; Sequence 14, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 14
; LENGTH: 297
; TYPE: DNA
```

```
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 700101196H1
US-09-987-899-14

Alignment Scores:
Pred. No.: 1.93e-18 Length: 297
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-14 (1-297)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 12 ATGGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 47
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 48 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 101
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 102 CGCTCTCCAGAAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 152

RESULT 18
US-09-987-899-21
; Sequence 21, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 21
; LENGTH: 298
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700099783H1
US-09-987-899-21

Alignment Scores:
Pred. No.: 1.94e-18 Length: 298
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-21 (1-298)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 48 ATGGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 83
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 84 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 137
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58

/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 700101196H1
US-09-987-899-14

Alignment Scores:
Pred. No.: 1.93e-18 Length: 297
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-14 (1-297)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 12 ATGGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 47
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 48 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 101
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 102 CGCTCTCCAGAAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 152

RESULT 18
US-09-987-899-21
; Sequence 21, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 21
; LENGTH: 298
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700099783H1
US-09-987-899-21

Alignment Scores:
Pred. No.: 1.94e-18 Length: 298
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-21 (1-298)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 48 ATGGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 83
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 84 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 137
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58

/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 700101196H1
US-09-987-899-14

Alignment Scores:
Pred. No.: 1.93e-18 Length: 305
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-16 (1-305)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 42 ATGGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 77
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 78 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 131
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 132 CGCTCTCCAGAAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 182

RESULT 20
US-09-987-899-29
; Sequence 29, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 29
; LENGTH: 307
```

```
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700211770H1
US-09-987-899-29

Alignment Scores:
Pred. No.: 2.01e-18 Length: 307
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-29 (1-307)
Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 50 ATGGGCGCCACCGTGATGGCTCGTCGGCCACC-----85
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLyseSerThrAlaSerLeuProValAlaArg 40
Db 86 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 139
Qy 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgIleArgCys 58
Db 140 CGCTCTCCAGAACGCTCGCAACGTC---AGCAACGCGGGAAGGATCCGGTGC 190

RESULT 21
US-09-987-899-15
; Sequence 15, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 15
; LENGTH: 309
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700097309H1
US-09-987-899-15

Alignment Scores:
Pred. No.: 2.02e-18 Length: 309
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-15 (1-309)
Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 48 ATGGGCGCCACCGTGATGGCTCGTCGGCCACC-----83
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLyseSerThrAlaSerLeuProValAlaArg 40
Db 84 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 137
```

```
Qy 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgIleArgCys 58
Db 138 CGCTCTCCAGAACGCTCGCAACGTC---AGCAACGCGGGAAGGATCCGGTGC 198

RESULT 22
US-09-987-899-30
; Sequence 30, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 30
; LENGTH: 311
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700095614H1
US-09-987-899-30

Alignment Scores:
Pred. No.: 2.04e-18 Length: 311
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-30 (1-311)
Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 42 ATGGGCGCCACCGTGATGGCTCGTCGGCCACC-----77
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLyseSerThrAlaSerLeuProValAlaArg 40
Db 78 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 131
Qy 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgIleArgCys 58
Db 132 CGCTCTCCAGAACGCTCGCAACGTC---AGCAACGCGGGAAGGATCCGGTGC 182

RESULT 23
US-09-987-899-68
; Sequence 68, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 68
```

```
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(312)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 700215027H1
US-09-987-899-68

Alignment Scores:
Pred. No.: 2,05e-18 Length: 312
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-68 (1-312)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 43 ATGGCGCCACCGTGATGAGCGCTCGTCGGCCACC----- 78
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 79 -----GCCGTCCGCTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 132
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 133 CGCTCTCTCAGAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 183

RESULT 24
US-09-987-899-11
; Sequence 11, Application US/09987899
; Publication NO. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 11
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700098235H1
US-09-987-899-11

Alignment Scores:
Pred. No.: 2,07e-18 Length: 315
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-11 (1-315)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 48 ATGGCGCCACCGTGATGAGCGCTCGTCGGCCACC----- 83

; LENGTH: 312
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(312)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 700215027H1
US-09-987-899-68

Alignment Scores:
Pred. No.: 2,05e-18 Length: 312
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-68 (1-312)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 43 ATGGCGCCACCGTGATGAGCGCTCGTCGGCCACC----- 78
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 79 -----GCCGTCCGCTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 132
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 133 CGCTCTCTCAGAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 183

RESULT 24
US-09-987-899-11
; Sequence 11, Application US/09987899
; Publication NO. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 11
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700098235H1
US-09-987-899-11

Alignment Scores:
Pred. No.: 2,07e-18 Length: 315
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-11 (1-315)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 48 ATGGCGCCACCGTGATGAGCGCTCGTCGGCCACC----- 83
```

```
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 84 -----GCCGTCCGCTCCAGGGGCTCAAGTCCACCGCCAGGCTCCCGTCGCCCGC 137
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 138 CGCTCTCTCAGAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 188

RESULT 25
US-09-987-899-10
; Sequence 10, Application US/09987899
; Publication NO. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 10
; LENGTH: 317
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700099925H1
US-09-987-899-10

Alignment Scores:
Pred. No.: 2,09e-18 Length: 317
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-10 (1-317)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 50 ATGGCGCCACCGTGATGAGCGCTCGTCGGCCACC----- 85
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 86 -----GCCGTCCGCTCCAGGGGCTCAAGTCCACCGCCAGGCTCCCGTCGCCCGC 139
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 140 CGCTCTCTCAGAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 190

RESULT 26
US-09-987-899-4
; Sequence 4, Application US/09987899
; Publication NO. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
```



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; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 4
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 70098783H1
US-09-987-899-4

Alignment Scores:
Pred. No.: 2.1e-18 Length: 319
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-4 (1-319)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 41 ATGGCGCCACCGTGATGCTCGTCCGCCACC----- 76
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 77 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCTCCCGGTGCGCCGC 130
QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58
Db 131 CGCTCTCCAGAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 181

RESULT 27
US-09-987-899-231
; Sequence 231, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 231
; LENGTH: 344
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3062-047-Q1-K1-B2
US-09-987-899-231

Alignment Scores:
Pred. No.: 2.3e-18 Length: 344
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-231 (1-344)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 46 ATGGCGCCACCGTGATGCTCGTCCGCCACC----- 81

; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 4
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 70098783H1
US-09-987-899-4

Alignment Scores:
Pred. No.: 2.1e-18 Length: 319
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-4 (1-319)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 41 ATGGCGCCACCGTGATGCTCGTCCGCCACC----- 76
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 77 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCTCCCGGTGCGCCGC 130
QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58
Db 131 CGCTCTCCAGAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 181

RESULT 27
US-09-987-899-231
; Sequence 231, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 231
; LENGTH: 344
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3062-047-Q1-K1-B2
US-09-987-899-231

Alignment Scores:
Pred. No.: 2.3e-18 Length: 344
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-231 (1-344)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 46 ATGGCGCCACCGTGATGCTCGTCCGCCACC----- 81

; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 4
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 70098783H1
US-09-987-899-4

Alignment Scores:
Pred. No.: 2.1e-18 Length: 319
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-4 (1-319)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 41 ATGGCGCCACCGTGATGCTCGTCCGCCACC----- 76
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 77 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCTCCCGGTGCGCCGC 130
QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58
Db 131 CGCTCTCCAGAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 181

RESULT 27
US-09-987-899-231
; Sequence 231, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 231
; LENGTH: 344
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3062-047-Q1-K1-B2
US-09-987-899-231

Alignment Scores:
Pred. No.: 2.3e-18 Length: 344
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-231 (1-344)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 46 ATGGCGCCACCGTGATGCTCGTCCGCCACC----- 81

; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 4
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 70098783H1
US-09-987-899-4

Alignment Scores:
Pred. No.: 2.1e-18 Length: 319
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-4 (1-319)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 41 ATGGCGCCACCGTGATGCTCGTCCGCCACC----- 76
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 77 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCTCCCGGTGCGCCGC 130
QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58
Db 131 CGCTCTCCAGAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 181

RESULT 27
US-09-987-899-231
; Sequence 231, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 231
; LENGTH: 344
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3066-002-Q1-K1-B12
US-09-987-899-215

Alignment Scores:
Pred. No.: 2.82e-18 Length: 409
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-215 (1-409)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 50 ATGGCGCCACCGTGATGCTCGTCCGCCACC----- 85
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 86 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCTCCCGGTGCGCCGC 139
QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58
Db 140 CGCTCTCCAGAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 190

RESULT 29
US-09-987-899-244
; Sequence 244, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
```

;  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 244  
; LENGTH: 415  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB84-027-Q1-E1-H12  
US-09-987-899-244

Alignment Scores:  
Pred. No.: 2,87e-18 Length: 415  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-244 (1-415)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
DB 99 ATGGGCCCCACCGTGATGCGCTCGTCGGCCACC----- 134  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
DB 135 -----GCCGTGCTCCGTTCCAGGGGCTCAAAGTCCACCGCCAGCCTCCCGTCGCCCGC 188  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
DB 189 CGCTCTCTCCAGAACCTCGGCAACGTC-----AGCAACGGCGGAAGGATCCGGTGC 239

## RESULT 30

US-09-987-899-210  
; Sequence 210, Application US/09987899  
; Publication No. US20040116682A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; FILE OF INVENTION: With the Carbon Assimilation Pathway  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 210  
; LENGTH: 438  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3078-018-Q1-K1-H8  
US-09-987-899-210

Alignment Scores:  
Pred. No.: 3,06e-18 Length: 438  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-210 (1-438)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
DB 99 ATGGGCCCCACCGTGATGCGCTCGTCGGCCACC----- 134

DB 41 ATGGGCCCCACCGTGATGCGCTCGTCGGCCACC----- 76  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
DB 77 -----GCCGTGCTCCGTTCCAGGGGCTCAAAGTCCACCGCCAGCCTCCCGTCGCCCGC 130  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
DB 131 CGCTCTCTCCAGAACCTCGGCAACGTC-----AGCAACGGCGGAAGGATCCGGTGC 181

Search completed: April 2, 2006, 02:11:05  
Job time : 276.022 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 2, 2006, 01:09:48 ; Search time 181.109 Seconds  
(without alignments)  
1278.753 Million cell updates/sec

Title: US-10-628-525A-34

Perfect score: 282

Sequence: 1 MATVMMASATATRTNPAQ.....ARRSRSLGNVAGRGIRC 58

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-Q=/abss/ABSSWEB\_spool/US10628525/runat\_31032006\_095139\_17270/app\_query.fasta.1  
-DB=Published Applications NA New -QWFI=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1  
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-TRANS-human40 cdi -LIST=150 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR\_MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abes05h  
-USER=US10628525 @CGN 1 1 2249 @runat\_31032006\_095139\_17270 -NCPU=6 -ICPU=3  
-NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New:  
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2: /SIDSS/ptodata/2/pubpna/US06\_NEW\_PUB.seq:  
3: /SIDSS/ptodata/2/pubpna/US07\_NEW\_PUB.seq:  
4: /SIDSS/ptodata/2/pubpna/PTCT\_NEW\_PUB.seq:  
5: /SIDSS/ptodata/2/pubpna/US09\_NEW\_PUB.seq:  
6: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq:  
7: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq:  
8: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq:  
9: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq:  
10: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq:  
11: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq:  
12: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq:  
13: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq:  
14: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq:  
15: /SIDSS/ptodata/2/pubpna/US60\_NEW\_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description      |
|------------|-------|-------------|--------|----|------------------|
| 1          | 196.5 | 69.7        | 416    | 14 | US-11-192-801-25 |
| 2          | 196.5 | 69.7        | 416    | 14 | US-11-192-801-30 |

|                   |                   |                   |                   |                   |                   |                  |                  |                  |                   |                   |                  |                    |                   |                   |                  |                   |                    |                   |                   |                    |                    |                    |                   |                   |                   |                   |                   |                    |                   |                   |                    |                   |                    |                    |                    |                   |                   |                   |                   |                   |                    |                     |                   |                   |                   |                   |                   |                   |                    |                   |                   |                   |                   |                    |                    |                     |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|--------------------|-------------------|-------------------|------------------|-------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|---------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|---------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| Sequence 17, Appl | Sequence 36, Appl | Sequence 19, Appl | Sequence 21808, A | Sequence 29, Appl | Sequence 29, Appl | Sequence 5, Appl | Sequence 5, Appl | Sequence 5, Appl | Sequence 13282, A | Sequence 22, Appl | Sequence 2328, A | Sequence 539532, A | Sequence 353, App | Sequence 12, Appl | Sequence 1, Appl | Sequence 5026, Ap | Sequence 811437, A | Sequence 3445, Ap | Sequence 18507, A | Sequence 121813, A | Sequence 220043, A | Sequence 833452, A | Sequence 12875, A | Sequence 23191, A | Sequence 1418, Ap | Sequence 542, App | Sequence 91751, A | Sequence 705160, A | Sequence 197, App | Sequence 197, App | Sequence 593669, A | Sequence 22252, A | Sequence 223970, A | Sequence 308843, A | Sequence 308842, A | Sequence 127, App | Sequence 18569, A | Sequence 20394, A | Sequence 40, Appl | Sequence 52, Appl | Sequence 551881, A | Sequence 1165290, A | Sequence 3253, Ap | Sequence 3253, Ap | Sequence 84, Appl | Sequence 1093, Ap | Sequence 173, App | Sequence 173, App | Sequence 529331, A | Sequence 3641, Ap | Sequence 3641, Ap | Sequence 25001, A | Sequence 23747, A | Sequence 708199, A | Sequence 571741, A | Sequence 1185150, A | Sequence 13, Appl | Sequence 25, Appl | Sequence 25, Appl | Sequence 37329, A | Sequence 37329, A | Sequence 11, Appl | Sequence 20037, A | Sequence 9890, Ap | Sequence 42914, A | Sequence 42914, A |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|--------------------|-------------------|-------------------|------------------|-------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|---------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|---------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|



; CURRENT APPLICATION NUMBER: US/11/192,801  
; CURRENT FILING DATE: 2005-07-29  
; PRIOR APPLICATION NUMBER: US/10/232,665  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US/09/377,466  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 416  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: modified  
; OTHER INFORMATION: cauliflower mosaic virus promoter AS4  
US-11-192-801-30

Alignment Scores:  
Pred. No.: 9-19e-14 Length: 416  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservative: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 14 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-192-801-30 (1-416)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 16 ATGGCGCCACCGTGATGATGGCTCTCGGCCACC-----51  
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 52 -----GCCGTGCTCGTTCTGGGGCTCAAGTCCACGCCAGCTTCCCGTCGCCCGC 105  
Qy 41 ArgSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 106 CGCTCTCCAGAGACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 156

## RESULT 3

US-11-192-801-17  
; Sequence 17, Application US/11/192801  
; Publication No. US20050273882A1  
; GENERAL INFORMATION:  
; APPLICANT: Romano, Charles P.  
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
; CURRENT APPLICATION NUMBER: US/11/192,801  
; CURRENT FILING DATE: 2005-07-29  
; PRIOR APPLICATION NUMBER: US/10/232,665  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US/09/377,466  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 3450  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: expression  
; OTHER INFORMATION: cassette  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (14)..(235)  
; OTHER INFORMATION: P-CaMV.AS4  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: (240)..(304)  
; OTHER INFORMATION: L-Ta.hcb1  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (318)..(805)

; OTHER INFORMATION: I-Os.Act1  
; FEATURE:  
; NAME/KEY: transit peptide  
; LOCATION: (825)..(971)  
; OTHER INFORMATION: amino terminal TS-2m.rbcS  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (972)..(1134)  
; OTHER INFORMATION: I-2m.rbcS  
; FEATURE:  
; NAME/KEY: transit peptide  
; LOCATION: (1135)..(1221)  
; OTHER INFORMATION: carboxy terminus TS-2m.rbcS  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1222)..(3180)  
; OTHER INFORMATION: Cry3Bb1 variant 11231mv1  
; FEATURE:  
; NAME/KEY: terminator  
; LOCATION: (3198)..(3431)  
; OTHER INFORMATION: T-Ta.hsp17  
US-11-192-801-17

Alignment Scores:  
Pred. No.: 7-33e-13 Length: 3450  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservative: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 14 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-192-801-17 (1-3450)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 825 ATGGCGCCACCGTGATGATGGCTCTCGGCCACC-----860  
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 861 -----GCCGTGCTCGTTCTGGGGCTCAAGTCCACGCCAGCTTCCCGTCGCCCGC 914  
Qy 41 ArgSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 915 CGCTCTCCAGAGACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 965

## RESULT 4

US-11-192-801-36  
; Sequence 36, Application US/11/192801  
; Publication No. US20050273882A1  
; GENERAL INFORMATION:  
; APPLICANT: Romano, Charles P.  
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
; CURRENT APPLICATION NUMBER: US/11/192,801  
; CURRENT FILING DATE: 2005-07-29  
; PRIOR APPLICATION NUMBER: US/10/232,665  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US/09/377,466  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 36  
; LENGTH: 3455  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: expression  
; OTHER INFORMATION: cassette  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (14)..(235)  
; OTHER INFORMATION: P-CaMV.AS4  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (318)..(805)

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/ NAME/KEY: 5'UTR
/ LOCATION: (240)..(304)
/ OTHER INFORMATION: L-Ta.hcb1
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: (318)..(805)
/ OTHER INFORMATION: I-Os.Act1
/ FEATURE:
/ NAME/KEY: transit_peptide
/ LOCATION: (825)..(971)
/ OTHER INFORMATION: TS-Zm.rbcS amino terminal coding sequence upstream
/ OTHER INFORMATION: of Zea mays rbcS intron
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: (972)..(1134)
/ OTHER INFORMATION: I-Zm.rbcS
/ FEATURE:
/ NAME/KEY: transit_peptide
/ LOCATION: (1135)..(1221)
/ OTHER INFORMATION: TS-Zm.rbcS carboxy terminus coding sequence
/ OTHER INFORMATION: downstream of Zea mays rbcS intron
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1222)..(3180)
/ OTHER INFORMATION: variant Cry3BB1 coding sequence encoding v11231
/ FEATURE:
/ NAME/KEY: terminator
/ LOCATION: (3198)..(3431)
/ OTHER INFORMATION: T-Ta.hsp17
US-11-192-801-36

Alignment Scores:
Pred. No.: 7.34e-13 Length: 3455
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 14 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-192-801-36 (1-3455)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 825 ATGGCGCCACCGTGATGCGCTCGTCGCCACC----- 860

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 861 -----GCCGTCGCTCCGTTCTTGGGGCTCAAGTCCACCGCAGCCTCCCGTCGCCGC 914

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 915 CGCTCTCCAGAGCCTCGGCACGTC---AGCAACGGCGGAGGATCGGTGC 965

RESULT 5
US-11-192-801-13
/ Sequence 13, Application US/11192801
/ Publication No. US20050273882A1
/ GENERAL INFORMATION:
/ APPLICANT: Romano, Charles P.
/ TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
/ FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
/ CURRENT APPLICATION NUMBER: US/11/192,801
/ CURRENT FILING DATE: 2005-07-29
/ PRIOR APPLICATION NUMBER: US/10/232,665
/ PRIOR FILING DATE: 2002-08-29
/ PRIOR APPLICATION NUMBER: US/09/377,466
/ PRIOR FILING DATE: 1999-08-19
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 13
/ LENGTH: 4149
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
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/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: expression
/ OTHER INFORMATION: cassette
/ FEATURE:
/ NAME/KEY: promoter
/ LOCATION: (25)..(640)
/ OTHER INFORMATION: P-CaMv.35S
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: (669)..(1472)
/ OTHER INFORMATION: I-Zm.Hsp70
/ FEATURE:
/ NAME/KEY: transit_peptide
/ LOCATION: (1489)..(1635)
/ OTHER INFORMATION: amino terminal TS-Zm.rbcS
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: (1636)..(1798)
/ OTHER INFORMATION: I-Zm.rbcS
/ FEATURE:
/ NAME/KEY: transit_peptide
/ LOCATION: (1799)..(1885)
/ OTHER INFORMATION: carboxy terminus TS-Zm.rbcS
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1885)..(3843)
/ OTHER INFORMATION: Cry3Bb1 variant v11231
/ FEATURE:
/ NAME/KEY: terminator
/ LOCATION: (3871)..(4127)
/ OTHER INFORMATION: T-AGRTcu.nos 3' transcription termination and
/ OTHER INFORMATION: polyadenylation sequence
US-11-192-801-13

Alignment Scores:
Pred. No.: 8.78e-13 Length: 4149
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 14 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-192-801-13 (1-4149)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 1488 ATGGCGCCACCGTGATGCGCTCGTCGCCACC----- 1523

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 1524 -----GCCGTCGCTCCGTTCTTGGGGCTCAAGTCCACCGCAGCCTCCCGTCGCCGC 1577

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 1578 CGCTCTCCAGAGCCTCGGCACGTC---AGCAACGGCGGAGGATCGGTGC 1628

RESULT 6
US-10-840-688-19
/ Sequence 19, Application US/10840688
/ Publication No. US2005028968A1
/ GENERAL INFORMATION:
/ APPLICANT: Weaver, Lisa M
/ APPLICANT: Mitsky, Timothy A
/ APPLICANT: Rapp, William D
/ APPLICANT: Gruys, Kenneth J
/ APPLICANT: Liang, Jihong
/ TITLE OF INVENTION: Plants with Increased Levels of One or More Amino Acids
/ FILE REFERENCE: REN-00-095
/ CURRENT APPLICATION NUMBER: US/10/840,688
/ CURRENT FILING DATE: 2004-05-06
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 19
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US-11-087-084-5  
; Sequence 5, Application US/11087084  
; Publication No. US20050273883A1  
; GENERAL INFORMATION:  
; APPLICANT: Metz, James  
; APPLICANT: Barclay, William  
; APPLICANT: Platt, James  
; APPLICANT: Kuner, Jerry  
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORPA of a PUFA Polyketide Synthase  
; FILE REFERENCE: 2997-29  
; CURRENT APPLICATION NUMBER: US/11/087,084  
; CURRENT FILING DATE: 2005-03-21  
; PRIOR APPLICATION NUMBER: 09/231,899  
; PRIOR FILING DATE: 1999-01-14  
; PRIOR APPLICATION NUMBER: 60/284,066  
; PRIOR FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: 60/298,796  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/323,269  
; PRIOR FILING DATE: 2001-09-18  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5  
; LENGTH: 4509  
; TYPE: DNA  
; ORGANISM: Schizochytrium sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(4509)  
US-11-087-084-5

|                        | Pred. No.: | Score:        | Length: |
|------------------------|------------|---------------|---------|
| Alignment Scores:      | 478        | 70.00         | 4509    |
| Percent Similarity:    | 56.9%      | Conservative: | 19      |
| Best Local Similarity: | 32.8%      | Mismatches:   | 14      |
| Query Match:           | 24.8%      | Indels:       | 23      |
| DB:                    | 14         | Gaps:         | 2       |

US-10-628-525A-34 (1-58) x US-11-087-084-5 (1-4509)

|                                                         | QY                                                               | Db   | QY                                                  | Db                                                            | QY   | Db |
|---------------------------------------------------------|------------------------------------------------------------------|------|-----------------------------------------------------|---------------------------------------------------------------|------|----|
| 2                                                       | AlaProThrValMetMetMetAlaSerSerAlaThraAlaThrArgThrAsnProAlaGlnAla | 21   | 2372                                                | TGGCCAAAGCGCCCGGCCGCGGCAGCTCAACGCGCGCACGACCAGGGCCAGTACTCTCG   | 2431 | 22 |
| -----                                                   | SerAlaValalaproPheGlnGlyLeuLysSerThrAlaSerLeuProValAla           | 39   | 2432                                                | ACGCCGTGTCACATTTGTCGCGCAGCGCGCAAGAAGAGCCCTCGGCTACGCCACGGTTCCA | 2491 | 40 |
| ArqArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyVargileArg | 57                                                               | 2492 | AGACGGTCAACCCGAAGACTGGTTCTTCGCTGTCACCTTTTGTTGACTCGG | 2545                                                          |      |    |

RESULT 13  
US-11-087-085-5  
; Sequence 5, Application US/11087085  
; Publication No. US20050273884A1  
; GENERAL INFORMATION:  
; APPLICANT: Metz, James  
; APPLICANT: Barclay, William  
; APPLICANT: Platt, James  
; APPLICANT: Kuner, Jerry  
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORPA of a PUFA Polyketide Synthase  
; FILE REFERENCE: 2997-29  
; CURRENT APPLICATION NUMBER: US/11/087,085  
; CURRENT FILING DATE: 2005-03-21  
; PRIOR APPLICATION NUMBER: 09/231,899  
; PRIOR FILING DATE: 1999-01-14  
; PRIOR APPLICATION NUMBER: 60/284,066  
; PRIOR FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: 60/298,796

```

; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/323,269
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 4509
; TYPE: DNA
; ORGANISM: Schizochytrium sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4509)
US-11-087-085-5

Alignment Scores:
Pred. No.: 478 Length: 4509
Score: 70.00 Matches: 19
Percent Similarity: 56.9% Conservative: 14
Best Local Similarity: 32.8% Mismatches: 23
Query Match: 24.8% Indels: 2
DB: 14 Gaps: 1

US-10-628-525A-34 (1-58) x US-11-087-085-5 (1-4509)

Qy 2 AlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAla 21
Db 2372 TCGCCACGCGCCGCCAGCGCGCCAGCTCAACGCGCGCACGACCGGGCCAGTACCTCG 2431
Qy 22 -----SerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAla 39
Db 2432 ACGCGTGCACATGTCTCCGCGACGGCGCAAGAGAGCCTCGGCTACGCCACCGGTCCA 2491
Qy 40 ArgArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArg 57
Db 2492 AGACGGTCAACCGACGACTGGTCTTCGTCGCCACACTTTTGGTTTGACTCGG 2545

RESULT 14
US-11-096-568A-13282
; Sequence 13282, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Poly
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 13282
; LENGTH: 746
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(746)
; OTHER INFORMATION: Ceres Seq. ID no. 15174052
US-11-096-568A-13282

Alignment Scores:
Pred. No.: 107 Length: 746
Score: 69.00 Matches: 16
Percent Similarity: 50.9% Conservative: 11
Best Local Similarity: 30.2% Mismatches: 26
Query Match: 24.5% Indels: 0
DB: 11 Gaps: 0

US-10-628-525A-34 (1-58) x US-11-096-568A-13282 (1-746)

Qy 3 ProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAlaSer 22
Db 130 CCTCTCCGGCGCGGTGTCGGCTGCAGTCGCCACGACCCACTACCACTCCGGCGGCT 189
Qy 23 AlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArgArgSer 42

```







```
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 811437
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-811437

Alignment Scores:
Pred. No.: 145          Length: 450
Score: 66.00           Matches: 16
Percent Similarity: 63.9% Conservative: 7
Best Local Similarity: 44.4% Mismatches: 13
Query Match: 23.4%      Indels: 0
DB: 6                  Gaps: 0

US-10-628-525A-34 (1-58) x US-09-925-065A-811437 (1-450)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 379 ATGGCTCCGTCAGCTCATGTGCAACCTCTGCGCTCTGCGGTTCGTGATTCTCTCGCTCA 320

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeu 36
Db 319 GCCTCCCAAGTAGCTAGGATTACAGGTGCCGCGCACCATGCTGGCTG 272

RESULT 24
US-11-136-527-3446/c
; Sequence 3446, Application US/11136527
; Publication No. US2005028750A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William M
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3446
; LENGTH: 6000
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3446

Alignment Scores:
Pred. No.: 2,11e+03     Length: 6000
Score: 65.50           Matches: 27
Percent Similarity: 56.2% Conservative: 9
Best Local Similarity: 42.2% Mismatches: 14
Query Match: 23.2%      Indels: 14
DB: 14                 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-136-527-3446 (1-6000)

QY 4 ThrValMetMetAlaSerSerAlaThrAla-ThrArgThrAsnProAlaGlnAlaSerAl 23
Db 242 AGCATGGTGACACCCAGCAGCTGCGCAGTGGACACCGCAAAACCCAGCACACGCTCTTG 183

QY 23 aVal-----AlaProPhe--GlnGlyLeuLysSerThrAlaSer----- 35
Db 182 TGCACTCGATGTGGGCTCCGTGGTGGGGTCTCACTCCACCGAGTCAGCCACGGG 123

QY 36 -----LeuProValAlaArgArgSerSerArgSerLeuGlyAsnValAlaSer 51
Db 122 TCCGAGAGCCCCCTGGCGCTTGGCCGAGCGCGGCGTCTCTCCCATGGTGGCGGCA 63

QY 52 AsnGly 53
Db 62 AACGGT 57
```

## RESULT 25

```
US-11-096-568A-18507/c
; Sequence 18507, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 18507
; LENGTH: 1517
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1517)
; OTHER INFORMATION: Ceres Seq. ID no. 12365500
US-11-096-568A-18507
```

## Alignment Scores:

```
Pred. No.: 625          Length: 1517
Score: 65.00           Matches: 23
Percent Similarity: 54.2% Conservative: 9
Best Local Similarity: 39.0% Mismatches: 24
Query Match: 23.0%      Indels: 3
DB: 11                 Gaps: 1
```

US-10-628-525A-34 (1-58) x US-11-096-568A-18507 (1-1517)

```
QY 2 AlaProThr-----ValMetMetAlaSerSerAlaThrAla-ThrArgThrAsnProAl 19
Db 768 GCGCCCACTCGCGCTTGTGTCATGACAGCATGCGCTCGCTGAGTCGAGCGGCGTCC 709

QY 19 aGlnAlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAl 39
Db 708 ACAGGCTCGGCTCGGGCTGTGTACTCGGGTGTGTCGTACAGCACCGCGAGCGCGGCGC 649

QY 39 aArgArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgLeuArg 57
Db 648 GCGGCGAGCAGCGCGTAGTTCGAAGCACGCTGGGCACAGAGCGTTCGCGCGCGCGG 594
```

## RESULT 26

```
US-09-925-065A-121813/c
; Sequence 121813, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121813
; LENGTH: 616
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-121813
```

**Alignment Scores:**

|                        |       |               |     |
|------------------------|-------|---------------|-----|
| Pred. No.:             | 295   | Length:       | 616 |
| Score:                 | 64.50 | Matches:      | 20  |
| Percent Similarity:    | 54.4% | Conservative: | 11  |
| Best Local Similarity: | 35.1% | Mismatches:   | 21  |
| Query Match:           | 22.9% | Indels:       | 5   |
| DB:                    | 6     | Gaps:         | 2   |

US-10-628-525A-34 (1-58) x US-09-925-065A-121813 (1-616)

|    |     |                                                              |     |
|----|-----|--------------------------------------------------------------|-----|
| Qy | 1   | MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln | 20  |
|    |     |                                                              |     |
| Db | 437 | GTCTCAACCACTGAACACTCTGTGACCTGAATCCCACTGTTGTTCTCACT           | 384 |
|    |     |                                                              |     |
|    |     |                                                              |     |
| Qy | 21  | AlaSerAlaValAlaProPheClnGlyLeuIysSerThrAla                   | 37  |
|    |     |                                                              |     |
| Db | 383 | AAACACGCCCTGCCCAATTCCTTACCTAGAGCCCACTGGGCACACTTACAGCCTTCT    | 324 |
|    |     |                                                              |     |
| Qy | 38  | ValAlaArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGly             | 54  |
|    |     |                                                              |     |
| Db | 323 | ACCTCTACCAAGAGCTCCAGTCTCTCTCATCATGGGGGAGTGAAGGGGGA           | 273 |
|    |     |                                                              |     |
|    |     |                                                              |     |

RESULT 27

US-10-301-480-220043/c

; Sequence 220043, Application US/10301480

; Publication No. US20060057564A1

**; GENERAL INFORMATION:**

; APPLICANT: Wang, David G.

**TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms**

; TITLE OF INVENTION: in the Human Genome

FILE REFERENCE: 108827.137

;; CURRENT APPLICATION NUMBER: US/10/301,480

1 ; CURRENT FILING DATE: 2002-11-21  
2 ;  
3 ; PRIORITY INFORMATION STATEMENT: 35 USC 119(e)  
4 ;

; PRIOR APPLICATION NUMBER: US 10/215,598  
 ; PRIOR FILING DATE 2002 08 08

; PRIOR FILING DATE: 2002-08-09  
 ; PRIOR APPLICATION NUMBER: US 60/311 606

; PRIOR APPLICATION NUMBER: US 60/311,695  
: PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10  
: NUMBER OF SEQ ID NOS: 122618

; NUMBER OF SEQ ID NOS: 1226616  
: SOFTWARE: FastSeq for Windows Version 4.0

```

; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
; SEQ ID NO 220043

```

: LENGTH: 619

TYPE: DNA

**ORGANISM: Homo sapien**

US-10-301-480-220043

**Alignment Scores:**

|                        |       |               |     |
|------------------------|-------|---------------|-----|
| Pred. No.:             | 297   | Length:       | 619 |
| Score:                 | 64.50 | Matches:      | 20  |
| Percent Similarity:    | 54.4% | Conservative: | 11  |
| Best Local Similarity: | 35.1% | Mismatches:   | 21  |
| Query Match:           | 22.9% | Indels:       | 5   |
| DB:                    | 10    | Gaps:         | 2   |

US-10-628-525A-34 (1-58) x US-10-301-480-220043 (1-619)

|    |     |                                                              |     |
|----|-----|--------------------------------------------------------------|-----|
| QY | 1   | MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln | 20  |
| Db | 437 | GTCTCACCACACTGAACACTACTCGACCTGAATCCACTGTGTCTCACT-----GTCCAG  | 384 |
| QY | 21  | AlaSerAlaValAlaProPheGlnGlyLeuLysserThrAla-----SerIeuPro     | 37  |
| Db | 383 | AAACAGCGCCTGCCCATTTCTTACCTAGAGCCACTGGGCACACTACAGCCTTCTCT     | 324 |
| QY | 38  | ValAlaAlaArgSerSerArgSerIeuGlyAsnValAlaSerAsnGlyGly          | 54  |
| Db | 323 | ACCTCTACCAGCAGCTCCAGTCTCTTCATCATGGGGGCGATCAAGGGGA            | 273 |

**RESULT 28**

US-10-301-480-833452/c

; Sequence 833452, Application US/10301480

; Publication No. US20060057564A1

**GENERAL INFORMATION:**

; APPLICANT: Wang, David G.



```
Db 1219 CCGTCGGCGGTGCACCTCTCGCGGCTACGACATCCCGGCCAGACCGCGTCTTCATCA 1278
Qy 23 AlavalalaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArgArgSer 42
Db 1279 ACACCTTCGCCATGGCGCGG-----ACCCGAGATCT 1311
Qy 43 SerArgSerLeuGlyAanValAlaSerAasnGlyGlyArg 55
Db 1312 GGGAGGAGCGCGTGGAGTACTCGCCGCGAGCGGTTCGAGG 1350

RESULT 30
US-11-096-568A-23191
; Sequence 23191, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23191
; LENGTH: 1347
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1347)
; OTHER INFORMATION: Ceres Seq. ID no. 12411590
US-11-096-568A-23191

Alignment Scores:
Pred. No.: 727 Length: 1347
Score: 64.00 Matches: 19
Percent Similarity: 51.2% Conservative: 3
Best Local Similarity: 44.2% Mismatches: 13
Query Match: 22.7% Indels: 8
DB: 11 Gaps: 1

US-10-628-525A-34 (1-58) x US-11-096-568A-23191 (1-1347)
Qy 3 ProThrValMetMetAlaSerAlaThrAlaThrArgThrAsnProAlaGlnAlaSer 22
Db 493 CCGCGACGCGGCGAGGTCCTCAGACGCGCCACGTCCTCCACTTCGCGTCCCGCGCGCC 552
Qy 23 AlavalalaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArgArgSer 42
Db 553 GCC-----TGACGGCTTCGTCTCCAAGGCGGAGGCGCC 588

Qy 43 SerArgSer 45
Db 589 AGGCGGAGC 597
```

Search completed: April 2, 2006, 02:04:56  
Job time : 232.109 secs

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GenCore version 5.1.7

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 20:18:18 ; Search time 1585.5 Seconds  
(without alignments)  
2022.653 Million cell updates/sec

Title: US-10-628-525A-34

Perfect score: 282

Sequence: 1 MATVMMASATATRTNPAQ.....ARRSSRLGNVASNGGRIRC 58

Scoring table:

|                           |  |
|---------------------------|--|
| BLOSUM62                  |  |
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| Ygapop 10.0 , Ygapext 0.5 |  |
| Fgapop 6.0 , Fgapext 7.0  |  |
| Delop 6.0 , Delext 7.0    |  |

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-TRANS-human40.cdi -LIST=150 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Pending Patents\_NA\_Main:\*

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- 3: /cgn2\_6/ptodata/1/pna/PCTUSC\_COMB.seq:\*
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- 5: /cgn2\_6/ptodata/1/pna/US075\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pna/US076\_COMB.seq:\*
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77: /cgn2\_6/ptodata/1/pna/US602B\_COMB.seq:\*

78: /cgn2\_6/ptodata/1/pna/US603\_COMB.seq:\*

79: /cgn2\_6/ptodata/1/pna/US604A\_COMB.seq:\*

80: /cgn2\_6/ptodata/1/pna/US604B\_COMB.seq:\*

81: /cgn2\_6/ptodata/1/pna/US605\_COMB.seq:\*

82: /cgn2\_6/ptodata/1/pna/US606\_COMB.seq:\*

83: /cgn2\_6/ptodata/1/pna/US607\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description         |
|------------|-------|-------------|--------|-------|---------------------|
| 1          | 203.5 | 72.2        | 183    | 42    | US-10-140-410-1     |
| 2          | 203.5 | 72.2        | 183    | 75    | US-60-166-268-1     |
| 3          | 203.5 | 72.2        | 185    | 11    | US-08-113-561A-14   |
| 4          | 203.5 | 72.2        | 188    | 30    | US-09-696-664A-651  |
| 5          | 203.5 | 72.2        | 228    | 22    | US-09-262-979-69    |
| 6          | 203.5 | 72.2        | 228    | 23    | US-09-304-517A-3880 |
| 7          | 203.5 | 72.2        | 228    | 23    | US-09-371-146A-3880 |

|    |       |      |     |    |                      |                    |     |       |      |     |    |                      |                    |
|----|-------|------|-----|----|----------------------|--------------------|-----|-------|------|-----|----|----------------------|--------------------|
| 8  | 203.5 | 72.2 | 228 | 39 | US-09-985-678-3880   | Sequence 3880, Ap  | 81  | 203.5 | 72.2 | 297 | 23 | US-09-304-517A-15920 | Sequence 15920, A  |
| 9  | 203.5 | 72.2 | 228 | 39 | US-09-987-899-69     | Sequence 69, Appl  | 82  | 203.5 | 72.2 | 297 | 23 | US-09-371-146A-15920 | Sequence 15920, A  |
| 10 | 203.5 | 72.2 | 229 | 22 | US-09-262-979-84     | Sequence 84, Appl  | 83  | 203.5 | 72.2 | 297 | 33 | US-09-985-678-15920  | Sequence 15920, A  |
| 11 | 203.5 | 72.2 | 229 | 23 | US-09-304-517A-28585 | Sequence 28585, A  | 84  | 203.5 | 72.2 | 297 | 39 | US-09-987-899-14     | Sequence 14, Appl  |
| 12 | 203.5 | 72.2 | 229 | 23 | US-09-371-146A-28585 | Sequence 28585, A  | 85  | 203.5 | 72.2 | 298 | 22 | US-09-262-979-21     | Sequence 21, Appl  |
| 13 | 203.5 | 72.2 | 229 | 39 | US-09-985-678-28585  | Sequence 28585, A  | 86  | 203.5 | 72.2 | 298 | 22 | US-09-304-517A-15447 | Sequence 15447, A  |
| 14 | 203.5 | 72.2 | 229 | 39 | US-09-987-899-84     | Sequence 84, Appl  | 87  | 203.5 | 72.2 | 298 | 23 | US-09-371-146A-15447 | Sequence 15447, A  |
| 15 | 203.5 | 72.2 | 230 | 22 | US-09-262-979-264    | Sequence 264, Appl | 88  | 203.5 | 72.2 | 298 | 39 | US-09-985-678-15447  | Sequence 15447, A  |
| 16 | 203.5 | 72.2 | 230 | 23 | US-09-304-517A-97485 | Sequence 97485, A  | 89  | 203.5 | 72.2 | 298 | 39 | US-09-987-899-21     | Sequence 21, Appl  |
| 17 | 203.5 | 72.2 | 230 | 23 | US-09-394-745-33403  | Sequence 33403, A  | 90  | 203.5 | 72.2 | 305 | 22 | US-09-262-979-16     | Sequence 16, Appl  |
| 18 | 203.5 | 72.2 | 230 | 27 | US-09-565-306-53165  | Sequence 53165, A  | 91  | 203.5 | 72.2 | 305 | 23 | US-09-304-517A-15586 | Sequence 15586, A  |
| 19 | 203.5 | 72.2 | 230 | 29 | US-09-654-617-326566 | Sequence 326566, A | 92  | 203.5 | 72.2 | 305 | 23 | US-09-371-146A-15586 | Sequence 15586, A  |
| 20 | 203.5 | 72.2 | 230 | 29 | US-09-684-016-326566 | Sequence 326566, A | 93  | 203.5 | 72.2 | 305 | 39 | US-09-985-678-15586  | Sequence 15586, A  |
| 21 | 203.5 | 72.2 | 230 | 39 | US-09-985-678-97485  | Sequence 97485, A  | 94  | 203.5 | 72.2 | 305 | 39 | US-09-987-899-16     | Sequence 16, Appl  |
| 22 | 203.5 | 72.2 | 230 | 39 | US-09-987-899-264    | Sequence 264, Appl | 95  | 203.5 | 72.2 | 307 | 22 | US-09-262-979-29     | Sequence 29, Appl  |
| 23 | 203.5 | 72.2 | 235 | 22 | US-09-262-979-79     | Sequence 79, Appl  | 96  | 203.5 | 72.2 | 307 | 23 | US-09-304-517A-32053 | Sequence 32053, A  |
| 24 | 203.5 | 72.2 | 235 | 23 | US-09-304-517A-5011  | Sequence 5011, Ap  | 97  | 203.5 | 72.2 | 307 | 23 | US-09-371-146A-32053 | Sequence 32053, A  |
| 25 | 203.5 | 72.2 | 235 | 23 | US-09-371-146A-5011  | Sequence 5011, Ap  | 98  | 203.5 | 72.2 | 307 | 39 | US-09-985-678-32053  | Sequence 32053, A  |
| 26 | 203.5 | 72.2 | 235 | 39 | US-09-985-678-5011   | Sequence 5011, Ap  | 99  | 203.5 | 72.2 | 307 | 39 | US-09-987-899-29     | Sequence 29, Appl  |
| 27 | 203.5 | 72.2 | 235 | 39 | US-09-987-899-79     | Sequence 79, Appl  | 100 | 203.5 | 72.2 | 309 | 22 | US-09-262-979-15     | Sequence 15, Appl  |
| 28 | 203.5 | 72.2 | 236 | 22 | US-09-262-979-70     | Sequence 70, Appl  | 101 | 203.5 | 72.2 | 309 | 23 | US-09-304-517A-14558 | Sequence 14558, A  |
| 29 | 203.5 | 72.2 | 236 | 23 | US-09-304-517A-4574  | Sequence 4574, Ap  | 102 | 203.5 | 72.2 | 309 | 23 | US-09-371-146A-14558 | Sequence 14558, A  |
| 30 | 203.5 | 72.2 | 236 | 23 | US-09-371-146A-4574  | Sequence 4574, Ap  | 103 | 203.5 | 72.2 | 309 | 29 | US-09-654-617-302670 | Sequence 302670, A |
| 31 | 203.5 | 72.2 | 236 | 39 | US-09-985-678-4574   | Sequence 4574, Ap  | 104 | 203.5 | 72.2 | 309 | 29 | US-09-684-016-302670 | Sequence 302670, A |
| 32 | 203.5 | 72.2 | 236 | 39 | US-09-987-899-70     | Sequence 70, Appl  | 105 | 203.5 | 72.2 | 309 | 39 | US-09-985-678-14558  | Sequence 14558, A  |
| 33 | 203.5 | 72.2 | 238 | 22 | US-09-262-979-66     | Sequence 66, Appl  | 106 | 203.5 | 72.2 | 309 | 39 | US-09-987-899-15     | Sequence 15, Appl  |
| 34 | 203.5 | 72.2 | 238 | 22 | US-09-304-517A-4331  | Sequence 4331, Ap  | 107 | 203.5 | 72.2 | 311 | 22 | US-09-262-979-30     | Sequence 30, Appl  |
| 35 | 203.5 | 72.2 | 238 | 23 | US-09-371-146A-4331  | Sequence 4331, Ap  | 108 | 203.5 | 72.2 | 311 | 23 | US-09-304-517A-13973 | Sequence 13973, A  |
| 36 | 203.5 | 72.2 | 238 | 39 | US-09-985-678-4331   | Sequence 4331, Ap  | 109 | 203.5 | 72.2 | 311 | 23 | US-09-371-146A-13973 | Sequence 13973, A  |
| 37 | 203.5 | 72.2 | 238 | 39 | US-09-987-899-66     | Sequence 66, Appl  | 110 | 203.5 | 72.2 | 311 | 39 | US-09-985-678-13973  | Sequence 13973, A  |
| 38 | 203.5 | 72.2 | 249 | 22 | US-09-262-979-71     | Sequence 71, Appl  | 111 | 203.5 | 72.2 | 311 | 39 | US-09-987-899-30     | Sequence 30, Appl  |
| 39 | 203.5 | 72.2 | 249 | 23 | US-09-304-517A-4896  | Sequence 4896, Ap  | 112 | 203.5 | 72.2 | 312 | 22 | US-09-262-979-68     | Sequence 68, Appl  |
| 40 | 203.5 | 72.2 | 249 | 23 | US-09-371-146A-4896  | Sequence 4896, Ap  | 113 | 203.5 | 72.2 | 312 | 39 | US-09-987-899-68     | Sequence 68, Appl  |
| 41 | 203.5 | 72.2 | 249 | 39 | US-09-985-678-4896   | Sequence 4896, Ap  | 114 | 203.5 | 72.2 | 315 | 23 | US-09-262-979-11     | Sequence 11, Appl  |
| 42 | 203.5 | 72.2 | 249 | 39 | US-09-987-899-71     | Sequence 71, Appl  | 115 | 203.5 | 72.2 | 315 | 23 | US-09-304-517A-14943 | Sequence 14943, A  |
| 43 | 203.5 | 72.2 | 264 | 22 | US-09-262-979-53     | Sequence 53, Appl  | 116 | 203.5 | 72.2 | 315 | 23 | US-09-371-146A-14943 | Sequence 14943, A  |
| 44 | 203.5 | 72.2 | 264 | 23 | US-09-304-517A-4344  | Sequence 4344, Ap  | 117 | 203.5 | 72.2 | 315 | 29 | US-09-654-617-302708 | Sequence 302708, A |
| 45 | 203.5 | 72.2 | 264 | 23 | US-09-371-146A-4344  | Sequence 4344, Ap  | 118 | 203.5 | 72.2 | 315 | 29 | US-09-684-016-302708 | Sequence 302708, A |
| 46 | 203.5 | 72.2 | 264 | 39 | US-09-985-678-4344   | Sequence 4344, Ap  | 119 | 203.5 | 72.2 | 315 | 39 | US-09-985-678-14943  | Sequence 14943, A  |
| 47 | 203.5 | 72.2 | 264 | 39 | US-09-987-899-53     | Sequence 53, Appl  | 120 | 203.5 | 72.2 | 315 | 39 | US-09-987-899-11     | Sequence 11, Appl  |
| 48 | 203.5 | 72.2 | 265 | 22 | US-09-262-979-40     | Sequence 40, Appl  | 121 | 203.5 | 72.2 | 317 | 22 | US-09-262-979-10     | Sequence 10, Appl  |
| 49 | 203.5 | 72.2 | 265 | 39 | US-09-987-899-40     | Sequence 40, Appl  | 122 | 203.5 | 72.2 | 317 | 23 | US-09-304-517A-15498 | Sequence 15498, A  |
| 50 | 203.5 | 72.2 | 272 | 22 | US-09-262-979-45     | Sequence 45, Appl  | 123 | 203.5 | 72.2 | 317 | 23 | US-09-371-146A-15498 | Sequence 15498, A  |
| 51 | 203.5 | 72.2 | 272 | 23 | US-09-304-517A-3749  | Sequence 3749, Ap  | 124 | 203.5 | 72.2 | 317 | 29 | US-09-654-617-302753 | Sequence 302753, A |
| 52 | 203.5 | 72.2 | 272 | 23 | US-09-371-146A-3749  | Sequence 3749, Ap  | 125 | 203.5 | 72.2 | 317 | 29 | US-09-684-016-302753 | Sequence 302753, A |
| 53 | 203.5 | 72.2 | 272 | 39 | US-09-985-678-3749   | Sequence 3749, Ap  | 126 | 203.5 | 72.2 | 317 | 39 | US-09-985-678-15498  | Sequence 15498, A  |
| 54 | 203.5 | 72.2 | 272 | 39 | US-09-987-899-45     | Sequence 45, Appl  | 127 | 203.5 | 72.2 | 317 | 39 | US-09-987-899-10     | Sequence 10, Appl  |
| 55 | 203.5 | 72.2 | 276 | 22 | US-09-262-979-26     | Sequence 26, Appl  | 128 | 203.5 | 72.2 | 319 | 22 | US-09-262-979-4      | Sequence 4, Appl   |
| 56 | 203.5 | 72.2 | 276 | 22 | US-09-262-979-51     | Sequence 51, Appl  | 129 | 203.5 | 72.2 | 319 | 23 | US-09-304-517A-15087 | Sequence 15087, A  |
| 57 | 203.5 | 72.2 | 276 | 23 | US-09-304-517A-4852  | Sequence 4852, Ap  | 130 | 203.5 | 72.2 | 319 | 23 | US-09-371-146A-15087 | Sequence 15087, A  |
| 58 | 203.5 | 72.2 | 276 | 23 | US-09-304-517A-51543 | Sequence 51543, A  | 131 | 203.5 | 72.2 | 319 | 39 | US-09-985-678-15087  | Sequence 15087, A  |
| 59 | 203.5 | 72.2 | 276 | 23 | US-09-371-146A-4852  | Sequence 4852, Ap  | 132 | 203.5 | 72.2 | 319 | 39 | US-09-987-899-4      | Sequence 4, Appl   |
| 60 | 203.5 | 72.2 | 276 | 23 | US-09-371-146A-51543 | Sequence 51543, A  | 133 | 203.5 | 72.2 | 344 | 22 | US-09-262-979-231    | Sequence 231, App  |
| 61 | 203.5 | 72.2 | 276 | 39 | US-09-985-678-4852   | Sequence 4852, Ap  | 134 | 203.5 | 72.2 | 344 | 23 | US-09-304-517A-93185 | Sequence 93185, A  |
| 62 | 203.5 | 72.2 | 276 | 39 | US-09-985-678-1543   | Sequence 1543, A   | 135 | 203.5 | 72.2 | 344 | 39 | US-09-985-678-93185  | Sequence 93185, A  |
| 63 | 203.5 | 72.2 | 276 | 39 | US-09-987-899-26     | Sequence 26, Appl  | 136 | 203.5 | 72.2 | 344 | 39 | US-09-987-899-231    | Sequence 231, App  |
| 64 | 203.5 | 72.2 | 276 | 39 | US-09-987-899-51     | Sequence 51, Appl  | 137 | 203.5 | 72.2 | 349 | 23 | US-09-394-745-51919  | Sequence 51919, A  |
| 65 | 203.5 | 72.2 | 284 | 22 | US-09-262-979-32     | Sequence 32, Appl  | 138 | 203.5 | 72.2 | 349 | 27 | US-09-565-306-43160  | Sequence 43160, A  |
| 66 | 203.5 | 72.2 | 284 | 23 | US-09-304-517A-15717 | Sequence 15717, A  | 139 | 203.5 | 72.2 | 349 | 34 | US-09-873-402A-17842 | Sequence 17842, A  |
| 67 | 203.5 | 72.2 | 284 | 23 | US-09-371-146A-15717 | Sequence 15717, A  | 140 | 203.5 | 72.2 | 349 | 76 | US-60-209-830-17799  | Sequence 17799, A  |
| 68 | 203.5 | 72.2 | 284 | 39 | US-09-985-678-15717  | Sequence 15717, A  | 141 | 203.5 | 72.2 | 357 | 23 | US-09-304-517A-77557 | Sequence 77557, A  |
| 69 | 203.5 | 72.2 | 284 | 39 | US-09-987-899-32     | Sequence 32, Appl  | 142 | 203.5 | 72.2 | 357 | 27 | US-09-371-146A-77557 | Sequence 77557, A  |
| 70 | 203.5 | 72.2 | 286 | 22 | US-09-262-979-37     | Sequence 37, Appl  | 143 | 203.5 | 72.2 | 357 | 27 | US-09-553-094-18378  | Sequence 18378, A  |
| 71 | 203.5 | 72.2 | 286 | 23 | US-09-304-517A-32361 | Sequence 32361, A  | 144 | 203.5 | 72.2 | 357 | 39 | US-09-985-678-77557  | Sequence 77557, A  |
| 72 | 203.5 | 72.2 | 286 | 23 | US-09-371-146A-32361 | Sequence 32361, A  | 145 | 203.5 | 72.2 | 357 | 75 | US-60-130-181-1499   | Sequence 1499, Ap  |
| 73 | 203.5 | 72.2 | 286 | 39 | US-09-985-678-32361  | Sequence 32361, A  | 146 | 203.5 | 72.2 | 364 | 23 | US-09-304-517A-76804 | Sequence 76804, A  |
| 74 | 203.5 | 72.2 | 286 | 39 | US-09-987-899-37     | Sequence 37, Appl  | 147 | 203.5 | 72.2 | 364 | 23 | US-09-371-146A-76804 | Sequence 76804, A  |
| 75 | 203.5 | 72.2 | 291 | 22 | US-09-262-979-47     | Sequence 47, Appl  | 148 | 203.5 | 72.2 | 364 | 27 | US-09-553-094-16426  | Sequence 16426, A  |
| 76 | 203.5 | 72.2 | 291 | 23 | US-09-304-517A-14794 | Sequence 14794, A  | 149 | 203.5 | 72.2 | 364 | 39 | US-09-985-678-76804  | Sequence 76804, A  |
| 77 | 203.5 | 72.2 | 291 | 23 | US-09-371-146A-14794 | Sequence 14794, A  | 150 | 203.5 | 72.2 | 364 | 75 | US-60-130-179-950    | Sequence 950, App  |
| 78 | 203.5 | 72.2 | 291 | 39 | US-09-985-678-14794  | Sequence 14794, A  |     |       |      |     |    |                      |                    |
| 79 | 203.5 | 72.2 | 291 | 39 | US-09-987-899-47     | Sequence 47, Appl  |     |       |      |     |    |                      |                    |
| 80 | 203.5 | 72.2 | 291 | 22 | US-09-262-979-14     | Sequence 14, Appl  |     |       |      |     |    |                      |                    |

ALIGNMENTS

RESULT 1  
US-10-140-410-1  
; Sequence 1, Application US/10140410  
; GENERAL INFORMATION:  
; APPLICANT: Caimi, Perry G.  
; TITLE OF INVENTION: Fructose Polymer Synthesis in Monocot Plastids  
; FILE REFERENCE: BB1347 US NA  
; CURRENT APPLICATION NUMBER: US/10/140,410  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR FILING DATE: PCT/US00/31788  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: 60/166,268  
; PRIOR FILING DATE: 1999-11-18  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 1  
; LENGTH: 183  
; TYPE: DNA  
; ORGANISM: Zea mays

Alignment Scores:  
Pred. No.: 1,13e-19 Length: 183  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 42 Gaps: 2

US-10-628-525A-34 (1-58) x US-10-140-410-1 (1-183)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
DB 1 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 36  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
DB 37 -----GCCGTCGCTCGTTCAGGGGCTTAAAGTCCACCGCCAGCCTCCCGTGGCCGC 90  
QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyValArgIleArgCys 58  
DB 91 CGCTCTCTAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGAAATCCGGTGC 141

RESULT 2  
US-60-166-268-1  
; Sequence 1, Application US/60166268  
; GENERAL INFORMATION:  
; APPLICANT: Caimi, Perry G.  
; TITLE OF INVENTION: Fructose Polymer Synthesis in Monocot Plastids  
; FILE REFERENCE: BB1347 US PRV  
; CURRENT APPLICATION NUMBER: US/60/166,268  
; CURRENT FILING DATE: 1999-11-18  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 1  
; LENGTH: 183  
; TYPE: DNA  
; ORGANISM: Zea mays

Alignment Scores:  
Pred. No.: 1,13e-19 Length: 183  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 75 Gaps: 2

US-10-628-525A-34 (1-58) x US-60-166-268-1 (1-183)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
DB 1 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 36  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
DB 37 -----GCCGTCGCTCGTTCAGGGGCTTAAAGTCCACCGCCAGCCTCCCGTGGCCGC 90  
QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyValArgIleArgCys 58  
DB 91 CGCTCTCTAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGAAATCCGGTGC 141

## RESULT 3

US-08-113-561A-14  
; Sequence 14, Application US/08113561A  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Thomas R. et al.  
; TITLE OF INVENTION: Methods and Compositions for the  
; TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants  
; TITLE OF INVENTION: and Cells Thereof  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/113,561A  
; FILING DATE: 25-AUG-1993  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/565,844  
; FILING DATE: 09-AUG-1990

; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: DEKM:055/PAR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 713/789-2679  
; TELEX: 79-0924  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 185 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-113-561A-14

Alignment Scores:  
Pred. No.: 1,16e-19 Length: 185  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 11 Gaps: 2

US-10-628-525A-34 (1-58) x US-08-113-561A-14 (1-185)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
DB 42 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 77  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40



; CURRENT APPLICATION NUMBER: US/09/371,146A  
; CURRENT FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: US 09/304,517  
; PRIOR FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 294310  
; SEQ ID NO 3880  
; LENGTH: 228  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-371-146A-3880

Alignment Scores:  
Pred. No.: 1.63e-19 Length: 228  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-371-146A-3880 (1-228)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db ATGGCGCCACCGTGATGATGGCTCGTGGCCACC----- 72  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db -----GCCGTGCTCGTTCAGGGGGCTCAAGTCCACGCCAGCCTCCCGCTGCGCCGC 126  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgCys 58  
Db 127 CGCTCTCCAGAGCTTCGGCAACGTC---AGCACGGCGGAAGGATCCGGTGC 177

## RESULT 8

US-09-985-678-3880  
; Sequence 3880, Application US/09985678  
; GENERAL INFORMATION:

; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; TITLE OF INVENTION: Annotated Plant Genes  
; FILE REFERENCE: 16517.255/38-21(15097)F  
; CURRENT APPLICATION NUMBER: US/09/985,678  
; CURRENT FILING DATE: 2001-11-05  
; PRIOR APPLICATION NUMBER: US 09/304,517  
; PRIOR FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 295529  
; SEQ ID NO 3880  
; LENGTH: 228  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-985-678-3880

Alignment Scores:  
Pred. No.: 1.63e-19 Length: 228  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-985-678-3880 (1-228)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db ATGGCGCCACCGTGATGATGGCTCGTGGCCACC----- 72  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db -----GCCGTGCTCGTTCAGGGGGCTCAAGTCCACGCCAGCCTCCCGCTGCGCCGC 126  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgCys 58  
Db 127 CGCTCTCCAGAGCTTCGGCAACGTC---AGCACGGCGGAAGGATCCGGTGC 177

## RESULT 9

US-09-987-899-69  
; Sequence 69, Application US/09987899  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 69  
; LENGTH: 228  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700042688H1  
US-09-987-899-69

Alignment Scores:  
Pred. No.: 1.63e-19 Length: 228  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-69 (1-228)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db ATGGCGCCACCGTGATGATGGCTCGTGGCCACC----- 72  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db -----GCCGTGCTCGTTCAGGGGGCTCAAGTCCACGCCAGCCTCCCGCTGCGCCGC 126  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgCys 58  
Db 127 CGCTCTCCAGAGCTTCGGCAACGTC---AGCACGGCGGAAGGATCCGGTGC 177

## RESULT 10

US-09-262-979-84  
; Sequence 84, Application US/09262979  
; GENERAL INFORMATION:

; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With The  
; FILE REFERENCE: 38-21(15091)B  
; CURRENT APPLICATION NUMBER: US/09/262,979  
; CURRENT FILING DATE: 1999-03-04  
; EARLIER APPLICATION NUMBER: US 60/076,912  
; EARLIER FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 84  
; LENGTH: 229  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700198026H1  
US-09-262-979-84



```
Alignment Scores:
Pred. No.: 1.64e-19 Length: 229
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 22 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-262-979-84 (1-229)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 52 ATGGCGCCACCGTGATGATGGCTCGTGGCCACC----- 87
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 88 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCAGCCAGCTCCCGTCGCCCGC 141
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 142 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 192

RESULT 11
US-09-304-517A-28585
; Sequence 28585, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 28585
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Zea mays
US-09-304-517A-28585

Alignment Scores:
Pred. No.: 1.64e-19 Length: 229
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-304-517A-28585 (1-229)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 52 ATGGCGCCACCGTGATGATGGCTCGTGGCCACC----- 87
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 88 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCAGCCAGCTCCCGTCGCCCGC 141
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 142 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 192

RESULT 12
US-09-371-146A-28585
; Sequence 28585, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE: 38-21(15097)C
; CURRENT APPLICATION NUMBER: US/09/371,146A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
```

```
; NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 28585
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Zea mays
US-09-371-146A-28585

Alignment Scores:
Pred. No.: 1.64e-19 Length: 229
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-371-146A-28585 (1-229)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 52 ATGGCGCCACCGTGATGATGGCTCGTGGCCACC----- 87
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 88 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCAGCCAGCTCCCGTCGCCCGC 141
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 142 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 192

RESULT 13
US-09-985-678-28585
; Sequence 28585, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517.255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 28585
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Zea mays
US-09-985-678-28585

Alignment Scores:
Pred. No.: 1.64e-19 Length: 229
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 39 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-985-678-28585 (1-229)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 52 ATGGCGCCACCGTGATGATGGCTCGTGGCCACC----- 87
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 88 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCAGCCAGCTCCCGTCGCCCGC 141
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 142 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 192

RESULT 14
US-09-987-899-84
; Sequence 84, Application US/09987899
```

```

; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 1517.258
; CURRENT APPLICATION NUMBER: US/09/262,979
; PRIOR FILING DATE: 2001-11-16
; PRIOR FILING DATE: 1999-03-04
; PRIOR FILING DATE: 1999-03-04
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 84
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700198026H1
; US-09-987-899-84

Alignment Scores:
Pred. No.: 1.64e-19 Length: 229
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 39 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-84 (1-229)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 52 ATGGCGCCACCGTGATGATGCGTCCGCCACC----- 87
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 88 -----GCCGTGCTCGTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCCGCCGC 141
Qy 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgileArgCys 58
Db 142 CGTCTCTCCAGAACCTCCGCCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 192

RESULT 15
US-09-262-979-264
; Sequence 264, Application US/09262979
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With The
; FILE REFERENCE: 38-21(15091)B
; CURRENT APPLICATION NUMBER: US/09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 264
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3068-029-Q1-K1-F6
; US-09-262-979-264

Alignment Scores:
Pred. No.: 1.66e-19 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0

; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With The
; FILE REFERENCE: 38-21(15091)B
; CURRENT APPLICATION NUMBER: US/09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 264
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3068-029-Q1-K1-F6
; US-09-262-979-264

Alignment Scores:
Pred. No.: 1.66e-19 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
```

```

Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 22 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-262-979-264 (1-230)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGATGCGTCCGCCACC----- 72
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTGCTCGTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCCGCCGC 126
Qy 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgileArgCys 58
Db 127 CGTCTCTCCAGAACCTCCGCCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 16
US-09-304-517A-97485
; Sequence 97485, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 97485
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
; US-09-304-517A-97485

Alignment Scores:
Pred. No.: 1.66e-19 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-304-517A-97485 (1-230)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGATGCGTCCGCCACC----- 72
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTGCTCGTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCCGCCGC 126
Qy 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgileArgCys 58
Db 127 CGTCTCTCCAGAACCTCCGCCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 17
US-09-394-745-33403
; Sequence 33403, Application US/09394745
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(15454)B
; CURRENT APPLICATION NUMBER: US/09/394,745
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 57264
; SEQ ID NO 33403
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
```

```
/ OTHER INFORMATION: Clone ID: LIB3068-029-Q1-K1-P6
US-09-394-745-33403

Alignment Scores:
Pred. No.: 1.66e-19 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-394-745-33403 (1-230)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGATGCGCTCGTGGCCACC----- 72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACGCCGAGCTCCCGTGGCCGC 126

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 127 CGCTCCTCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 177

RESULT 18
US-09-565-306-53165
; Sequence 53165, Application US/09565306
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalugudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15459)C
; CURRENT APPLICATION NUMBER: US/09/565,306
; CURRENT FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 53165
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3068-029-Q1-K1-P6
US-09-565-306-53165

Alignment Scores:
Pred. No.: 1.66e-19 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 27 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-565-306-53165 (1-230)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGATGCGCTCGTGGCCACC----- 72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACGCCGAGCTCCCGTGGCCGC 126

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 127 CGCTCCTCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 177

RESULT 19
US-09-654-617-326566
; Sequence 326566, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
```

```
/ TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 326566
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
US-09-654-617-326566

Alignment Scores:
Pred. No.: 1.66e-19 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 29 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-654-617-326566 (1-230)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGATGCGCTCGTGGCCACC----- 72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACGCCGAGCTCCCGTGGCCGC 126

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 127 CGCTCCTCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 177

RESULT 20
US-09-684-016-326566
; Sequence 326566, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 326566
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
US-09-684-016-326566

Alignment Scores:
Pred. No.: 1.66e-19 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 29 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-684-016-326566 (1-230)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGATGCGCTCGTGGCCACC----- 72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACGCCGAGCTCCCGTGGCCGC 126

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 127 CGCTCCTCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 177
```

```
RESULT 21
US-09-985-678-97485
; Sequence 97485, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517.255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 97485
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
US-09-985-678-97485

Alignment Scores:
Pred. No.: 1.66e-19 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 39 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-985-678-97485 (1-230)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCAGCTCCCGTCGCCCGC 126
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 127 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 22
US-09-987-899-264
; Sequence 264, Application US/09987899
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 264
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3068-029-Q1-K1-P6
US-09-987-899-264

Alignment Scores:
Pred. No.: 1.66e-19 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 39 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-985-678-97485 (1-230)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCAGCTCCCGTCGCCCGC 126
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 127 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 23
US-09-262-979-79
; Sequence 79, Application US/09262979
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; FILE REFERENCE: 38-21(15091)B
; CURRENT APPLICATION NUMBER: US/09/262,979
; CURRENT FILING DATE: 1999-03-04
; EARLIER APPLICATION NUMBER: US 60/076,912
; EARLIER FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 79
; LENGTH: 235
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700046244H1
US-09-262-979-79

Alignment Scores:
Pred. No.: 1.72e-19 Length: 235
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 22 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-262-979-79 (1-235)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 47 ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 82
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 83 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCAGCTCCCGTCGCCCGC 136
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 137 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 187

RESULT 24
US-09-304-517A-5011
; Sequence 5011, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
```

```
Query Match: 72.2% Indels: 11
DB: 39 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-264 (1-230)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCAGCTCCCGTCGCCCGC 126
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 127 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 23
US-09-262-979-79
; Sequence 79, Application US/09262979
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; FILE REFERENCE: 38-21(15091)B
; CURRENT APPLICATION NUMBER: US/09/262,979
; CURRENT FILING DATE: 1999-03-04
; EARLIER APPLICATION NUMBER: US 60/076,912
; EARLIER FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 79
; LENGTH: 235
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700046244H1
US-09-262-979-79

Alignment Scores:
Pred. No.: 1.72e-19 Length: 235
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 22 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-262-979-79 (1-235)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 47 ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 82
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 83 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCAGCTCCCGTCGCCCGC 136
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 137 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 187

RESULT 24
US-09-304-517A-5011
; Sequence 5011, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
```

; NUMBER OF SEQ ID NOS: 295529  
; SEQ ID NO 5011  
; LENGTH: 235  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-304-517A-5011

Alignment Scores:  
Pred. No.: 1-72e-19 Length: 235  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservatives: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-304-517A-5011 (1-235)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThraAsnProAlaGln 20  
Db 47 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 82  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 83 -----GCCGTCCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCCTCCCGTCGCCCGC 136  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyCys 58  
Db 137 CGCTCTCCAGAGCTCGGCCAAGCTC---AGCAACGGCGGAAGGATCCGGTGC 187

## RESULT 25

US-09-371-146A-5011  
; Sequence 5011, Application US/09371146A  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; TITLE OF INVENTION: ANNOTATED PLANT GENES  
; FILE REFERENCE: 38-21(15097)C  
; CURRENT APPLICATION NUMBER: US/09/371,146A  
; CURRENT FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: US 09/304,517  
; PRIOR FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 294310  
; SEQ ID NO 5011  
; LENGTH: 235  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-371-146A-5011

Alignment Scores:  
Pred. No.: 1-72e-19 Length: 235  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservatives: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-371-146A-5011 (1-235)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThraAsnProAlaGln 20  
Db 47 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 82  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 83 -----GCCGTCCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCCTCCCGTCGCCCGC 136  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyCys 58  
Db 137 CGCTCTCCAGAGCTCGGCCAAGCTC---AGCAACGGCGGAAGGATCCGGTGC 187

## RESULT 26

US-09-985-678-5011  
; Sequence 5011, Application US/09985678

; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; TITLE OF INVENTION: Annotated Plant Genes  
; FILE REFERENCE: 16517.255/38-21(15097)F  
; CURRENT APPLICATION NUMBER: US/09/985,678  
; CURRENT FILING DATE: 2001-11-05  
; PRIOR APPLICATION NUMBER: US 09/304,517  
; PRIOR FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 295529  
; SEQ ID NO 5011  
; LENGTH: 235  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-985-678-5011

Alignment Scores:  
Pred. No.: 1-72e-19 Length: 235  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservatives: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 39 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-985-678-5011 (1-235)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThraAsnProAlaGln 20  
Db 47 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 82  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 83 -----GCCGTCCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCCTCCCGTCGCCCGC 136  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyCys 58  
Db 137 CGCTCTCCAGAGCTCGGCCAAGCTC---AGCAACGGCGGAAGGATCCGGTGC 187

## RESULT 27

US-09-987-899-79  
; Sequence 79, Application US/09987899  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; TITLE OF INVENTION: With the Carbon Assimilation Pathway  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 79  
; LENGTH: 235  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700046244H1  
US-09-987-899-79

Alignment Scores:  
Pred. No.: 1-72e-19 Length: 235  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservatives: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 39 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-79 (1-235)

```
Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 47 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC-----82
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 83 -----GCCGTCGTCGTCCTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 136
Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 137 CGCTCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 187

RESULT 28
US-09-262-979-70
; Sequence 70, Application US/09262979
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; FILE REFERENCE: 38-21(15091)B
; CURRENT APPLICATION NUMBER: US/09/262,979
; CURRENT FILING DATE: 1999-03-04
; EARLIER APPLICATION NUMBER: US 60/076,912
; EARLIER FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 70
; LENGTH: 236
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700044947H1
US-09-262-979-70

Alignment Scores:
Pred. No.: 1,73e-19 Length: 236
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 22 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-262-979-70 (1-236)
Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 13 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC-----48
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 49 -----GCCGTCGTCGTCCTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 102
Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 103 CGCTCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 153

RESULT 29
US-09-304-517A-4574
; Sequence 4574, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 29529
; SEQ ID NO 4574
; LENGTH: 236
; TYPE: DNA
```

```
; ORGANISM: Zea mays
US-09-304-517A-4574

Alignment Scores:
Pred. No.: 1,73e-19 Length: 236
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 22 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-304-517A-4574 (1-236)
Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 13 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC-----48
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 49 -----GCCGTCGTCGTCCTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 102
Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 103 CGCTCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 153

RESULT 30
US-09-371-146A-4574
; Sequence 4574, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE: 38-21(15097)C
; CURRENT APPLICATION NUMBER: US/09/371,146A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 4574
; LENGTH: 236
; TYPE: DNA
; ORGANISM: Zea mays
US-09-371-146A-4574

Alignment Scores:
Pred. No.: 1,73e-19 Length: 236
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-371-146A-4574 (1-236)
Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 13 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC-----48
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 49 -----GCCGTCGTCGTCCTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 102
Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 103 CGCTCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 153

Search completed: April 2, 2006, 03:27:39
Job time : 1588.5 secs
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GenCore version 5.1.7  
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QM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 21:21:57 ; Search time 108.468 Seconds  
(without alignments)  
1603.719 Million cell updates/sec

Title: US-10-628-525A-34

Perfect score: 282

Sequence: 1 MAPTVWASSATATRNPAQ.....ARRSSRLGNVASNGGRIRC 58

Scoring table:

BLOSUM62 Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6698573 seqs, 1499593917 residues

Total number of hits satisfying chosen parameters: 13397146

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-Q=/abs/ABSSWEB spool/US10628525/runat\_31032006\_095132\_17106/app query.fasta\_1  
-DB=Pending Patents NA.New -QFMT=fastap -SUFFIX=p2n.rdpn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=150 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR\_MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abss06h  
-USER=US10628525 @CGN 1.1.1552 @runat\_31032006\_095132\_17106 -NCPU=6 -ICPU=3  
-NO WMAP -NEG SCORES=0 -WAIT -DSBLOK=100 -LONGLOG\_DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Pending Patents NA.New :  
1: /SID55/ptodata/2/pna/US06\_PCT\_NEW\_COMB.seq :  
2: /SID55/ptodata/2/pna/US06\_NEW\_COMB.seq :  
3: /SID55/ptodata/2/pna/US07\_NEW\_COMB.seq :  
4: /SID55/ptodata/2/pna/US08\_NEW\_COMB.seq :  
5: /SID55/ptodata/2/pna/US09\_NEW\_COMB.seq :  
6: /SID55/ptodata/2/pna/US10\_NEW\_COMB.seq :  
7: /SID55/ptodata/2/pna/US10\_NEW\_COMB.seq :  
8: /SID55/ptodata/2/pna/US11\_NEW\_COMB.seq :  
9: /SID55/ptodata/2/pna/US11\_NEW\_COMB.seq :  
10: /SID55/ptodata/2/pna/US11\_NEW\_COMB.seq :  
11: /SID55/ptodata/2/pna/US11\_NEW\_COMB.seq :  
12: /SID55/ptodata/2/pna/US60\_NEW\_COMB.seq :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                           |
|------------|-------|-------------|--------|----|---------------------------------------|
| 1          | 203.5 | 72.2        | 188    | 8  | US-11-330-364-651 Sequence 651, App   |
| 2          | 203.5 | 72.2        | 228    | 8  | US-11-244-330A-69 Sequence 69, App    |
| 3          | 203.5 | 72.2        | 229    | 8  | US-11-244-330A-84 Sequence 84, App    |
| 4          | 203.5 | 72.2        | 230    | 8  | US-11-244-330A-264 Sequence 264, App  |
| 5          | 203.5 | 72.2        | 230    | 8  | US-11-353-150-53165 Sequence 53165, A |

|    |       |      |      |    |                     |                    |
|----|-------|------|------|----|---------------------|--------------------|
| 6  | 203.5 | 72.2 | 235  | 8  | US-11-244-330A-79   | Sequence 79, App   |
| 7  | 203.5 | 72.2 | 236  | 8  | US-11-244-330A-70   | Sequence 70, App   |
| 8  | 203.5 | 72.2 | 238  | 8  | US-11-244-330A-66   | Sequence 66, App   |
| 9  | 203.5 | 72.2 | 249  | 8  | US-11-244-330A-71   | Sequence 71, App   |
| 10 | 203.5 | 72.2 | 264  | 8  | US-11-244-330A-53   | Sequence 53, App   |
| 11 | 203.5 | 72.2 | 265  | 8  | US-11-244-330A-40   | Sequence 40, App   |
| 12 | 203.5 | 72.2 | 272  | 8  | US-11-244-330A-45   | Sequence 45, App   |
| 13 | 203.5 | 72.2 | 276  | 8  | US-11-244-330A-26   | Sequence 26, App   |
| 14 | 203.5 | 72.2 | 276  | 8  | US-11-244-330A-51   | Sequence 51, App   |
| 15 | 203.5 | 72.2 | 284  | 8  | US-11-244-330A-32   | Sequence 32, App   |
| 16 | 203.5 | 72.2 | 286  | 8  | US-11-244-330A-37   | Sequence 37, App   |
| 17 | 203.5 | 72.2 | 291  | 8  | US-11-244-330A-47   | Sequence 47, App   |
| 18 | 203.5 | 72.2 | 297  | 8  | US-11-244-330A-14   | Sequence 14, App   |
| 19 | 203.5 | 72.2 | 298  | 8  | US-11-244-330A-16   | Sequence 16, App   |
| 20 | 203.5 | 72.2 | 305  | 8  | US-11-244-330A-29   | Sequence 29, App   |
| 21 | 203.5 | 72.2 | 307  | 8  | US-11-244-330A-15   | Sequence 15, App   |
| 22 | 203.5 | 72.2 | 309  | 8  | US-11-244-330A-30   | Sequence 30, App   |
| 23 | 203.5 | 72.2 | 311  | 8  | US-11-244-330A-68   | Sequence 68, App   |
| 24 | 203.5 | 72.2 | 312  | 8  | US-11-244-330A-11   | Sequence 11, App   |
| 25 | 203.5 | 72.2 | 315  | 8  | US-11-244-330A-10   | Sequence 10, App   |
| 26 | 203.5 | 72.2 | 317  | 8  | US-11-244-330A-4    | Sequence 4, App    |
| 27 | 203.5 | 72.2 | 319  | 8  | US-11-244-330A-231  | Sequence 231, App  |
| 28 | 203.5 | 72.2 | 344  | 8  | US-11-353-150-43160 | Sequence 43160, A  |
| 29 | 203.5 | 72.2 | 349  | 8  | US-11-329-388-18378 | Sequence 18378, A  |
| 30 | 203.5 | 72.2 | 357  | 8  | US-11-329-388-16426 | Sequence 16426, A  |
| 31 | 203.5 | 72.2 | 364  | 8  | US-11-329-388-16940 | Sequence 16940, A  |
| 32 | 203.5 | 72.2 | 375  | 8  | US-11-329-388-16940 | Sequence 16940, A  |
| 33 | 203.5 | 72.2 | 409  | 8  | US-11-244-330A-215  | Sequence 215, App  |
| 34 | 203.5 | 72.2 | 409  | 8  | US-11-329-388-14858 | Sequence 14858, A  |
| 35 | 203.5 | 72.2 | 409  | 8  | US-11-353-150-43494 | Sequence 43494, A  |
| 36 | 203.5 | 72.2 | 415  | 8  | US-11-244-330A-244  | Sequence 244, App  |
| 37 | 203.5 | 72.2 | 438  | 8  | US-11-244-330A-210  | Sequence 210, App  |
| 38 | 203.5 | 72.2 | 438  | 8  | US-11-353-150-68984 | Sequence 68984, A  |
| 39 | 203.5 | 72.2 | 441  | 8  | US-11-244-330A-229  | Sequence 229, App  |
| 40 | 203.5 | 72.2 | 443  | 8  | US-11-244-330A-235  | Sequence 235, App  |
| 41 | 203.5 | 72.2 | 617  | 8  | US-11-330-364-12143 | Sequence 12143, A  |
| 42 | 203.5 | 72.2 | 1242 | 1  | PCT-US05-45517-219  | Sequence 219, App  |
| 43 | 203.5 | 72.2 | 1242 | 10 | US-11-303-745-219   | Sequence 219, App  |
| 44 | 202.5 | 71.8 | 197  | 8  | US-11-244-330A-270  | Sequence 270, App  |
| 45 | 202.5 | 71.8 | 197  | 8  | US-11-329-388-13647 | Sequence 13647, A  |
| 46 | 202.5 | 71.8 | 198  | 8  | US-11-244-330A-99   | Sequence 99, App   |
| 47 | 202.5 | 71.8 | 258  | 8  | US-11-244-330A-48   | Sequence 48, App   |
| 48 | 202.5 | 71.8 | 268  | 8  | US-11-244-330A-54   | Sequence 54, App   |
| 49 | 202.5 | 71.8 | 269  | 8  | US-11-244-330A-62   | Sequence 62, App   |
| 50 | 202.5 | 71.8 | 276  | 8  | US-11-244-330A-44   | Sequence 44, App   |
| 51 | 202.5 | 71.8 | 278  | 8  | US-11-244-330A-22   | Sequence 22, App   |
| 52 | 202.5 | 71.8 | 283  | 8  | US-11-244-330A-31   | Sequence 31, App   |
| 53 | 202.5 | 71.8 | 286  | 8  | US-11-244-330A-41   | Sequence 41, App   |
| 54 | 202.5 | 71.8 | 290  | 8  | US-11-244-330A-35   | Sequence 35, App   |
| 55 | 202.5 | 71.8 | 291  | 8  | US-11-244-330A-25   | Sequence 25, App   |
| 56 | 202.5 | 71.8 | 291  | 8  | US-11-244-330A-34   | Sequence 34, App   |
| 57 | 202.5 | 71.8 | 291  | 8  | US-11-244-330A-49   | Sequence 49, App   |
| 58 | 202.5 | 71.8 | 296  | 8  | US-11-244-330A-38   | Sequence 38, App   |
| 59 | 202.5 | 71.8 | 310  | 8  | US-11-244-330A-23   | Sequence 23, App   |
| 60 | 202.5 | 71.8 | 316  | 8  | US-11-244-330A-9    | Sequence 9, App    |
| 61 | 202.5 | 71.8 | 381  | 8  | US-11-244-330A-220  | Sequence 220, App  |
| 62 | 202.5 | 71.8 | 384  | 10 | US-11-227-183A-553  | Sequence 553, App  |
| 63 | 202.5 | 71.8 | 386  | 8  | US-11-329-388-15097 | Sequence 15097, A  |
| 64 | 202.5 | 71.8 | 411  | 8  | US-11-244-330A-221  | Sequence 221, App  |
| 65 | 202.5 | 71.8 | 414  | 8  | US-11-244-330A-213  | Sequence 213, App  |
| 66 | 202.5 | 71.8 | 414  | 8  | US-11-329-388-15586 | Sequence 15586, A  |
| 67 | 202.5 | 71.8 | 433  | 8  | US-11-244-330A-211  | Sequence 211, App  |
| 68 | 202.5 | 71.8 | 434  | 8  | US-11-244-330A-223  | Sequence 223, App  |
| 69 | 202.5 | 71.8 | 434  | 8  | US-11-244-330A-424  | Sequence 224, App  |
| 70 | 202.5 | 71.8 | 434  | 8  | US-11-329-388-13655 | Sequence 13655, A  |
| 71 | 202.5 | 71.8 | 434  | 8  | US-11-329-388-15585 | Sequence 15585, A  |
| 72 | 202.5 | 71.8 | 435  | 8  | US-11-329-388-15375 | Sequence 15375, A  |
| 73 | 202.5 | 71.8 | 446  | 10 | US-11-227-183A-2995 | Sequence 2995, App |
| 74 | 202.5 | 71.8 | 450  | 8  | US-11-329-388-15092 | Sequence 15092, A  |
| 75 | 202.5 | 71.8 | 478  | 8  | US-11-353-150-19891 | Sequence 19891, A  |
| 76 | 202.5 | 71.8 | 283  | 8  | US-11-244-330A-39   | Sequence 39, App   |
| 77 | 199.5 | 70.7 | 226  | 8  | US-11-244-330A-97   | Sequence 97, App   |
| 78 | 198.5 | 70.4 |      |    |                     |                    |



```
; LENGTH: 228
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700042688H1
US-11-244-330A-69

Alignment Scores:
Pred. No.: 7,07e-17 Length: 228
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservatives: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-69 (1-228)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGGCTCGTCGGCCACC-----72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLeuSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGGCCGC 126
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 127 CGCTCTCCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 3
US-11-244-330A-84
; Sequence 84, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091))D/US
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 84
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700198026H1
US-11-244-330A-84

Alignment Scores:
Pred. No.: 7,11e-17 Length: 229
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservatives: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-84 (1-229)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 52 ATGGCGCCACCGTGATGGCTCGTCGGCCACC-----87
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLeuSerThrAlaSerLeuProValAlaArg 40
Db 127 CGCTCTCCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 4
US-11-244-330A-264
; Sequence 264, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091))D/US
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 264
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3068-029-Q1-K1-F6
US-11-244-330A-264

Alignment Scores:
Pred. No.: 7,16e-17 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservatives: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-264 (1-230)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGGCTCGTCGGCCACC-----72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLeuSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGGCCGC 126
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 127 CGCTCTCCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 5
US-11-353-150-53165
; Sequence 53165, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 16517.365 - 38-21(15459))D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
```

```
; SEQ ID NO 53165
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3068-029-Q1-K1-F6
US-11-353-150-53165

Alignment Scores:
Pred. No.: 7,16e-17 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-353-150-53165 (1-230)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 37 ATGGCGCCACCCTGATGATGCTCGTCGCCACC----- 72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
DB 73 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGGCTCCCGTCGCCCGC 126
QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58
DB 127 CGCTCTCCAGAACGCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 6
US-11-244-330A-79
; Sequence 79, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 79
; LENGTH: 235
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700046244H1
US-11-244-330A-79

Alignment Scores:
Pred. No.: 7,41e-17 Length: 236
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-79 (1-236)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 13 ATGGCGCCACCCTGATGATGCTCGTCGCCACC----- 48
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
DB 49 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGGCTCCCGTCGCCCGC 102
QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58
DB 103 CGCTCTCCAGAACGCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 153

RESULT 8
US-11-244-330A-66
; Sequence 66, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
```

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; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 66
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700044245H1
US-11-244-330A-66

Alignment Scores:
Pred. No.: 7,5e-17 Length: 238
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-66 (1-238)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 14 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 49
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 50 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGTGGCCGC 103
QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 104 CGCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 154

RESULT 9
US-11-244-330A-71
; Sequence 71, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; PRIOR FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 71
; LENGTH: 249
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700045847H1
US-11-244-330A-71

Alignment Scores:
Pred. No.: 7,98e-17 Length: 249
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-71 (1-249)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 14 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 49
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 50 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGTGGCCGC 103
QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 104 CGCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 154

US-10-628-525A-34 (1-58) x US-11-244-330A-53 (1-264)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 46 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 81
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 82 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGTGGCCGC 135
QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 136 CGCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 186

RESULT 11
US-11-244-330A-40
; Sequence 40, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
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; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 40
; LENGTH: 265
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700025653H1
US-11-244-330A-40

Alignment Scores:
Pred. No.:      8,69e-17      Length:      265
Score:          203.50      Matches:      47
Percent Similarity: 81.0%      Conservative: 0
Best Local Similarity: 81.0%      Mismatches: 0
Query Match:    72.2%      Indels:      11
DB:             8          Gaps:          2

US-10-628-525A-34 (1-58) x US-11-244-330A-40 (1-265)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 21 ATGGGCCCCACCGTGATGATGGCTCGTCGGCCACC----- 56
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerIleuProValAlaArg 40
Db 57 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 110
QY 41 ArgSerSerArgSerIleuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 111 CGCTCTCTCAGAAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 161

RESULT 12
US-11-244-330A-45
; Sequence 45, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 45
; LENGTH: 272
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700042186H1
US-11-244-330A-45

Alignment Scores:
Pred. No.:      9e-17      Length:      272
Score:          203.50      Matches:      47
Percent Similarity: 81.0%      Conservative: 0
Best Local Similarity: 81.0%      Mismatches: 0
Query Match:    72.2%      Indels:      11
DB:             8          Gaps:          2
```

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US-10-628-525A-34 (1-58) x US-11-244-330A-45 (1-272)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 43 ATGGGCCCCACCGTGATGATGGCTCGTCGGCCACC----- 78
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerIleuProValAlaArg 40
Db 79 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 132
QY 41 ArgSerSerArgSerIleuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 133 CGCTCTCTCAGAAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 183

RESULT 13
US-11-244-330A-26
; Sequence 26, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 26
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700045728H1
US-11-244-330A-26

Alignment Scores:
Pred. No.:      9.18e-17      Length:      276
Score:          203.50      Matches:      47
Percent Similarity: 81.0%      Conservative: 0
Best Local Similarity: 81.0%      Mismatches: 0
Query Match:    72.2%      Indels:      11
DB:             8          Gaps:          2

US-10-628-525A-34 (1-58) x US-11-244-330A-26 (1-276)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 41 ATGGGCCCCACCGTGATGATGGCTCGTCGGCCACC----- 76
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerIleuProValAlaArg 40
Db 77 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 130
QY 41 ArgSerSerArgSerIleuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 131 CGCTCTCTCAGAAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 181

RESULT 14
US-11-244-330A-51
; Sequence 51, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
```

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
 ; TITLE OF INVENTION: With the Carbon Assimilation Pathway  
 ; FILE REFERENCE: 16517.339 (38-21(15091)D/US)  
 ; CURRENT APPLICATION NUMBER: US/11/244,330A  
 ; CURRENT FILING DATE: 2005-10-06  
 ; PRIOR APPLICATION NUMBER: US 09/987,899  
 ; PRIOR FILING DATE: 2001-11-16  
 ; PRIOR APPLICATION NUMBER: US 09/262,979  
 ; PRIOR FILING DATE: 1999-03-04  
 ; PRIOR APPLICATION NUMBER: US 60/076,712  
 ; PRIOR FILING DATE: 1998-03-06  
 ; NUMBER OF SEQ ID NOS: 7341  
 ; SEQ ID NO 51  
 ; LENGTH: 276  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: 700433801H1  
 US-11-244-330A-51

Alignment Scores:  
 Pred. No.: 9,18e-17 Length: 276  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservatives: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 81.0% Indels: 11  
 DB: 8 Gaps: 2  
 US-10-628-525A-34 (1-58) x US-11-244-330A-51 (1-276)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThrArgThrAsnProAlaGln 20  
 DB 46 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 81  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 DB 82 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 135  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgileArgCys 58  
 DB 136 CGCTCTCTCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 186

RESULT 15  
 US-11-244-330A-32  
 ; Sequence 32, Application US/11244330A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheikh, Nordine  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Miller, Phillip W.  
 ; APPLICANT: O Connell, Keith M.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
 ; TITLE OF INVENTION: With the Carbon Assimilation Pathway  
 ; FILE REFERENCE: 16517.339 (38-21(15091)D/US)  
 ; CURRENT APPLICATION NUMBER: US/11/244,330A  
 ; CURRENT FILING DATE: 2005-10-06  
 ; PRIOR APPLICATION NUMBER: US 09/987,899  
 ; PRIOR FILING DATE: 2001-11-16  
 ; PRIOR APPLICATION NUMBER: US 09/262,979  
 ; PRIOR FILING DATE: 1999-03-04  
 ; PRIOR APPLICATION NUMBER: US 60/076,712  
 ; PRIOR FILING DATE: 1998-03-06  
 ; NUMBER OF SEQ ID NOS: 7341  
 ; SEQ ID NO 32  
 ; LENGTH: 284  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: 700100637H1  
 US-11-244-330A-32

Alignment Scores:  
 Pred. No.: 9,55e-17 Length: 284  
 Score: 203.50 Matches: 47

Percent Similarity: 81.0% Conservatives: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 8 Gaps: 2  
 US-10-628-525A-34 (1-58) x US-11-244-330A-32 (1-284)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThrArgThrAsnProAlaGln 20  
 DB 50 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 85  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 DB 86 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 139  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgileArgCys 58  
 DB 140 CGCTCTCTCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 190

RESULT 16  
 US-11-244-330A-37  
 ; Sequence 37, Application US/11244330A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheikh, Nordine  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Miller, Phillip W.  
 ; APPLICANT: O Connell, Keith M.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
 ; TITLE OF INVENTION: With the Carbon Assimilation Pathway  
 ; FILE REFERENCE: 16517.339 (38-21(15091)D/US)  
 ; CURRENT APPLICATION NUMBER: US/11/244,330A  
 ; CURRENT FILING DATE: 2005-10-06  
 ; PRIOR APPLICATION NUMBER: US 09/987,899  
 ; PRIOR FILING DATE: 2001-11-16  
 ; PRIOR APPLICATION NUMBER: US 09/262,979  
 ; PRIOR FILING DATE: 1999-03-04  
 ; PRIOR APPLICATION NUMBER: US 60/076,712  
 ; PRIOR FILING DATE: 1998-03-06  
 ; NUMBER OF SEQ ID NOS: 7341  
 ; SEQ ID NO 37  
 ; LENGTH: 286  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: 700212658H1  
 US-11-244-330A-37

Alignment Scores:  
 Pred. No.: 9,64e-17 Length: 286  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservatives: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-37 (1-286)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThrArgThrAsnProAlaGln 20  
 DB 48 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 83  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 DB 84 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 137  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgileArgCys 58  
 DB 138 CGCTCTCTCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 188

RESULT 17  
 US-11-244-330A-47  
 ; Sequence 47, Application US/11244330A  
 ; GENERAL INFORMATION:



```
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 47
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700097886H1
US-11-244-330A-47

Alignment Scores:
Pred. No.: 9,87e-17 Length: 291
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-47 (1-291)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 57 ATGGGCCCCACCGTGATGATGCGCTCGTGGCCACC-----92
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 93 -----GCCGTGCGTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGCGCCGCGC 146
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 147 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 197

RESULT 18
US-11-244-330A-14
; Sequence 14, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 14
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700101196H1
US-11-244-330A-14

Alignment Scores:
Pred. No.: 9,87e-17 Length: 291
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-47 (1-291)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 57 ATGGGCCCCACCGTGATGATGCGCTCGTGGCCACC-----92
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 93 -----GCCGTGCGTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGCGCCGCGC 146
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 147 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 197

RESULT 19
US-11-244-330A-21
; Sequence 21, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 21
; LENGTH: 298
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700099783H1
US-11-244-330A-21

Alignment Scores:
Pred. No.: 1,02e-16 Length: 298
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-21 (1-298)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 48 ATGGGCCCCACCGTGATGATGCGCTCGTGGCCACC-----83
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 84 -----GCCGTGCGTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGCGCCGCGC 137
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 138 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 188

US-11-244-330A-14
```

```
Alignment Scores:
Pred. No.: 1,02e-16 Length: 297
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-14 (1-297)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 12 ATGGGCCCCACCGTGATGATGCGCTCGTGGCCACC-----47
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 48 -----GCCGTGCGTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGCGCCGCGC 101
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 102 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 152
```

```
RESULT 20
US-11-244-330A-16
; Sequence 16, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244.330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 16
; LENGTH: 305
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700100270H1
US-11-244-330A-16

Alignment Scores:
Pred. No.: 1.05e-16 Length: 305
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-16 (1-305)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 42 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 77
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
DB 78 -----GCCGTGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCGC 131
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
DB 132 CGCTCTCCAGAGCCTCGGCACAGTC---AGCACGGCGGAGGATCCGGTGC 182

RESULT 21
US-11-244-330A-29
; Sequence 29, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244.330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 29
; LENGTH: 307
; TYPE: DNA
```

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; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700211770H1
US-11-244-330A-29

Alignment Scores:
Pred. No.: 1.06e-16 Length: 307
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-29 (1-307)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 50 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 85
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
DB 86 -----GCCGTGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCGC 139
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
DB 140 CGCTCTCCAGAGCCTCGGCACAGTC---AGCACGGCGGAGGATCCGGTGC 190

RESULT 22
US-11-244-330A-15
; Sequence 15, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244.330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 15
; LENGTH: 309
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700097309H1
US-11-244-330A-15

Alignment Scores:
Pred. No.: 1.07e-16 Length: 309
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-15 (1-309)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 48 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 83
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
DB 84 -----GCCGTGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCGC 137
```



QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 48 ATGGCGCCACCGATGATGGCTCGTGGCCACC----- 83  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 84 -----GCCGTGCGTCCGTTCCAGGGCTCAAGTCCACGCCAGCCTCCCGTCCGCCGC 137  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 138 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 188

## RESULT 26

US-11-244-330A-10  
; Sequence 10, Application US/11244330A  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)  
; CURRENT APPLICATION NUMBER: US/11/244,330A  
; PRIOR FILING DATE: 2005-10-06  
; PRIOR APPLICATION NUMBER: US 09/987,899  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 10  
; LENGTH: 317  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURES:  
; OTHER INFORMATION: Clone ID: 700999925H1  
US-11-244-330A-10

Alignment Scores:  
Pred. No.: 1,11e-16 Length: 317  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-10 (1-317)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 50 ATGGCGCCACCGATGATGGCTCGTGGCCACC----- 85  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 86 -----GCCGTGCGTCCGTTCCAGGGCTCAAGTCCACGCCAGCCTCCCGTCCGCCGC 139  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 140 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 190

## RESULT 27

US-11-244-330A-4  
; Sequence 4, Application US/11244330A  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)

; CURRENT APPLICATION NUMBER: US/11/244,330A  
; CURRENT FILING DATE: 2005-10-06  
; PRIOR APPLICATION NUMBER: US 09/987,899  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 4  
; LENGTH: 319  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURES:  
; OTHER INFORMATION: Clone ID: 700998783H1  
US-11-244-330A-4

## Alignment Scores:

Pred. No.: 1,12e-16 Length: 319  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-4 (1-319)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 41 ATGGCGCCACCGATGATGGCTCGTGGCCACC----- 76  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 77 -----GCCGTGCGTCCGTTCCAGGGCTCAAGTCCACGCCAGCCTCCCGTCCGCCGC 130  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 131 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 181

## RESULT 28

US-11-244-330A-231  
; Sequence 231, Application US/11244330A  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)  
; CURRENT APPLICATION NUMBER: US/11/244,330A  
; CURRENT FILING DATE: 2005-10-06  
; PRIOR APPLICATION NUMBER: US 09/987,899  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 231  
; LENGTH: 344  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURES:  
; OTHER INFORMATION: Clone ID: LIB3062-047-Q1-K1-B2  
US-11-244-330A-231

Alignment Scores:  
Pred. No.: 1,24e-16 Length: 344  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11

```
DB: 8 Gaps: 2
US-10-628-525A-34 (1-58) x US-11-244-330A-231 (1-344)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 46 ATGGCCCCACCGTGATGGCTCGTCGGCCACC----- 81
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLeuSerThrAlaSerLeuProValAlaArg 40
DB 82 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCCTCCCGTCGCCCGC 135
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58
DB 136 CGCTCCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 186
RESULT 29
US-11-353-150-43160
; Sequence 43160, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Comer, Timothy W.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 16517.357 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; PRIOR FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 43160
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3062-047-Q1-K1-B2
US-11-353-150-43160
Alignment Scores:
Pred. No.: 1.27e-16 Length: 349
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2
US-10-628-525A-34 (1-58) x US-11-353-150-43160 (1-349)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 51 ATGGCGCCACCGTGATGGCTCGTCGGCCACC----- 86
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLeuSerThrAlaSerLeuProValAlaArg 40
DB 87 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCCTCCCGTCGCCCGC 140
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58
DB 141 CGCTCCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 191
RESULT 30
US-11-329-388-18378
; Sequence 18378, Application US/11329388
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 16517.357 - 38-21(15503)C/US
; CURRENT APPLICATION NUMBER: US/11/329,388
```

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; CURRENT FILING DATE: 2006-01-11
; PRIOR APPLICATION NUMBER: 09/553,094
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 18831
; SEQ ID NO 18378
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB84-027-Q1-E1-H12
US-11-329-388-18378
Alignment Scores:
Pred. No.: 1.31e-16 Length: 357
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2
US-10-628-525A-34 (1-58) x US-11-329-388-18378 (1-357)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 41 ATGGCGCCACCGTGATGGCTCGTCGGCCACC----- 76
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLeuSerThrAlaSerLeuProValAlaArg 40
DB 77 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCCTCCCGTCGCCCGC 130
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58
DB 131 CGCTCCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 181
Search completed: April 2, 2006, 04:09:37
Job time : 110.468 secs
```

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, ~~using frame plus p2n model~~

Run on: April 1, 2006, 04:29:01 ; Search time 1155.21 Seconds  
(without alignments)  
2853.949 Million cell updates/sec

Title: US-10-628-525A-35

Perfect score: 297

Sequence: 1 MAQILAPSTQWQRIYKTSPTSP.....KKVAHSAKFRVMAVNSGNT 58

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/abs/ABSSWEB.spool/US10628525/runat\_31032006\_095113\_16622/app\_query.fasta\_1  
-DB=GenEmbl -OPMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdd -LIST=150  
-DOCALLIGN=200 -THR\_SCORE=pcp -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs06h  
-USER=US10628525 @CGN\_1\_1\_4375 @runat\_31032006\_095113\_16622 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DISPATCH=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*  
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2: gb.in.\*  
3: gb.env.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pr.\*  
9: gb.ro.\*  
10: gb.sts.\*  
11: gb.sy.\*  
12: gb.un.\*  
13: gb.vi.\*  
14: gb.htg.\*  
15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 297   | 100.0       | 1540   | 15 | PEACHGS2A   |
| 2          | 265   | 89.2        | 1489   | 15 | PSU22971    |
| 3          | 240   | 80.8        | 1577   | 15 | AF031082    |

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| 4  | 223   | 75.1 | 1552   | 15 | AY225150    |
| 5  | 223   | 75.1 | 131577 | 14 | AC148968    |
| 6  | 222   | 74.7 | 1595   | 15 | AF124244    |
| 7  | 217   | 73.1 | 564    | 15 | AY962529    |
| 8  | 217   | 73.1 | 1293   | 15 | AY187005    |
| 9  | 217   | 73.1 | 1293   | 15 | AY187006    |
| 10 | 217   | 73.1 | 1436   | 15 | AY187004    |
| 11 | 217   | 73.1 | 1696   | 15 | AF459587    |
| 12 | 210   | 70.7 | 1541   | 15 | AF353620    |
| 13 | 201   | 67.7 | 1632   | 15 | BT013265    |
| 14 | 199   | 67.0 | 1523   | 15 | AY426758    |
| 15 | 195.5 | 65.8 | 1510   | 15 | PVGSCH      |
| 16 | 180   | 60.6 | 1666   | 15 | AF169795    |
| 17 | 179   | 60.3 | 1590   | 15 | NSGS2AA     |
| 18 | 174   | 58.6 | 1640   | 15 | AY162465    |
| 19 | 174   | 58.6 | 1665   | 15 | AF162466    |
| 20 | 172   | 57.9 | 1537   | 15 | AF019561    |
| 21 | 126   | 42.4 | 5232   | 15 | BNA271909   |
| 22 | 124   | 41.8 | 1575   | 15 | BNGSL2      |
| 23 | 124   | 41.8 | 1597   | 15 | BNGSL2      |
| 24 | 117   | 39.4 | 1579   | 15 | AF145480    |
| 25 | 115   | 38.7 | 1324   | 15 | AY122977    |
| 26 | 115   | 38.7 | 1473   | 15 | AF428461    |
| 27 | 115   | 38.7 | 1519   | 15 | AY081252    |
| 28 | 115   | 38.7 | 1548   | 15 | S69727      |
| 29 | 115   | 38.7 | 1570   | 15 | AF428319    |
| 30 | 115   | 38.7 | 1580   | 15 | AY091114    |
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| 33 | 115   | 38.7 | 63989  | 15 | AB013393    |
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| 36 | 83    | 27.9 | 110000 | 1  | CR931997_21 |
| 37 | 75    | 25.3 | 158560 | 8  | AC024614    |
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| 40 | 73    | 24.6 | 1543   | 6  | AX430070    |
| 41 | 73    | 24.6 | 2418   | 6  | AX430071    |
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| 47 | 72.5  | 24.4 | 211489 | 5  | BX323451    |
| 48 | 72.5  | 24.4 | 285929 | 14 | BX571956    |
| 49 | 72    | 24.2 | 163375 | 9  | AC146896    |
| 50 | 72    | 24.2 | 173841 | 9  | AL732391    |
| 51 | 72    | 24.2 | 189211 | 9  | AC093447    |
| 52 | 71.5  | 24.1 | 636    | 5  | AY035309    |
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| 55 | 71    | 23.9 | 3415   | 5  | AF286875    |
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| 57 | 71    | 23.9 | 110000 | 1  | AE006470_12 |
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| 59 | 70.5  | 23.7 | 2320   | 9  | BC089846    |
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| 61 | 70.5  | 23.7 | 73423  | 14 | AC135749    |
| 62 | 70.5  | 23.7 | 149256 | 8  | AC110603    |
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| 64 | 70.5  | 23.7 | 171843 | 5  | BX511232    |
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| 67 | 70.5  | 23.7 | 276713 | 14 | AC097881    |
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| 70 | 70    | 23.6 | 110000 | 1  | AE016822_19 |
| 71 | 70    | 23.6 | 139958 | 14 | AC141936    |
| 72 | 70    | 23.6 | 223959 | 9  | AC122922    |
| 73 | 69.5  | 23.4 | 1062   | 6  | BD163619    |
| 74 | 69.5  | 23.4 | 1062   | 6  | AX121502    |
| 75 | 69.5  | 23.4 | 1192   | 6  | AX773599    |
| 76 | 69.5  | 23.4 | 1539   | 6  | AR616032    |

|                    |              |
|--------------------|--------------|
| AY225150           | Medicago     |
| AC148968           | Medicago     |
| AF124244           | Medicago     |
| AY962529           | Lotus cor    |
| AY187005           | Lotus cor    |
| AY187006           | Lotus cor    |
| AY187004           | Lotus cor    |
| AF459587           | Lotus jap    |
| AF353620           | Glycine m    |
| BT013265           | Lycopersi    |
| AY426758           | Nicotiana    |
| X12738             | French Bean  |
| AF169795           | Juglans n    |
| X66940             | N. sylvestri |
| AY162465           | Crataegus    |
| AF162466           | Spiraea n    |
| AF019561           | Daucus ca    |
| AJ271909           | Brassica     |
| X72751             | B. napus mRN |
| Y12458             | Brassica na  |
| AF145480           | Mesembrya    |
| AY122977           | Arabidops    |
| AF428461           | Arabidops    |
| AY081252           | Arabidops    |
| S69727             | light-regul  |
| AF428319           | Arabidops    |
| AY091114           | Arabidops    |
| AY088222           | Arabidops    |
| AB015045           | Arabidops    |
| AB013393           | Arabidops    |
| X71361             | A. officinal |
| AY026353           | Beta vulg    |
| Continuation (22 o |              |
| AC024614           | Homo sapi    |
| AL162754           | Neisseria    |
| AF246375           | Acidithio    |
| AX430070           | Sequence     |
| AX430071           | Sequence     |
| AX430069           | Sequence     |
| AF006007           | Danio rer    |
| AF210640           | Danio rer    |
| Continuation (25 o |              |
| CR383684           | Zebrafish    |
| BX323451           | Zebrafish    |
| BX571956           | Danio rer    |
| AC146896           | Mus muscu    |
| AL732391           | Mouse DNA    |
| AC093447           | Mus muscu    |
| AY035309           | Cyprinus     |
| AY120894           | Cyprinus     |
| AB062114           | Xiphophor    |
| AF286875           | Oryzias l    |
| AJ001312           | Oreochrom    |
| Continuation (13 o |              |
| BC089846           | Rattus no    |
| BC056709           | Danio rer    |
| AC135749           | Rattus no    |
| AC110603           | Homo sapi    |
| BX511232           | Zebrafish    |
| BX511232           | Zebrafish    |
| AC145948           | Gallus ga    |
| AC132397           | Rattus no    |
| AC097881           | Rattus no    |
| AY929160           | Acanthopa    |
| DQ013309           | Oligocott    |
| Continuation (20 o |              |
| AC141936           | Rattus no    |
| AC122922           | Mus muscu    |
| BD163619           | Nevel pol    |
| AX121502           | Sequence     |
| AX773599           | Sequence     |
| AR616032           | Sequence     |

|     |      |      |        |    |              |                    |
|-----|------|------|--------|----|--------------|--------------------|
| 77  | 69.5 | 23.4 | 1539   | 6  | AR616033     | Sequence           |
| 78  | 69.5 | 23.4 | 1539   | 6  | AX065785     | Sequence           |
| 79  | 69.5 | 23.4 | 1539   | 6  | AX065787     | Sequence           |
| 80  | 69.5 | 23.4 | 110000 | 1  | BA000036_13  | Continuation (14 o |
| 81  | 69.5 | 23.4 | 152732 | 14 | AC074204     | Mus muscu          |
| 82  | 69.5 | 23.4 | 163710 | 9  | AC140404     | Mus muscu          |
| 83  | 69.5 | 23.4 | 182898 | 9  | AC133198     | Mus muscu          |
| 84  | 69.5 | 23.4 | 187260 | 9  | AC087802     | Mus muscu          |
| 85  | 69.5 | 23.4 | 193694 | 14 | AC120728     | Rattus no          |
| 86  | 69.5 | 23.4 | 228349 | 9  | AC079044     | Mus muscu          |
| 87  | 69.5 | 23.4 | 248439 | 14 | AC098173     | Rattus no          |
| 88  | 69.5 | 23.4 | 349459 | 1  | BX927151     | Corynebact         |
| 89  | 69.5 | 23.4 | 349980 | 6  | AY127147     | Sequence           |
| 90  | 69   | 23.2 | 656    | 5  | AY971578     | Rachycent          |
| 91  | 69   | 23.2 | 698    | 5  | AF187726     | Platichth          |
| 92  | 69   | 23.2 | 933    | 4  | AY675174     | Bos tauru          |
| 93  | 69   | 23.2 | 1374   | 2  | DQ004584     | Sesamia n          |
| 94  | 69   | 23.2 | 1422   | 4  | BTAS34372    | Bos tauru          |
| 95  | 69   | 23.2 | 1433   | 4  | BTAS19787    | Bos tauru          |
| 96  | 69   | 23.2 | 2064   | 5  | AB062113     | Xiphophor          |
| 97  | 69   | 23.2 | 2073   | 5  | AY423555     | Dicentrar          |
| 98  | 69   | 23.2 | 2132   | 4  | AY589091S4   | Bos tauru          |
| 99  | 69   | 23.2 | 2971   | 5  | FRHSP702     |                    |
| 100 | 69   | 23.2 | 4791   | 15 | OHSC70A      |                    |
| 101 | 69   | 23.2 | 5352   | 5  | FRHSP704     |                    |
| 102 | 69   | 23.2 | 7784   | 11 | AB078779     | Cloning v          |
| 103 | 69   | 23.2 | 110000 | 1  | BA000013     | Continuation (2 of |
| 104 | 69   | 23.2 | 139522 | 15 | AC145061     |                    |
| 105 | 69   | 23.2 | 196404 | 14 | AC150221     |                    |
| 106 | 69   | 23.2 | 209102 | 14 | AC162401     |                    |
| 107 | 69   | 23.2 | 230210 | 14 | AC164267     |                    |
| 108 | 69   | 23.2 | 250519 | 9  | AC140288     |                    |
| 109 | 69   | 23.2 | 278550 | 14 | AC152220     |                    |
| 110 | 68.5 | 23.1 | 1830   | 2  | AY274366     |                    |
| 111 | 68.5 | 23.1 | 54929  | 8  | AL731868     |                    |
| 112 | 68.5 | 23.1 | 110000 | 14 | AL732359_08  |                    |
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| 124 | 68   | 22.9 | 1934   | 8  | AB169323     |                    |
| 125 | 68   | 22.9 | 2681   | 4  | BOVHSP111    |                    |
| 126 | 68   | 22.9 | 34589  | 6  | AR659795     |                    |
| 127 | 68   | 22.9 | 35645  | 8  | AC133914     |                    |
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| 145 | 67.5 | 22.7 | 1338   | 6  | BD211491     |                    |
| 146 | 67.5 | 22.7 | 1578   | 6  | CQ719025     |                    |
| 147 | 67.5 | 22.7 | 1932   | 15 | MDJ583       |                    |
| 148 | 67.5 | 22.7 | 2103   | 6  | BD156167     |                    |
| 149 | 67.5 | 22.7 | 2103   | 6  | AX876511     |                    |

|     |      |      |      |   |          |           |
|-----|------|------|------|---|----------|-----------|
| 150 | 67.5 | 22.7 | 2103 | 8 | AK001328 | Homo sapi |
|-----|------|------|------|---|----------|-----------|

ALIGNMENTS

RESULT 1

PEACHGS2A

LOCUS

DEFINITION

PEACHGS2A 1540 bp mRNA linear PLN 27-APR-1993

Pisum sativum glutamine synthetase (chloroplast GS2) mRNA, complete

cds.

ACCESSION

M20664 J03878

VERSION

M20664.1 GI:169058

KEYWORDS

glutamine synthetase (chloroplast GS2).

SOURCE

Pisum sativum (pea)

ORGANISM

Pisum sativum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;

Pisum.

REFERENCE

1 (bases 1 to 1540)

AUTHORS

Tingey,S.V., Tsai,F.Y., Edwards,J.W., Walker,E.L. and Coruzzi,G.M.

TITLE

Chloroplast and cytosolic glutamine synthetase are encoded by

homologous nuclear genes which are differentially expressed in vivo

JOURNAL

J. Biol. Chem. 263 (20), 9651-9657 (1988)

PUBMED

2898472

COMMENT

Original source text: P.sativum (strain sparkle) 21 day old plant

root, cDNA to mRNA, clone PGS185.

Draft entry and computer-readable sequence [1] kindly submitted by

G. Coruzzi, 14-SEP-1988.

FEATURES

source

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68..1360

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ORIGIN

Unreported.

Alignment Scores:

Pred. No.: 2,348-25 Length: 1540

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Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 15 Gaps: 0

US-10-628-525A-35 (1-58) x PEACHGS2A (1-1540)

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68 ATGGCGCAGATTTTGGCACCCTTCGACGCATATGGCAGATGAGATCAGAAAACCTCTCT 127

QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40

128 TGTGCAACTCCCAATCACATCAAAAGATGTGGAGTCTTCTTGTGTTATGAAACAACTAAGAAA 187

QY 41 ValAlaHisSerAlaIlePheArgValMetAlaValAsnSerGluAsnGlyThr 58

DB 188 GTTGGCATTCTGCTAAATTTAGATTATGGCAGTCAACTCTGAAATATGGCACC 241

RESULT 2



PSU22971  
LOCUS  
DEFINITION Pisum sativum glutamine synthetase (GS2) gene, nuclear gene  
U22971.1 GI:1045309  
Pisum sativum (pea)  
Pisum sativum  
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
1 (bases 1 to 1489)  
Tjaden, G., Edwards, J.W. and Coruzzi, G.M.  
cis elements and trans-acting factors affecting regulation of a nonphotosynthetic light-regulated gene for chloroplast glutamine synthetase  
Plant Physiol. 108 (3), 1109-1117 (1995)  
7630938  
2 (bases 1 to 1489)  
Tjaden, G.  
Direct Submission  
Submitted (17-MAR-1995) Gabrielle Tjaden, Biology Department, New York University, 1009 Main Building, New York, NY 10003, USA  
JOURNAL Location/Qualifiers  
1. 1489  
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Score: 265.00 Matches: 52  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 89.2% Indels: 0  
DB: 15 Gaps: 0

US-10-628-525A-35 (1-58) x PSU22971 (1-1489)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
DB 1334 ATGGCGCAGATTTTGGCACCTTCGACGCAATGCGATGAGATCAAAAACCTCTCT 1393  
QY 21 CysAlaThrProIleThrSerLysMetTpsSerSerLeuValMetLysGlnThrLysLys 40  
DB 1394 TTGGCAACTCCATCATCAACAGATGTGGAGTTCTTTGTTATGAAACAACATAAGAAA 1453

QY 41 ValAlaHisSerAlaLysPheArgValMetAlaVal 52  
DB 1454 GTTGGCGCATTTCTGTAATAATTAGATTATGCGAGTC 1489  
RESULT 3  
AF031082  
LOCUS  
DEFINITION Canavalia lineata glutamine synthetase (gln) mRNA, nuclear gene  
encoding chloroplast protein, complete cds.  
AF031082  
VERSION AF031082.1 GI:6578119  
KEYWORDS  
SOURCE Canavalia lineata  
ORGANISM Canavalia lineata  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Canavalia.  
1 (bases 1 to 1577)  
Choi, Y.A., Kim, S.G. and Kwon, Y.M.  
The plastidic glutamine synthetase activity is directly modulated by means of redox change at two unique cysteine residues  
Plant Sci. 149 (2), 175-182 (1999)  
2 (bases 1 to 1577)  
Choi, Y.A. and Kwon, Y.M.  
Direct Submission  
Submitted (23-OCT-1997) Biology, Seoul National University, Seoul 151-742, Korea  
JOURNAL Location/Qualifiers  
1. 1577  
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Alignment Scores:  
Pred. No.: 1.34e-18 Length: 1577  
Score: 240.00 Matches: 46  
Percent Similarity: 87.9% Conservative: 5  
Best Local Similarity: 79.3% Mismatches: 7  
Query Match: 80.8% Indels: 0  
DB: 15 Gaps: 0

US-10-628-525A-35 (1-58) x AF031082 (1-1577)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
DB 91 ATGGCACAATTTTGGCACCTTCAGCAATGCGATGAGATCAAGAAACATCACCC 150  
QY 21 CysAlaThrProIleThrSerLysMetTpsSerSerLeuValMetLysGlnThrLysLys 40  
DB 151 AATGCAAGTCCCGTCATCAACATGTGGAGTTCTTTGTTATGAAACAACATAAGAAA 210  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58

|                                              |                                                                                                                                                                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
|----------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------|
| Db                                           | 211                                                                                                                                                                                                  | GCTACAGTTCGCTAAATTAGAGTCTGCGCAATCAAGTCTGAAATGGCACC                                                                                                                                                                                                                                                                                                                                                                                       | 264             |
| RESULT 4                                     |                                                                                                                                                                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| LOCUS                                        | AY225150                                                                                                                                                                                             | 1552 bp mRNA linear                                                                                                                                                                                                                                                                                                                                                                                                                      | PLN 15-MAY-2003 |
| DEFINITION                                   | Medicago truncatula glutamine synthetase (GS2) mRNA, complete cds;                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| ACCESSION                                    | AY225150                                                                                                                                                                                             |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| VERSION                                      | AY225150.1                                                                                                                                                                                           | GI:28629469                                                                                                                                                                                                                                                                                                                                                                                                                              |                 |
| KEYWORDS                                     |                                                                                                                                                                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| SOURCE                                       | Medicago truncatula (barrel medic)                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| ORGANISM                                     | Medicago truncatula                                                                                                                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| REFERENCE                                    | 1 (bases 1 to 1552)                                                                                                                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| AUTHORS                                      | Melo, P.M., Lima, L.M., Santos, I.M., Carvalho, H.G. and Cullimore, J.V.                                                                                                                             |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| TITLE                                        | Expression of the Plastid-Located Glutamine Synthetase of Medicago truncatula. Accumulation of the Precursor in Root Nodules Reveals an in Vivo Control at the Level of Protein Import into Plastids |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| JOURNAL                                      | Plant Physiol. 132 (1), 390-399 (2003)                                                                                                                                                               |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| PUBMED                                       | 12746544                                                                                                                                                                                             |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| REFERENCE                                    | 2 (bases 1 to 1552)                                                                                                                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| AUTHORS                                      | Melo, P., Lima, L., Carvalho, H. and Cullimore, J.                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| TITLE                                        | Direct Submission                                                                                                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| JOURNAL                                      | Submitted (24-JAN-2003) Institute for Molecular and Cellular Biology, Rua do Campo Alegre, 823, Porto 4150, Portugal                                                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| FEATURES                                     | source                                                                                                                                                                                               |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
|                                              | 1..1552                                                                                                                                                                                              | /organism="Medicago truncatula"                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
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| gene                                         | 1..1552                                                                                                                                                                                              | /db_xref="taxon:3880"                                                                                                                                                                                                                                                                                                                                                                                                                    |                 |
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|                                              |                                                                                                                                                                                                      | /protein_id="AAO37651.1"                                                                                                                                                                                                                                                                                                                                                                                                                 |                 |
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| ORIGIN                                       |                                                                                                                                                                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| Alignment Scores:                            |                                                                                                                                                                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| Pred. No.:                                   | 1.36e-16                                                                                                                                                                                             | Length:                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1552            |
| Score:                                       | 223.00                                                                                                                                                                                               | Matches:                                                                                                                                                                                                                                                                                                                                                                                                                                 | 47              |
| Percent Similarity:                          | 88.9%                                                                                                                                                                                                | Conservative:                                                                                                                                                                                                                                                                                                                                                                                                                            | 1               |
| Best Local Similarity:                       | 87.0%                                                                                                                                                                                                | Mismatches:                                                                                                                                                                                                                                                                                                                                                                                                                              | 6               |
| Query Match:                                 | 75.1%                                                                                                                                                                                                | Indels:                                                                                                                                                                                                                                                                                                                                                                                                                                  | 0               |
| DB:                                          | 15                                                                                                                                                                                                   | Gaps:                                                                                                                                                                                                                                                                                                                                                                                                                                    | 0               |
| US-10-628-525A-35 (1-58) x AY225150 (1-1552) |                                                                                                                                                                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                          |                 |
| Qy                                           | 1                                                                                                                                                                                                    | MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro                                                                                                                                                                                                                                                                                                                                                                             | 20              |
| Db                                           | 41                                                                                                                                                                                                   | ATGGACACAGATTTGGCTCTCTTCTACAAATGTCAGGCAAGATCACAAAAATCTCTCC                                                                                                                                                                                                                                                                                                                                                                               | 100             |
| Qy                                           | 21                                                                                                                                                                                                   | CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys                                                                                                                                                                                                                                                                                                                                                                             | 40              |
| Db                                           | 101                                                                                                                                                                                                  | GTTCGAACTCCAAATTCATCAAGATGTGGAGTTCTTTGGTTATGAAACAAACAGAAA                                                                                                                                                                                                                                                                                                                                                                                | 160             |
| Qy                                           | 41                                                                                                                                                                                                   | ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer                                                                                                                                                                                                                                                                                                                                                                                               | 54              |

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ORIGIN
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Best Local Similarity: 87.0% Mismatches: 6
Query Match: 75.1% Indels: 0
DB: 14 Gaps: 0

US-10-628-525A-35 (1-58) x AC148968 (1-131577)
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Qy 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLys 40
Db 14664 GTTGCACACTCAATCTCATCAAGATGTGGAGTCTTTGGTTATGAAACAAACAGAAA 14605
Qy 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
Db 14604 GTTCACAGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 14563

RESULT 6
LOCUS AF124244
DEFINITION Medicago sativa glutamine synthetase precursor (gln) mRNA, nuclear
ACCESSION AF124244
VERSION AF124244.2 GI:45827172
KEYWORDS Medicago sativa
SOURCE Medicago sativa
ORGANISM Medicago sativa
REFERENCE 1 (bases 1 to 1595)
AUTHORS Zozaya-Garza,M. and Sengupta-Gopalan,C.
TITLES Glutamine synthetase gene isolation from an alfalfa leaf cDNA
JOURNAL Library (Accession No. AF124244) (PGR99-054)
REFERENCE 2 (bases 1 to 1595)
AUTHORS Plant Physiol. 119 (4), 1568 (1999)
TITLES Zozaya-Garza,M. and Sengupta-Gopalan,C.
JOURNAL Direct Submission
REFERENCE 3 (bases 1 to 1595)
AUTHORS Submitted (27-JAN-1999) Molecular Biology, New Mexico State
TITLES University, College Av., Las Cruces, NM 80003, USA
JOURNAL Zozaya-Garza,M. and Sengupta-Gopalan,C.
REFERENCE 30-MAR-2004 Molecular Biology, New Mexico State
AUTHORS University, College Av., Las Cruces, NM 80003, USA
TITLES Sequence update by submitter
REMARK On Mar 30, 2004 this sequence version replaced gi:4731321.
COMMENT Location/Qualifiers
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ORIGIN
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Pred. No.: 1.84e-16 Length: 1595
Score: 222.00 Matches: 46
Percent Similarity: 88.9% Conservative: 2
Best Local Similarity: 85.2% Mismatches: 6
Query Match: 74.7% Indels: 0
DB: 15 Gaps: 0

US-10-628-525A-35 (1-58) x AF124244 (1-1595)
Qy 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 88 ATGGCACAGATTTGGCTCTTCTATACAAATGTACAGCAAGATCACAAAACATCTCTCC 147
Qy 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLys 40
Db 148 GTTGCACACTCCGATCTCATCAAGATGTGGAGTCTTTGGTTATGAAACAAACAGAAA 207
Qy 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
Db 208 GTTGCACAGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 249

RESULT 7
LOCUS AH014864S1
DEFINITION Lotus corniculatus var. japonicus glutamine synthetase precursor
ACCESSION AY962529
VERSION AY962529.1 GI:63176998
KEYWORDS Lotus
SEGMENT 1 of 2
SOURCE Lotus corniculatus var. japonicus (Lotus japonicus)
ORGANISM Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteeae;
Lotus.
REFERENCE 1 (bases 1 to 564)
AUTHORS Arcondeguy,T., Betti,M. and Marquez,A.J.
TITLES Direct Submission
JOURNAL Submitted (15-MAR-2005) Bioquimica Vegetal y Biologia Molecular,
University of Seville, Avenida Prof. Garcia Gonzales, Seville
41080, Spain
FEATURES
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ORIGIN

Alignment Scores:

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| Score:                 | 217.00   | Matches:      | 42  |
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| Best Local Similarity: | 72.4%    | Mismatches:   | 9   |
| Query Match:           | 73.1%    | Indels:       | 0   |
| DB:                    | 15       | Gaps:         | 0   |

US-10-628-525A-35 (1-58) x AH014864S1 (1-564)

QY 1 MetAlaGInLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
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Db 1 ATGGCACAGATTTTGGCACCCCTCGACGCAATGGCAGAGAAATCACAAAACCTCTCCC 60  
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Db 61 AATGCAAGTCCCATACATCAACATGTGGAGTCTCTTTATTGTGGAACACAAACAGAAA 120  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58  
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Db 121 GTTGACAGTCTCTTAAGTTAGACTGCGCAATCAAGTCTGTGATGGTAGCACC 174

RESULT 8

AY187005

LOCUS

DEFINITION

AY187005

ACCESSION

AY187005.1 GI:37778504

KEYWORDS

SOURCE

ORGANISM

Lotus corniculatus var. japonicus (Lotus japonicus)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.

REFERENCE

1 (bases 1 to 1293)

Orea,A., Pajuelo,P., Pajuelo,E., Quidiello,C., Romero,J.M. and Marquez,A.J.

Isolation of photorespiratory mutants from Lotus japonicus deficient in glutamine synthetase

Physiol. Plantarum 115 (3), 352-361 (2002)

12081527

REFERENCE

2 (bases 1 to 1293)

Arcondéguy,T., Betti,M. and Marquez,A.J.

Lotus japonicus plastidic glutamine synthetase, PR1

Unpublished

JOURNAL

REFERENCE

3 (bases 1 to 1293)

Arcondéguy,T., Betti,M. and Marquez,A.J.

Direct Submission

TITLE

Submitted (26-NOV-2002) Bioquímica Vegetal y Biología Molecular, Facultad de Química, Apartado 553, Sevilla 41080, Spain

JOURNAL

FEATURES

source

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ORIGIN

Alignment Scores:

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| Pred. No.:             | 5,86e-16 | Length:       | 1293 |
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| Best Local Similarity: | 72.4%    | Mismatches:   | 9    |
| Query Match:           | 73.1%    | Indels:       | 0    |
| DB:                    | 15       | Gaps:         | 0    |

US-10-628-525A-35 (1-58) x AY187005 (1-1293)

QY 1 MetAlaGInLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
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Db 1 ATGGCACAGATTTTGGCACCCCTCGACGCAATGGCAGAGAAATCACAAAACCTCTCCC 60  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
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Db 61 AATGCAAGTCCCATACATCAACATGTGGAGTCTCTTTATTGTGGAACACAAACAGAAA 120  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58  
|||||  
Db 121 GTTGACAGTCTCTTAAGTTAGACTGCGCAATCAAGTCTGTGATGGTAGCACC 174

RESULT 9

AY187006

LOCUS

DEFINITION

AY187006

ACCESSION

AY187006.1 GI:37778508

KEYWORDS

SOURCE

ORGANISM

Lotus corniculatus var. japonicus (Lotus japonicus)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.

REFERENCE

1 (bases 1 to 1293)

Orea,A., Pajuelo,P., Pajuelo,E., Quidiello,C., Romero,J.M. and Marquez,A.J.

Isolation of photorespiratory mutants from Lotus japonicus deficient in glutamine synthetase

Physiol. Plantarum 115 (3), 352-361 (2002)

12081527

REFERENCE

2 (bases 1 to 1293)

Arcondéguy,T., Betti,M. and Marquez,A.J.

Lotus japonicus plastidic glutamine synthetase, PR2

Unpublished

JOURNAL

REFERENCE

3 (bases 1 to 1293)

Arcondéguy,T., Betti,M. and Marquez,A.J.

Direct Submission

TITLE

Submitted (26-NOV-2002) Bioquímica Vegetal y Biología Molecular, Facultad de Química, Apartado 553, Sevilla 41080, Spain

JOURNAL

FEATURES

source

1..1293

/organism="Lotus corniculatus var. japonicus"

/mol\_type="mRNA"

/variety="japonicus"

/db\_xref="taxon:34305"

/tissue\_type="leaves"

1..1293

/EC\_number="6.3.1.2"

/note="Ljpr2 mutant"

/codon\_start=1

/product="glutamine synthetase PR2 mutant"

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/db\_xref="GI:37778509"

CDS

CDS

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PTNKRRAAEIFSNPKVQAEIPWYIEQBYTLQTDVKWPLGWPVGPGPGPYCYCA
AGADKSFGRDISAHYKACLYAGINISGTNGEVMQWBYOVGPSVIGIEAGDHIWASR
YHLERITEQAGVVLTLDPKPIEGDNGAGAHYNTSKSMEEGGFEVIKKAILNLSLR
HODHIRAYGEGNERLLTGKHETADINTFSGVAVNRGCSIRVGRDTEKEGKYLEDRRP
ASNMDPVVTTALLAETILLWEPTLEAALAAQKIQLVK"

```

## ORIGIN

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Alignment Scores:
Pred. No.: 5,86e-16 Length: 1293
Score: 217,00 Matches: 42
Percent Similarity: 84.5% Conservatives: 7
Best Local Similarity: 72.4% Mismatches: 9
Query Match: 73.1% Indels: 0
DB: 15 Gaps: 0

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US-10-628-525A-35 (1-58) x AY187006 (1-1293)

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Qy 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 1 ATGGCACAGATTTTGGCACCTCGACGCAATGGCAGCAGAGATCACCAAAACCTCTCCC 60

Qy 21 CysAlaThrProIleThrSerLysMetTyrSerSerLeuValMetLysGlnThrLysLys 40
Db 61 AATGCAAGTCCCATATACATCAACATGTGGAGTCTTTATTATGGAAACAAACAGAAA 120

Qy 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 121 GTTGACGCTCTTAAGTTAGTACTGCGCATCAAGTCTGATGGTAGCACC 174

```

## RESULT 10

```

AY187004
LOCUS AY187004 1436 bp mRNA linear PLN 14-MAR-2005
DEFINITION Lotus corniculatus var. japonicus glutamine synthetase mRNA,
complete cds.

```

```

ACCESSION AY187004.2 GI:61103521
VERSION AY187004
KEYWORDS
SOURCE

```

```

ORGANISM
Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
Lotus.

```

```

REFERENCE
1 (bases 1 to 1436)
Arcondeguy,T., Betti,M. and Marquez,A.J.
Lotus japonicus plastidic glutamine synthetase
Unpublished

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```

REFERENCE
2 (bases 1 to 1436)
Arcondeguy,T., Betti,M. and Marquez,A.J.
Direct Submission
Submitted (26-NOV-2002) Biochimica Vegetal y Biologia Molecular,
University of Seville, Avenida Prof. Garcia Gonzales s/n, Seville
41080, Spain

```

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REFERENCE
3 (bases 1 to 1436)
Arcondeguy,T., Betti,M. and Marquez,A.J.
Direct Submission
Submitted (14-MAR-2005) Biochimica Vegetal y Biologia Molecular,
University of Seville, Avenida Prof. Garcia Gonzales s/n, Seville
41080, Spain

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REMARK
COMMENT Sequence update by submitter
On Mar 14, 2005 this sequence version replaced gi:26892200.
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Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:34305"
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1..1293
/BC_number="6.3.1.2"

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## CDS

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/db_xref="GI:26892201"

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PTNKRRAAEIFSNPKVQAEIPWYIEQBYTLQTDVKWPLGWPVGPGPGPYCYCA
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YHLERITEQAGVVLTLDPKPIEGDNGAGAHYNTSKSMEEGGFEVIKKAILNLSLR
HODHIRAYGEGNERLLTGKHETADINTFSGVAVNRGCSIRVGRDTEKEGKYLEDRRP
ASNMDPVVTTALLAETILLWEPTLEAALAAQKIQLVK"

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## ORIGIN

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Alignment Scores:
Pred. No.: 6,49e-16 Length: 1436
Score: 217,00 Matches: 42
Percent Similarity: 84.5% Conservatives: 7
Best Local Similarity: 72.4% Mismatches: 9
Query Match: 73.1% Indels: 0
DB: 15 Gaps: 0

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US-10-628-525A-35 (1-58) x AY187004 (1-1436)

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Qy 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 1 ATGGCACAGATTTTGGCACCTCGACGCAATGGCAGCAGAGATCACCAAAACCTCTCCC 60

```

```

Qy 21 CysAlaThrProIleThrSerLysMetTyrSerSerLeuValMetLysGlnThrLysLys 40
Db 61 AATGCAAGTCCCATATACATCAACATGTGGAGTCTTTATTATGGAAACAAACAGAAA 120

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Qy 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 121 GTTGACGCTCTTAAGTTAGTACTGCGCATCAAGTCTGATGGTAGCACC 174

```

## RESULT 11

```

AF459587
LOCUS AF459587 1696 bp mRNA linear PLN 23-JAN-2002
DEFINITION Lotus japonicus glutamine synthetase precursor, mRNA, complete cds;
nuclear gene for chloroplast product.

```

```

ACCESSION AF459587
VERSION AF459587.1 GI:18266052
KEYWORDS
SOURCE

```

```

ORGANISM
Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
Lotus.

```

```

REFERENCE
1 (bases 1 to 1696)
Simon-Rosin,U., Colebatch,G. and Udvardi,M.
CDNA encoding plastidic glutamine synthetase
Unpublished

```

```

REFERENCE
2 (bases 1 to 1696)
Simon-Rosin,U., Colebatch,G. and Udvardi,M.
Direct Submission
Submitted (16-DEC-2001) AG-Udvardi, Max-Planck-Institute for Plant
Molecular Physiology, Am Mühlenberg 1, Golm D-14476, Germany
Location/Qualifiers
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/protein_id="AAL67439.1"
/db_xref="GI:18266053"

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## FEATURES

source

## CDS

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AGADISFGDRDISAHYKACLIYAGINISGTIGEVMPQWQYVGVGIEAGDHIWA  
YLLERITQAGVVLIDPKPIGDWNGAGCHTNYSTKSMREDDGGFVKKAILNLS  
HODHIRAYGEGNERLTGKHETASINTFSWGVANRGCSIRVGRDTEKNGKYLEDRR  
ASNMDPVVYVTTALLAETLLWEPTLEAEALAAQIKLV"

ORIGIN

Alignment Scores:  
Pred. No.: 7,63e-16 Length: 1696  
Score: 217.00 Matches: 42  
Percent Similarity: 84.5% Conservative: 7  
Best Local Similarity: 72.4% Mismatches: 9  
Query Match: 73.1% Indels: 0  
DB: 15 Gaps: 0

US-10-628-525A-35 (1-58) x AF459587 (1-1696)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
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Db 147 ATGGCACAGATTTTGGCACCTCGAGCAATGGCAGACGAGATCAACAAACCTCTCCC 206  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
|||||  
Db 207 AATGCAAGTCCCATACATCAACATGTGGAGTCTCTTTATTGTGGAAACAAACAAAGAAA 266  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58  
|||||  
Db 267 GTTGACAGTGGCTTCTTAAGTTTAGTACTGGCAATCAAGTCTGTGTTAGTACACC 320

RESULT 12

AF353620  
LOCUS AF353620 1541 bp mRNA linear PLN 15-NOV-2001  
DEFINITION Glycine max glutamine synthetase precursor, mRNA, complete cds;  
nuclear gene for chloroplast product.  
ACCESSION AF353620  
VERSION AF353620.1 GI:13877510  
KEYWORDS Glycine max (soybean)  
SOURCE Glycine max  
ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

REFERENCE 1 (bases 1 to 1541)

AUTHORS Bemis,K.L.  
TITLE Characterization of chloroplast glutamine synthetase in soybean  
(Glycine max)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1541)

AUTHORS Bemis,K.L., Kahle,A., Moguel-Baoponda,S., Ortega,J.L. and  
Sengupta-Gopalan,C.

TITLE Direct Submission

JOURNAL Submitted (26-FEB-2001) Agronomy and Horticulture, New Mexico State  
University, Skeen Hall Rm W329. Espina St. and College Dr., Las  
Cruces, NM 88003, USA

FEATURES

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30..1328  
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/note="GS-2"  
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/db\_xref="GI:13877511"

CDS

translation="NAQILAPSTQWMSKSPNASPITSNMSSLLWKNQKVSPT  
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ORIGIN

Alignment Scores:  
Pred. No.: 4,69e-15 Length: 1541  
Score: 210.00 Matches: 43  
Percent Similarity: 86.2% Conservative: 7  
Best Local Similarity: 74.1% Mismatches: 6  
Query Match: 70.7% Indels: 2  
DB: 15 Gaps: 1

US-10-628-525A-35 (1-58) x AF353620 (1-1541)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
Db 30 ATGGCACAGATTTTGGCTCCCTCTACGCNATGGCAGATGAGATCTCAAAATCCTCTCCC 89  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
|||||  
Db 90 AATGCAAGTCCCATACATCAACATGTGGAGTCTCTTTATTGTGGAAACAAACAAAGAAA 149  
QY 41 ValAlaA-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56  
|||||  
Db 150 GTTCAACCACCAAGTCTGCTAAATTTAGAGTGTGGCAATTAAGTCTGACAA 203

RESULT 13

BT013265  
LOCUS BT013265 1632 bp mRNA linear PLN 11-MAY-2004  
DEFINITION Lycopersicon esculentum clone 134810R, mRNA sequence.  
ACCESSION BT013265  
VERSION BT013265.1 GI:47104680  
KEYWORDS FLI CDNA.  
SOURCE Lycopersicon esculentum (Solanum lycopersicum)  
ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 1632)

AUTHORS Kirkness,E.F., Wang,W. and Vazeille,A.

TITLE Direct Submission

JOURNAL Submitted (11-MAY-2004) The Institute for Genomic Research, 9712  
Medical Center Drive, Rockville, MD 20850, USA

FEATURES

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/clone="134810R"  
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/note="TCACH68"

ORIGIN

Alignment Scores:  
Pred. No.: 5,77e-14 Length: 1632  
Score: 201.00 Matches: 41  
Percent Similarity: 83.3% Conservative: 9  
Best Local Similarity: 68.3% Mismatches: 8  
Query Match: 67.7% Indels: 2  
DB: 15 Gaps: 1

US-10-628-525A-35 (1-58) x BT013265 (1-1632)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
Db 70 ATGGCTCAGATCTCGCTCCGCTCCATGCCAGATGAGATGACAAAGAGCTCAACC 129  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
|||||  
Db 130 GATGCTAGTCCCTTGACTTCAAGATGTGGAGCTCTGTGGTGTCTGAAGCAGAAACAAAAGA 189

|                                              |            |                                                                     |                 |
|----------------------------------------------|------------|---------------------------------------------------------------------|-----------------|
| Qy                                           | 41         | Vallala-----HisSerAlaLysPheArgValMetalAlaValenSerGluAsnGlyThr       | 58              |
| Db                                           | 190        | CACGCTCTTAAAGCTCTGCCAAATTAGAGTTTTTGCCCTACAGTCTGCAATGGCACC           | 249             |
| RESULT 14                                    |            |                                                                     |                 |
| AY426758                                     |            |                                                                     |                 |
| LOCUS                                        |            |                                                                     |                 |
| DEFINITION                                   | AY426758   | 1523 bp mRNA linear                                                 | PLN 02-AUG-2004 |
| ACCESSION                                    |            | Nicotiana attenuata glutamine synthetase GS58 mRNA, complete cds;   |                 |
| VERSION                                      |            | nuclear gene for plastid product.                                   |                 |
| KEYWORDS                                     | AY426758.1 | GI:40457327                                                         |                 |
| SOURCE                                       |            |                                                                     |                 |
| ORGANISM                                     |            | Nicotiana attenuata                                                 |                 |
| REFERENCE                                    |            | Nicotiana attenuata                                                 |                 |
| AUTHORS                                      |            | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  |                 |
| TITLE                                        |            | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  |                 |
|                                              |            | asterids; lamids; Solanales; Eucotyledons; Nicotiana.               |                 |
|                                              |            | 1 (bases 1 to 1523)                                                 |                 |
|                                              |            | Bubner,B., Gase,K. and Baldwin,I.T.                                 |                 |
|                                              |            | Two-fold differences are the detection limit for determining        |                 |
|                                              |            | transgene copy numbers in plants by real-time PCR                   |                 |
|                                              |            | (ex) BMC Biotechnol. 4 (1), 14 (2004)                               |                 |
| JOURNAL                                      |            | 15251044                                                            |                 |
| PUBMED                                       |            | 2 (bases 1 to 1523)                                                 |                 |
| REFERENCE                                    |            | Schittko,U. and Baldwin,I.T.                                        |                 |
| AUTHORS                                      |            | Direct Submission                                                   |                 |
| TITLE                                        |            | Submitted (03-OCT-2003) Molecular Ecology, Max Planck Institute for |                 |
| JOURNAL                                      |            | Chemical Ecology, Hans-Knoell-Strasse 8, Jena D-07745, Germany      |                 |
| FEATURES                                     |            | Location/Qualifiers                                                 |                 |
| source                                       |            | 1..1523                                                             |                 |
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|                                              |            | /mol_type="mRNA"                                                    |                 |
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|                                              |            | 51..1349                                                            |                 |
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|                                              |            | /translation="MAQILPASAQWQMRMTKSSTDANPLTSKMWSSVVLKQNKRLAVK          |                 |
|                                              |            | SSAKRFYPALQSDSGTVNRVEQLNLNLDVPTDKI IAEYTWIGSGIDMSKSRITISK           |                 |
|                                              |            | PVXHASLKPWNYDGPQAPEDSEVILYPOALPKDPFGGNNLIVICDAVTPAGE                |                 |
|                                              |            | PIPTNKHKAQLEIFSDSKVSEYFEGIEYTLQQNKPWLPWNFVGVPQGQPTT                 |                 |
|                                              |            | CGAGADSKFSDISDAHYKACLAFAGINISGTNGVPMQWEPQVSGVGIENGDLHLC             |                 |
|                                              |            | ARYLEKITQAGVVLSDLPKPIEGDWNAGCHTNYSITLSMRBEGGFEVIKKAILNLS            |                 |
|                                              |            | LRKHKEISAYGEGNERLTGKHETASIDKFSWGVNARGASIRVGRDTEKQKGKYLEDR           |                 |
|                                              |            | RPASNMDPYVVTGILLAEITTLWEPTLEAEALAAQKALNV"                           |                 |
| ORIGIN                                       |            |                                                                     |                 |
| Alignment Scores:                            |            |                                                                     |                 |
| Pred. No.:                                   | 9.3e-14    | Length:                                                             | 1523            |
| Score:                                       | 199.00     | Matches:                                                            | 40              |
| Percent Similarity:                          | 83.3%      | Conservative:                                                       | 10              |
| Best Local Similarity:                       | 66.7%      | Mismatches:                                                         | 8               |
| Query Match:                                 | 67.0%      | Indels:                                                             | 2               |
| DB:                                          | 15         | Gaps:                                                               | 1               |
| US-10-628-525A-35 (1-58) x AY426758 (1-1523) |            |                                                                     |                 |
| Qy                                           | 1          | MetAlaGlnIleLeuAlaProSerThrGlnTriDlnMetArgIleThrLysThrSerPro        | 20              |
| Db                                           | 51         | ATGGCTCAGATCTTGGCTCCATCTGCACANTGGCAGATGAGATGACAAAGAGCTCAACA         | 110             |
| Qy                                           | 21         | CyAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys         | 40              |
| Db                                           | 111        | GATGCTAATCCCTTGACTTCAAGAGATGTGGAGTCTCTGTGGTATTGAAGCAGATAAAGA        | 170             |
| Qy                                           | 41         | Vallala-----HisSerAlaLysPheArgValMetalAlaValenSerGluAsnGlyThr       | 58              |
| Db                                           | 171        | CTTGGCTTTAAAGAGCTCGCCAAATTAGAGTCTTTGGCTTCCAAATCTGATAGTGCACT         | 230             |
| RESULT 15                                    |            |                                                                     |                 |

[illegible]





```

Db      67 ATGGCTCAGATCTTGGCTCCATCAGGAGATGGCAGATGAGATGACAAAGAGCTCAACA 126
Qy      21 CyAAlaThrProLeThrSerLysMetTyrSerSerLeuValMetLysGlnThrLysLys 40
Db      127 GATGCTAATCCCTGACTTCAAGATGTCGAGTCTCTGTGTGTTGAAGATAATAAAGAA 166
Qy      41 ValAla-----HisSerAlaLysPheArgValMetAlaValAenSerGluAenGlyThr 58
Db      187 CTTCGCTGTTAAAGCTCTGCCAAATTTAGATCTTTTGCTCTGGAATCTGATAGTGGCACT 246

RESULT 18
LOCUS   AY162465
DEFINITION Crataegus crus-galli putative plastidic glutamine synthetase (GS2)
ACCESSION AY162465
VERSION   AY162465.1 GI:26892027
KEYWORDS Crataegus crus-galli (cockspur hawthorn)
SOURCE   Crataegus crus-galli
ORGANISM Crataegus crus-galli
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Crataegus.
REFERENCE 1 (bases 1 to 1640)
AUTHORS   Twigg,P.G. and Mahn,M.J.
TITLE     Cloning and Analysis of a Putative Chloroplast Localized Glutamine
          Synthetase from Crataegus crus-galli (Cockspur Hawthorn)
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 1640)
AUTHORS   Twigg,P.G. and Mahn,M.J.
TITLE     Direct Submission
JOURNAL   Submitted (11-OCT-2002) Biology, University of Nebraska-Kearney,
          905 W. 25th St., Kearney, NE 68849, USA
FEATURES             source
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     85..1383
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     /note="glutamate ammonia ligase"
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     PVEDPSLPKNYDGSQAPGEDSEVILYPAIFKDPFRGNNILVICDAYTPQGE
     PIPTNKRARAASIFKNKKVIDRVPWVGIEQVYLLQTDVWPLGWPIGGYPCGPQPY
     CGAGADKSGRDISDAHVKACIYAGINISGTVGEVMPGWQVQVPSVIGIEAGDHIWA
     SRYILERTIQAGVLTLDPKIEGDMGAGCHTNTYSTKMRDGDGFEVVKAILNLS
     LRHKEHISAYGSGNRRLLTGKHETASINTFSGVANRGCSIRVGRETEKQKGYLEDR
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ORIGIN
Alignment Scores:
Pred. No.:          9,12e-11      Length:          1640
Score:              174.00        Matches:          34
Percent Similarity: 76.7%         Conservative:     12
Best Local Similarity: 56.7%      Mismatches:       12
Query Match:        58.6%         Indels:           2
DB:                  15           Gaps:             1

US-10-628-525A-35 (1-58) x AY162465 (1-1640)

```

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Qy      1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db      85 ATGGCGCAGATTTTGGCACCCTTCAATGCGGATGAAGCTTACAAGGAGCTCAGCA 144
Qy      21 CyAAlaThrProLeThrSerLysMetTyrSerSerLeuValMetLysGlnThrLysLys 40
Db      145 ATGCGCAGTCCTATGACACGCAAGATGTGGGGTCTCTTGTGTGTAACACAGAA 204
Qy      41 -----ValAlaHisSerAlaLysPheArgValMetAlaValAenSerGluAenGlyThr 58
Db      205 GGACCAAGCTGGGAGCTCTACTAAATTTAGATGCTGCCACCAAGTCCGAGGTTATACC 264

RESULT 19
LOCUS   AY162466
DEFINITION Spiraera nipponica putative plastidic glutamine synthetase (GS2)
ACCESSION AY162466
VERSION   AY162466.1 GI:26892039
KEYWORDS Spiraera nipponica
SOURCE   Spiraera nipponica
ORGANISM Spiraera nipponica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Rosales; Rosaceae; Rosaceae incertae sedis;
Spiraera.
REFERENCE 1 (bases 1 to 1665)
AUTHORS   Twigg,P.G. and Mahn,M.J.
TITLE     Cloning and Analysis of a Putative Plastidic Glutamine Synthetase
          (GS2) from Spiraera nipponica (Snowmound Spirea)
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 1665)
AUTHORS   Twigg,P.G. and Mahn,M.J.
TITLE     Direct Submission
JOURNAL   Submitted (13-OCT-2002) Biology, University of Nebraska-Kearney,
          905 W. 25th St., Kearney, NE 68849, USA
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Score:              174.00        Matches:          36
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Best Local Similarity: 60.0%      Mismatches:      14
Query Match:        58.6%         Indels:           2
DB:                  15           Gaps:             1

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| Db                                           | 86 ATGGGCACATATTTGGCACCCTACACAAATGGCAGACGAAATTACAAAGAACGCAACC 145    |
| QY                                           | 21 CysAlaThrProIleThrSerIlyMetTrpSerSerLeuValMetIlyGlnThrIlySly 40   |
| Db                                           | 146 ATGCAAGTCCTATGACACGCAAGATGTGGGTTCTCTCTGTTGTAACAGACGACAGAAA 205   |
| QY                                           | 41 -----ValAlaHisSerAlaIlySlyPheArgValMetAlaValAsnSerGluAsnGlyThr 58 |
| Db                                           | 206 GGACCAACTAAGACCTCTACTAAATTTAGATGTTGGCCGTCAGTCTGAAGGTTTATACC 265  |
| RESULT 20                                    |                                                                      |
| AF019561                                     | 1537 bp mRNA linear PLN 01-OCT-1997                                  |
| LOCUS                                        | Daucus carota clone CGS201 glutamine synthetase (GS2) mRNA, nuclear  |
| DEFINITION                                   | gene encoding chloroplast protein, complete cds.                     |
| ACCESSION                                    | AF019561                                                             |
| KEYWORDS                                     | AF019561.1 GI:2454632                                                |
| SOURCE                                       | Daucus carota (carrot)                                               |
| ORGANISM                                     | Daucus carota                                                        |
| REFERENCE                                    | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;   |
| AUTHORS                                      | Higashi,K. and Kamada,H.                                             |
| TITLE                                        | A cDNA sequence of carrot glutamine synthetase                       |
| JOURNAL                                      | Unpublished                                                          |
| REFERENCE                                    | 2 (bases 1 to 1537)                                                  |
| AUTHORS                                      | Higashi,K. and Kamada,H.                                             |
| TITLE                                        | Direct Submission                                                    |
| JOURNAL                                      | Submitted (15-AUG-1997) Institute of Biological Sciences,            |
|                                              | University of Tsukuba, Ten-nohdai, 1-1-1, Tsukuba, Ibaraki 305,      |
|                                              | Japan                                                                |
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|                                              | PVEHPSLPKNYDGSSTGGQAPDDSEVILYPQALFKDPFRGNNILVICITYPQGE               |
|                                              | PIPTNKRKAQIFSDAKVLGEVPMFGEIQQEYTLMQDDVNPGLNNGVYFGPQPGY               |
|                                              | CAATGAKSFGRIIDSAHYKACLYAGINISGTNGEVMPCQWBFQVSPSVIGIAGDHWC            |
|                                              | ARYLLERTEOAGVVLTDPKPIDGMNMGACHTNYSTKSMREGGREVIKKAILNLS               |
|                                              | LRKHEHISAYGEGNERLTGKHETASIDFSKGVADRGCSIRVGEDTEKEGKGYLED              |
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| ORIGIN                                       |                                                                      |
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| Pred. No.:                                   | 1.48e-10 Length: 1537                                                |
| Score:                                       | 172.00 Matches: 36                                                   |
| Percent Similarity:                          | 70.0% Conservative: 6                                                |
| Best Local Similarity:                       | 60.0% Mismatches: 16                                                 |
| Query Match:                                 | 57.9% Indels: 2                                                      |
| DB:                                          | 15 Gaps: 1                                                           |

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| Db                                           | 17 ATGGCTCAGATCTTAGCTCCGTCAGTGAATGGCAATGAGATTACAAAAAATTTCTACC 76     |
| QY                                           | 21 CysAlaThrProIleThrSerIlyMetTrpSerSerLeuValMetIlyGlnThrIlySly 40   |
| Db                                           | 77 GAAAGTAAAGTTCAATGACATCAAGAATGTGGGTTCTCTATTCTTGAACAAACAGAGAAA 136  |
| QY                                           | 41 -----ValAlaHisSerAlaIlySlyPheArgValMetAlaValAsnSerGluAsnGlyThr 58 |
| Db                                           | 137 GCACCAGCTAGAAGTTCTTACCAAATATAGACATTAGCAGTCTGAGGATGGCACC 196      |
| RESULT 21                                    |                                                                      |
| BNA271909                                    | 5232 bp DNA linear PLN 15-APR-2005                                   |
| LOCUS                                        | Brassica napus gln gene for plastid glutamine synthetase, exons      |
| DEFINITION                                   | 1-12.                                                                |
| ACCESSION                                    | AJ271909                                                             |
| VERSION                                      | AJ271909.1 GI:6966929                                                |
| KEYWORDS                                     | gln gene; glutamine synthetase.                                      |
| SOURCE                                       | Brassica napus (rape)                                                |
| ORGANISM                                     | Brassica napus                                                       |
| REFERENCE                                    | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;   |
| AUTHORS                                      | Wojtyna,S., Ochs,G. and Wild,A.                                      |
| TITLE                                        | Cloning and Sequencing of genomic fragments coding for glutamine     |
| JOURNAL                                      | synthetase of Brassica napus                                         |
| REFERENCE                                    | 2 (bases 1 to 5232)                                                  |
| AUTHORS                                      | Wojtyna,S.                                                           |
| TITLE                                        | Direct Submission                                                    |
| JOURNAL                                      | Submitted (04-FEB-2000) Wojtyna S., Allgemeine Botanik, Johannes     |
|                                              | Gutenberg-Universitaet, Muellerweg 6, 55099 Mainz, GERMANY           |
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|                                              | 3630..3881,3961..4021,4107..4421)                                    |
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|                                              | /number=1                                                            |
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|                                              | 3961..4021,4107..4246)                                               |
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QY 41 ValAlaHisSerAlaLys---PheArgValMetAlaValAsnSerGluAsnGlyThr 58
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DEFINITION B.napus mRNA for plastidic glutamine synthetase isoform (BNGSR1-1)
related to the A-genome type of Brassica campestris.
ACCESSION X72751
VERSION X72751.1 GI:296222
KEYWORDS glutamine synthetase.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 1575)
AUTHORS Ochs,G., Schock,G. and Wild,A.
TITLE Chloroplastic glutamine synthetase from Brassica napus
JOURNAL Plant Physiol. 103 (1), 303-304 (1993)
PUBMED 7911583
REFERENCE 2
AUTHORS Ochs,G., Schock,G., Trischler,M., Kosemund,K. and Wild,A.
TITLE Complexity and expression of the glutamine synthetase multigene
family in the amphidiploid crop Brassica napus
JOURNAL Plant Mol. Biol. 39 (3), 395-405 (1999)
PUBMED 10092169
REFERENCE 3 (bases 1 to 1575)
AUTHORS Ochs,G.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-1993) G. Ochs, Inst fuer Allgemeine Botanik, Abt
Prof Dr A Wild, Johannes Gutenberg - Universitaet Mainz, Saarstr
21, 6500 Mainz, FRG
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Pred. No.: 7,3e-05 Length: 1575
Score: 124.00 Matches: 29
Percent Similarity: 69.5% Conservative: 12
Best Local Similarity: 49.2% Mismatches: 14
Query Match: 41.8% Indels: 4
DB: 15 Gaps: 2
US-10-628-525A-35 (1-58) x BNGLSL2 (1-1575)
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Db 95 ATGGCGCAGATCTTGGCAGCTTCTCCAAATGTCAAATGAGATTGACTAAACCCAGCTCC 154
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 155 ATTGCA-----TCGTCAAGTATGGAACCTGGTGTGTGTAACAGAGAAACAG 205
QY 41 ValAlaHisSerAlaLys---PheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 206 AGCAGCAGCAAGTCAGAGCTTCAAGATGATGGCTCTCCAAATCTGATAACAGCACA 262
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BNGSL2
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DEFINITION Brassica napus mRNA for plastidic glutamine synthetase isoform (BNGSL2).
ACCESSION Y12458
VERSION Y12458.1 GI:1934753
KEYWORDS gln gene; glutamine synthetase; plastidic isoform.
SOURCE Brassica napus
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1
AUTHORS Ochs,G., Schock,G., Trischler,M., Kosemund,K. and Wild,A.
TITLE Complexity and expression of the glutamine synthetase multigene
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JOURNAL family in the amphidiploid crop Brassica napus
PUBMED Plant Mol. Biol. 39 (3), 395-405 (1999)
REFERENCE 10092169
AUTHORS Ochs,G.
TITLE Direct Submission
JOURNAL Submitted (08-APR-1997) G. Ochs, Institut fuer Allgemeine Botanik,
Abteilung Prof. Dr. H. Paulsen, Johannes Gutenberg - Universitaet
Mainz, D-55099 Mainz, FRG
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Pred. No.: 7,4e-05 Length: 1597
Score: 124.00 Matches: 30
Percent Similarity: 70.5% Conservative: 13
Best Local Similarity: 49.2% Mismatches: 10
Query Match: 41.8% Indels: 8
DB: 15 Gaps: 3
US-10-628-525A-35 (1-58) x BNGSL2 (1-1597)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
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Db 157 ATTGCA-----TCTTCAAGTATGAGCTGGTGTGTGTAACAGAGAAACAG 207
QY 41 ValAlaHisSerAlaLys-----PheArgValMetAlaValAsnSerGluAsnGly 57
Db 208 -----ACACAGCAGCAAACTCAGAGCTTTAAAGCATGGCTCTCCAAATCTGATAACAGT 261
QY 58 Thr 58
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3'UTR

ORIGIN

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Score: 115.00 Matches: 28  
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DB: 15 Gaps: 2

US-10-628-525A-35 (1-58) x AY122977 (1-1324)

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Db 1 ATGGCTCAGATCTTAGCAGCTTCTCCACATGTCAGATGAGTGCTTAACACTCATCA 60  
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QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
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QY 41 ValAlaHisSerAlaLys---PheArgValMetAlaValAsnSerGluLysGlyThr 58  
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RESULT 26

AF428461

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

COMMENT

AF428461 1473 bp mRNA linear PLN 18-OCT-2001  
Arabidopsis thaliana AT5g35630/MJE4\_9 mRNA, complete cds.  
AF428461.1 GI:16226676  
FLI CDNA.  
Arabidopsis thaliana (thale cress)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
1 (bases 1 to 1473)  
Cheuk,R., Chen,H., Kim,C.J., Koesema,B., Meyers,M.C., Banh,J.,  
Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,  
Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,  
Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,  
Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K.,  
Toriumi,M., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,  
Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,  
Davis,R.W., Theologis,A. and Ecker,J.R.  
Arabidopsis cDNA clones  
Unpublished  
2 (bases 1 to 1473)  
Cheuk,R., Chen,H., Kim,C.J., Koesema,B., Meyers,M.C., Banh,J.,  
Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,  
Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,  
Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,  
Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K.,  
Toriumi,M., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,  
Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,  
Davis,R.W., Theologis,A. and Ecker,J.R.  
Direct Submission  
Submitted (05-OCT-2001) Salk Institute Genomic Analysis Laboratory  
(SIGNAL), Plant Biology Laboratory, The Salk Institute for  
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,  
USA  
RIKEN Genomic Sciences Center (GSC) members carried out the  
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN  
Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J.,  
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,  
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the  
sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H.,  
Kim,C.J., Koesema,B., Meyers,M.C., Shinn,P., Bath,J., Bowser,L.,  
Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G.,  
Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M.,  
Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A.,  
Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S.,  
Davis,R.W., Theologis,A., and Ecker,J.R.

Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to  
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)  
contributed equally to this work as PIs.

FEATURES

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/clone="RAPL09-71-I04 (R14930)"

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3'UTR

ORIGIN

Alignment Scores:

Pred. No.: 0.000795 Length: 1473  
Score: 115.00 Matches: 28  
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Best Local Similarity: 47.5% Mismatches: 18  
Query Match: 38.7% Indels: 2  
DB: 15 Gaps: 2

US-10-628-525A-35 (1-58) x AF428461 (1-1473)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
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Db 105 ATGGCTCAGATCTTAGCAGCTTCTCCACATGTCAGATGAGTGCTTAACACTCATCA 164  
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QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
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QY 41 ValAlaHisSerAlaLys---PheArgValMetAlaValAsnSerGluLysGlyThr 58  
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RESULT 27

AY081252

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AY081252 1519 bp mRNA linear PLN 24-MAR-2002  
Arabidopsis thaliana glutamate-ammonia ligase, chloroplast  
(AT5g35630) mRNA, complete cds.

AY081252

AY081252.1 GI:19698810

FLI CDNA.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;



REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

roids; eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 1519)  
Nguyen, M., Karlin-Neumann, G., Southwick, A., Lam, B., Miranda, M.,  
Pal, C. J., Bowser, L., Jones, T., Ban, J., Carninci, P., Chen, H.,  
Cheuk, R., Chung, M. K., Hayashizaki, Y., Ishida, J., Kamiya, A.,  
Kawai, J., Kim, C., Lin, J., Liu, S. X., Narusaka, M., Pham, P. K.,  
Sakano, H., Sakurai, T., Satou, M., Seki, M., Shim, P., Yamada, K.,  
Shinozaki, K., Ecker, J., Theologis, A., and Davis, R. W.  
Direct Submission  
Submitted (26-FEB-2002) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
USA  
e-mail for correspondence: arabseq@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the  
collection and clustering of RAPL cDNAs (RAPL cDNA: 'RIKEN  
Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J.,  
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,  
Hayashizaki, Y., and Shinozaki, K.

The Salk, Stanford, PGC (SSP) Consortium members carried out the  
sequencing and annotation of the RAPL cDNAs: Nguyen, M.,  
Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Pal, C. J.,  
Bowser, L., Jones, T., Ban, J., Chen, H., Cheuk, R., Chung, M. K.,  
Kim, C., Lin, J., Liu, S. X., Pham, P. K., Sakano, H., Shim, P.,  
Yamada, K., Ecker, J., Theologis, A., and Davis, R. W.

Nguyen, M. (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed  
equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R. W.  
(SSP/Stanford) contributed equally to this work as PIs.

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Query Match: 38.7% Indels: 2  
DB: 15 Gaps: 2

US-10-628-525A-35 (1-58) x AY081252 (1-1519)

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QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
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Db 119 GTCAATGTCATCA---TCATCCAAGTATTGAGGCTCTTGTGTGTTGAACAGAGACGAG 175  
QY 41 ValAlaHisSerAlaLys---PheAtgValMetAlaValAanSerGluAanGlyThr 58  
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RESULT 28  
S69727  
LOCUS  
DEFINITION  
light-regulated glutamine synthetase isoenzyme [Arabidopsis  
thaliana, mRNA, 1548 nt].  
ACCESSION  
S69727.1 GI:240069  
KEYWORDS  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE  
AUTHORS  
TITLE  
The glutamine synthetase gene family of Arabidopsis thaliana:  
light-regulation and differential expression in leaves, roots and  
seeds  
Mol. Gen. Genet. 230 (1-2), 145-154 (1991)  
JOURNAL  
PUBMED  
1684022  
REMARK  
GenBank staff at the National Library of Medicine created this  
entry [NCBI gibbsq 69727] from the original journal article.

FEATURES  
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Percent Similarity: 66.1% Conservative: 11  
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Query Match: 38.7% Indels: 2  
DB: 15 Gaps: 2

US-10-628-525A-35 (1-58) x S69727 (1-1548)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
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Db 132 GTCAATGTCATCA---TCATCCAAGTATTGAGGCTCTTGTGTGTTGAACAGAGACGAG 188  
QY 41 ValAlaHisSerAlaLys---PheArgValMetAlaValAanSerGluAanGlyThr 58  
Db 189 AGCAACAAACAAATCAGAGCTTGTAGATCTTGTGCTCTCCAAATCTGATAAGACTACT 245



The Salk, Stanford, PGECC (SSP) Consortium members carried out the sequencing and annotation of the RAPL cDNAs: Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Dang, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.

Search completed: April 1, 2006, 15:18:40  
Job time : 1178.21 secs

Yamada, K. (SSP/PGECC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGECC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

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## ORIGIN

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US-10-628-525A-35 (1-58) x AY091114 (1-1580)

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| Db | 167 | GTCATTGCATCA---TCATCCAAAGTTATGGAGCTCTGTGTGTGTTGAACACAGAGAAGCAG | 223 |
| Qy | 41  | ValAlaHisSerAlaLys---PheArgValMetAlaValAsnSerGluAsnGlyThr      | 58  |
| Db | 224 | AGCAACACAAAGTCAGAGCTTTAGAGTTCITGCTCTCCATCTGATCAACAGTACT        | 280 |

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 00:15:06 ; Search time 136.553 Seconds  
(without alignments)  
2830.777 Million cell updates/sec

Title: US-10-628-525A-35

Perfect score: 297

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Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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-Q=abas/ABSSWEB spool/US10628525/runat\_31032006\_095109\_16557/app\_query.fasta\_1  
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Database :

N Geneseq 21:\*

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5: Geneseqn2001ba:\*  
6: Geneseqn2002aa:\*  
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11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*  
14: Geneseqn2005as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 5    | 174.5 | 58.8 | 1508   | 13 | ADR65314    | Adr65314 Cotton cd |
| 6    | 155.5 | 52.4 | 1519   | 10 | ADD17886    | Add17886 DNA (Segi |
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| 13   | 73    | 24.6 | 2445   | 6  | ABL53627    | Ab153627 Breast pr |
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| C 15 | 70.5  | 23.7 | 386    | 10 | ADB50884    | Adb50884 Primary r |
| C 16 | 70.5  | 23.7 | 386    | 14 | ADX25897    | Adx25897 Novel cel |
| C 17 | 70.5  | 23.7 | 460    | 10 | ADE58674    | Ades58674 Rat gene |
| C 18 | 70.5  | 23.7 | 460    | 10 | ADE58670    | Ades58670 Rat gene |
| C 19 | 69.5  | 23.4 | 347    | 8  | ABX44826    | Abx44826 Bovine ES |
| C 20 | 69.5  | 23.4 | 1062   | 5  | AHH66383    | Ahh66383 C glutami |
| C 21 | 69.5  | 23.4 | 1192   | 11 | AD165758    | Ad165758 C. glutam |
| C 22 | 69.5  | 23.4 | 1539   | 4  | AAF71202    | Aaf71202 Corynebac |
| C 23 | 69.5  | 23.4 | 1539   | 4  | AAF71203    | Aaf71203 Corynebac |
| C 24 | 69.5  | 23.4 | 34980  | 5  | AHH68528    | Ahh68528 C glutami |
| C 25 | 69    | 23.2 | 1950   | 12 | ADQ37186    | Adq37186 Cell prol |
| C 26 | 68    | 22.9 | 86149  | 12 | ADQ97278    | Adq97278 Human can |
| C 27 | 68    | 22.9 | 110000 | 14 | AEA61124_0  | Aea61124 Human SLC |
| C 28 | 67.5  | 22.7 | 421    | 9  | ACH47744    | Ach47744 Human inf |
| C 29 | 67.5  | 22.7 | 939    | 4  | AAI63931    | Aai63931 Human pol |
| C 30 | 67.5  | 22.7 | 939    | 4  | AAI63931    | Aai63931 Human pol |
| C 31 | 67.5  | 22.7 | 939    | 4  | ABK43906    | Abk43906 DNA enco  |
| C 32 | 67.5  | 22.7 | 939    | 12 | ADI54293    | Adi54293 cDNA enco |
| C 33 | 67.5  | 22.7 | 939    | 12 | ADM24482    | Adm24482 Human PRO |
| C 34 | 67.5  | 22.7 | 1338   | 3  | AAZ39568    | Aaz39568 Human cal |
| C 35 | 67.5  | 22.7 | 1339   | 4  | ABK43612    | Abk43612 DNA enco  |
| C 36 | 67.5  | 22.7 | 1339   | 12 | ADI53999    | Adi53999 cDNA enco |
| C 37 | 67.5  | 22.7 | 1346   | 4  | AAI63854    | Aai63854 Human pol |
| C 38 | 67.5  | 22.7 | 1346   | 12 | ADM24405    | Adm24405 Human PRO |
| C 39 | 67.5  | 22.7 | 1658   | 3  | AACT7199    | Aac77199 Human ORF |
| C 40 | 67.5  | 22.7 | 2103   | 4  | AAH41175    | Aah41175 Human ORF |
| C 41 | 67.5  | 22.7 | 3739   | 4  | AACT75928   | Aac75928 Human ORF |
| C 42 | 67.5  | 22.7 | 174424 | 6  | ABL68122    | Ab168122 Ovary can |
| C 43 | 67.5  | 22.7 | 181343 | 12 | ADQ19573    | Adq19573 Human sof |
| C 44 | 67    | 22.6 | 381    | 8  | ABX41787    | Abx41787 Bovine ES |
| C 45 | 67    | 22.6 | 1366   | 6  | ABK63620    | Abk63620 Rat seque |
| C 46 | 67    | 22.6 | 1366   | 12 | ADP73022    | Adp73022 Renal tox |
| C 47 | 67    | 22.6 | 1926   | 11 | ADJ27276    | Adj27276 Mouse HSP |
| C 48 | 67    | 22.6 | 1929   | 4  | AAI10678    | Aai10678 Murine hs |
| C 49 | 67    | 22.6 | 1929   | 11 | ADJ27274    | Adj27274 Mouse HSP |
| C 50 | 67    | 22.6 | 3783   | 10 | ADP30533    | Adp30533 Rat angio |
| C 51 | 67    | 22.6 | 76994  | 12 | ADP64454    | Adp64454 Sorangium |
| C 52 | 67    | 22.6 | 158405 | 13 | ADV35010    | Adv35010 Murine CD |
| C 53 | 67    | 22.6 | 158405 | 13 | ADV35010    | Adv35010 Murine CD |
| C 54 | 66.5  | 22.4 | 1167   | 6  | ABL53626    | Ab153626 Breast pr |
| C 55 | 66.5  | 22.4 | 1596   | 3  | AAZ53282    | Aaz53282 Neisseria |
| C 56 | 66.5  | 22.4 | 49646  | 3  | AAA81457    | Aaa81457 N. mening |
| C 57 | 66.5  | 22.4 | 110000 | 3  | AAH81490_06 | Coniuntion (7 of   |
| C 58 | 66.5  | 22.4 | 34980  | 3  | AAF21608    | Aaf21608 Neisseria |
| C 59 | 66    | 22.2 | 503    | 10 | ADK12028    | Adk12028 Breast ca |
| C 60 | 66    | 22.2 | 525    | 6  | ABL63576    | Ab163576 Breast ca |
| C 61 | 66    | 22.2 | 525    | 6  | ABL67454    | Ab167454 Thyroid c |
| C 62 | 66    | 22.2 | 525    | 6  | ABN97056    | Abn97056 Gene #355 |
| C 63 | 66    | 22.2 | 604    | 6  | ABT10312    | Abt10312 Human bre |
| C 64 | 66    | 22.2 | 1172   | 12 | ADO42254    | Ado42254 Human NOV |
| C 65 | 66    | 22.2 | 1189   | 12 | ADO42252    | Ado42252 Human NOV |
| C 66 | 66    | 22.2 | 1189   | 12 | ADO42258    | Ado42258 Human NOV |
| C 67 | 66    | 22.2 | 1191   | 12 | ADO42248    | Ado42248 Human NOV |
| C 68 | 66    | 22.2 | 1191   | 12 | ADO42244    | Ado42244 Human NOV |
| C 69 | 66    | 22.2 | 1198   | 12 | ADO42256    | Ado42256 Human NOV |
| C 70 | 66    | 22.2 | 1207   | 12 | ADO42250    | Ado42250 Human NOV |
| C 71 | 66    | 22.2 | 1230   | 12 | ADO42246    | Ado42246 Human NOV |
| C 72 | 66    | 22.2 | 1230   | 12 | ADO42679    | Ado42679 Human NOV |
| C 73 | 66    | 22.2 | 1231   | 6  | AAD46541    | Aad46541 Human dia |
| C 74 | 66    | 22.2 | 1231   | 12 | ADO15614    | Ado15614 Human DGA |
| C 75 | 66    | 22.2 | 1233   | 6  | AAH46549    | Aah46549 Human DGA |
| C 76 | 66    | 22.2 | 1233   | 12 | ADO15631    | Ado15631 Human acy |
| C 77 | 66    | 22.2 | 1303   | 2  | AAZ33556    | Aaz33556 Human bre |

|     |    |      |      |    |           |                     |
|-----|----|------|------|----|-----------|---------------------|
| 78  | 66 | 22.2 | 1459 | 2  | AAT29043  | Aat29043 Oerskovia  |
| 79  | 66 | 22.2 | 1510 | 13 | ADR26804  | Adr26804 Breast ca  |
| 80  | 66 | 22.2 | 1570 | 3  | AA37103   | Aaa37103 Human PRO  |
| 81  | 66 | 22.2 | 1570 | 4  | AA54409   | Aaf54409 Primer #8  |
| 82  | 66 | 22.2 | 1570 | 4  | AA546092  | Aas46092 Human DNA  |
| 83  | 66 | 22.2 | 1570 | 8  | ACA89542  | ACA89542 cDNA enco  |
| 84  | 66 | 22.2 | 1570 | 8  | ACA73552  | ACA73552 Human sec  |
| 85  | 66 | 22.2 | 1570 | 8  | ACA05867  | ACA05867 Human sec  |
| 86  | 66 | 22.2 | 1570 | 8  | ACA66701  | ACA66701 cDNA enco  |
| 87  | 66 | 22.2 | 1570 | 8  | ACF20276  | Acf20276 Human sec  |
| 88  | 66 | 22.2 | 1570 | 8  | ACFI19662 | ACFI19662 Human sec |
| 89  | 66 | 22.2 | 1570 | 8  | ACD21950  | ACD21950 Human sec  |
| 90  | 66 | 22.2 | 1570 | 8  | ACFI13115 | ACFI13115 Human sec |
| 91  | 66 | 22.2 | 1570 | 8  | ACD25218  | ACD25218 Human sec  |
| 92  | 66 | 22.2 | 1570 | 8  | ACF00267  | ACF00267 Human sec  |
| 93  | 66 | 22.2 | 1570 | 8  | ACA72334  | ACA72334 Novel hum  |
| 94  | 66 | 22.2 | 1570 | 8  | ACD04848  | ACD04848 Novel hum  |
| 95  | 66 | 22.2 | 1570 | 8  | ACD18309  | ACD18309 Human sec  |
| 96  | 66 | 22.2 | 1570 | 8  | ACD08316  | ACD08316 Human sec  |
| 97  | 66 | 22.2 | 1570 | 8  | ACA88750  | ACA88750 Novel hum  |
| 98  | 66 | 22.2 | 1570 | 8  | ACA70192  | ACA70192 Human sec  |
| 99  | 66 | 22.2 | 1570 | 8  | ACD12414  | ACD12414 Novel hum  |
| 100 | 66 | 22.2 | 1570 | 8  | ACC74329  | ACC74329 Human sec  |
| 101 | 66 | 22.2 | 1570 | 8  | ACD15957  | ACD15957 Human sec  |
| 102 | 66 | 22.2 | 1570 | 8  | ACD25525  | ACD25525 Novel hum  |
| 103 | 66 | 22.2 | 1570 | 8  | ACD18002  | ACD18002 Human sec  |
| 104 | 66 | 22.2 | 1570 | 8  | ACC88289  | ACC88289 Human sec  |
| 105 | 66 | 22.2 | 1570 | 8  | ACD21643  | ACD21643 Human sec  |
| 106 | 66 | 22.2 | 1570 | 8  | ACD18710  | ACD18710 Human sec  |
| 107 | 66 | 22.2 | 1570 | 8  | ABX98320  | ABX98320 Human cDN  |
| 108 | 66 | 22.2 | 1570 | 8  | ACD14071  | ACD14071 Human PRO  |
| 109 | 66 | 22.2 | 1570 | 8  | ACD09851  | ACD09851 Human sec  |
| 110 | 66 | 22.2 | 1570 | 8  | ACC88596  | ACC88596 Human sec  |
| 111 | 66 | 22.2 | 1570 | 8  | ACD21336  | ACD21336 Human sec  |
| 112 | 66 | 22.2 | 1570 | 8  | ABX75708  | ABX75708 Human cDN  |
| 113 | 66 | 22.2 | 1570 | 8  | ABX97911  | ABX97911 Human PRO  |
| 114 | 66 | 22.2 | 1570 | 8  | ACA97387  | ACA97387 Novel hum  |
| 115 | 66 | 22.2 | 1570 | 8  | ACA57850  | ACA57850 Human PRO  |
| 116 | 66 | 22.2 | 1570 | 8  | ACD14378  | ACD14378 Human PRO  |
| 117 | 66 | 22.2 | 1570 | 8  | ACC91161  | ACC91161 Human sec  |
| 118 | 66 | 22.2 | 1570 | 8  | ACC88903  | ACC88903 Human sec  |
| 119 | 66 | 22.2 | 1570 | 8  | ACD07100  | ACD07100 Human PRO  |
| 120 | 66 | 22.2 | 1570 | 8  | ACA67551  | ACA67551 Human PRO  |
| 121 | 66 | 22.2 | 1570 | 8  | ACC81606  | ACC81606 Human sec  |
| 122 | 66 | 22.2 | 1570 | 8  | ACC89210  | ACC89210 Human sec  |
| 123 | 66 | 22.2 | 1570 | 8  | ACC86566  | ACC86566 Human sec  |
| 124 | 66 | 22.2 | 1570 | 8  | ACC89824  | ACC89824 Human sec  |
| 125 | 66 | 22.2 | 1570 | 8  | ACC93003  | ACC93003 Human sec  |
| 126 | 66 | 22.2 | 1570 | 8  | ACA72631  | ACA72631 Human PRO  |
| 127 | 66 | 22.2 | 1570 | 8  | ACA89149  | ACA89149 Human sec  |
| 128 | 66 | 22.2 | 1570 | 8  | ACA69885  | ACA69885 Human sec  |
| 129 | 66 | 22.2 | 1570 | 8  | ACA97028  | ACA97028 Novel hum  |
| 130 | 66 | 22.2 | 1570 | 8  | ACA91024  | ACA91024 Novel hum  |
| 131 | 66 | 22.2 | 1570 | 8  | ACA70806  | ACA70806 Human sec  |
| 132 | 66 | 22.2 | 1570 | 8  | ACA95316  | ACA95316 Novel hum  |
| 133 | 66 | 22.2 | 1570 | 8  | ACC86259  | ACC86259 Human sec  |
| 134 | 66 | 22.2 | 1570 | 8  | ACC90131  | ACC90131 Human sec  |
| 135 | 66 | 22.2 | 1570 | 8  | ACD12739  | ACD12739 Human sec  |
| 136 | 66 | 22.2 | 1570 | 8  | ACFI19969 | ACFI19969 Human sec |
| 137 | 66 | 22.2 | 1570 | 8  | ABX76913  | ABX76913 Human PRO  |
| 138 | 66 | 22.2 | 1570 | 8  | ACA73245  | ACA73245 Novel hum  |
| 139 | 66 | 22.2 | 1570 | 8  | ACA68788  | ACA68788 Novel hum  |
| 140 | 66 | 22.2 | 1570 | 8  | ACA74632  | ACA74632 cDNA enco  |
| 141 | 66 | 22.2 | 1570 | 8  | ACA70499  | ACA70499 Human sec  |
| 142 | 66 | 22.2 | 1570 | 8  | ACD14685  | ACD14685 Human PRO  |
| 143 | 66 | 22.2 | 1570 | 8  | ACA68357  | ACA68357 Novel hum  |
| 144 | 66 | 22.2 | 1570 | 8  | ABX98822  | ABX98822 Novel hum  |
| 145 | 66 | 22.2 | 1570 | 8  | ACC81299  | ACC81299 Human sec  |
| 146 | 66 | 22.2 | 1570 | 8  | ACA95623  | ACA95623 Novel hum  |
| 147 | 66 | 22.2 | 1570 | 8  | ACD04541  | ACD04541 Novel hum  |
| 148 | 66 | 22.2 | 1570 | 8  | ACC87982  | ACC87982 Human sec  |
| 149 | 66 | 22.2 | 1570 | 8  | ACFI12644 | ACFI12644 Human sec |
| 150 | 66 | 22.2 | 1570 | 8  | ACA96359  | ACA96359 Human PRO  |

ALIGNMENTS

RESULT 1

AAQ12539

AAQ12539 standard; DNA; 1589 BP.

ID AAQ12539

XX AAQ12539;

AC AAQ12539;

XX

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 25-SEP-1991 (first entry)

XX

DE GS2 promoter element.

XX

KW Glutamine synthetase isoenzyme; photosynthesis; light induction; tissue specific; transgenic plants; transcription; ss.

KW

XX Pisum sativum; cv "Sparkle".

OS

XX WO9109050-A.

PN

XX

PD 27-JUN-1991.

XX

XX

PF 08-DEC-1989; 89US-00448036.

XX

PR 08-DEC-1989; 89US-00448036.

XX

XX (UYRQ ) UNIV ROCKEFELLER.

PI

XX Coruzzi G, Edwards J, Walker EI;

XX

DR WPI; 1991-208085/28.

XX

PT Organ-specific, light-inducible plant promoter sequences - from Pisum sativum glutamine synthetase isoenzyme(s), used to introduce herbicide and pathogen resistance.

PT

XX Claim 1; Fig 5A; 70pp; English.

PS

XX The promoter was isolated from the nuclear gene for chloroplast GS2 glutamine synthetase. It is specific for photosynthetically active cells and is light inducible. It can be used to control the expression of glutamine synthetase as well as heterologous proteins in a tissue specific and/or light inducible manner. This control can be applied to e.g. manipulation of nutritional requirements or to induction of resistance to herbicides, or viral or pathogen infection. See also AAQ12540 and AAQ12541. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)

CC

XX SQ Sequence 1589 BP; 548 A; 252 C; 219 G; 570 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:

Score:

Length: 1589

Matches: 53

Percent Similarity: 100.0%

Conservative: 0

Best Local Similarity: 100.0%

Mismatches: 0

Query Match: 91.2%

Indels: 0

DB: 2

Gaps: 0

US-10-628-525A-35 (1-58) x AAQ12539 (1-1589)

OY 1 MetalAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIlySerPro 20

DB 1431 ATGGCGCGCATTTTGGCACCTTCGACGCAATGGCAGATGAGAAATCAGAAAAACCTCTCT 1490

OY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrIlyLys 40

DB 1491 TGTGCACTCCCAATCAGATGAGATGAGATTTCTTTGGTTATGAAACAAACTAAGAAA 1550

OY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsn 53

|||||

DB 1551 GTTGGCAGTTCGTAAATTTAGATTATGGCAGTCAAC 1589  
 RESULT 2  
 AAQ34621  
 ID AAQ34621 standard; DNA; 1601 BP.  
 XX  
 AC AAQ34621;  
 XX  
 25-MAR-2003 (revised)  
 DT 12-MAY-1993 (first entry)  
 XX  
 DE Chloroplast GS2 glutamine synthase promoter element.  
 XX  
 KW Plant organ specific; light inducible; heterologous protein; expression.  
 XX  
 OS Pisum sativum.  
 XX  
 FN WO9222582-A1.  
 XX  
 PD 23-DEC-1992.  
 XX  
 PF 12-JUN-1992; 92WO-US005170.  
 XX  
 PR 13-JUN-1991; 91US-00715751.  
 XX  
 PA (UYRQ ) UNIV ROCKEFELLER.  
 XX  
 PI Coruzzi GM, Edwards JW, Walker EL, Brears T;  
 XX  
 DR WPI; 1993-018084/02.  
 XX  
 PT Pure GS2, GS3A and GS3B promoter elements - which are light inducible or  
 PT phloem active, used, e.g. to impart herbicide or pathogen resistance.  
 XX  
 PS Claim 1; Page 54; 104pp; English.  
 XX  
 CC The sequence is that of the chloroplast GS2 glutamine synthetase promoter  
 CC element. It is inducible by light and directs levels of transcription in  
 CC photosynthetic cells of leaves and in non-photosynthetic cells of leaves  
 CC and in non-photosynthetic cells of the root tip. It may also be used to  
 CC control expression of heterologous proteins, e.g. for the manipulation of  
 CC nutritional requirements and the induction of resistance to herbicides  
 CC and pathogens, e.g. viruses. It may be used to design optimal gene fusion  
 CC systems and in the identification of promoter elements associated with  
 CC glutamine synthetase genes from any species of plant, bacteria or virus  
 CC using any method. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 1601 BP; 551 A; 259 C; 217 G; 574 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.41e-25 Length: 1601  
 Score: 268.00 Matches: 52  
 Percent Similarity: 100.0% Conservative: 1  
 Best Local Similarity: 98.1% Mismatches: 0  
 Query Match: 90.2% Indels: 0  
 DB: 2 Gaps: 0  
 US-10-628-525A-35 (1-58) x AAQ34621 (1-1601)  
 Qy 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 Db 1443 ATGGCGCAGATTTTGGCACCTTCGACGCAATGGCAGATGAGATCAAAAACCTCTCCT 1502  
 Qy 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 Db 1503 TGTGCAACTCCAAATCACATCAAAAGATGGGACTCTTTGGTTATGAACAACAACTAAGAAA 1562  
 Qy 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsn 53  
 Db 1563 GTTGGCAGTTCGTAAATTTAGATTATGGCAGTCAAC 1601  
 RESULT 3  
 ADK54299



Db 120 GATGCTAATCCCTTGACTTCAAGATGGAGTCTGTGGTGTGTTGAAGCAGATAAAGA 179

QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

Db 180 CTTGCTGTTAAAGACTCTGCCAAATTTAGAGCTTTGCTCTCCATCTCATAGTGGCACT 239

RESULT 4

ADK58446

ID ADK58446 standard; DNA; 1633 BP.

XX

AC ADK58446;

XX

DT 06-MAY-2004 (first entry)

XX

DE Plant DNA sequence which confers altered metabolic characteristic #5829.

XX

KW altered metabolic characteristic; plant; acid metabolism;

KW alcohol metabolism; fatty acid metabolism;

KW branched fatty acid metabolism; alkaloid metabolism;

KW amino acid metabolism; ester metabolism; glyceride metabolism;

KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;

KW terpene metabolism; isoprenoid metabolism; alkene metabolism;

KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;

KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.

XX

OS Unidentified.

XX

XX

PN WO2003020936-A1.

XX

PD 13-MAR-2003.

XX

PF 30-AUG-2002; 2002WO-US027884.

XX

PR 31-AUG-2001; 2001US-0316471P.

XX

PA (DOWC ) DOW CHEM CO.

PA (DOWC ) DOW AGROSCIENCES LLC.

XX

PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;

PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;

XX

DR WPI; 2003-313091/30.

XX

PT Novel genes that confer altered metabolic characteristics in Nicotiana

PT benthamiana plants, useful for altering the levels of metabolites e.g.

PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.

XX

PS Claim 1; SEQ ID NO 5829; 2576pp; English.

XX

CC The invention comprises DNA sequences which confer an altered metabolic

CC characteristic when they are expressed in a plant. The DNA sequences of

CC the invention are useful for producing plants with an altered metabolic

CC characteristic, such as: altered acid metabolism, alcohol metabolism,

CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other

CC base metabolism, altered amino acid metabolism, altered ester metabolism,

CC altered glyceride metabolism, altered phenolic metabolism, altered

CC carbohydrate metabolism, altered sterol, oxygenated terpene, or

CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon

CC metabolism, ketone or quinone metabolism. The DNA sequences of the

CC invention may be used to provide disease resistance in a plant and gene

CC shuffling or sexual PCR procedures. The present nucleic acid represents a

CC DNA sequence of the invention.

XX

SQ Sequence 1633 BP; 472 A; 322 C; 389 G; 450 T; 0 U; 0 Other;

US-10-628-525a-35 (1-58) x ADK58446 (1-1633)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

Db 74 ATGGCTCAGATCTTGGCTCCATCTGGCAATGGCAGATGAGATGACAAAGAGCTCAACA 133

QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

Db 134 GATGCTAATCCCTTGACTTCAAGATGTGGAGTCTGTGTGTTGAAGCAGATAAAGA 193

QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

Db 194 CTTGCTGTTAAAGACTCTGCCAAATTTGAGTCTTTGCTCTCCATCTCATAGTGGCACT 253

RESULT 5

ADR65314

ID ADR65314 standard; cDNA; 1508 BP.

XX

AC ADR65314;

XX

DT 02-DEC-2004 (first entry)

XX

DE Cotton cDNA sequence, SEQ ID 6095.

XX

KW Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;

KW drought tolerance; plant disease resistance; galactomannan; lignin;

KW plant growth regulator; heat tolerance; herbicide tolerance;

KW homologous recombination; extreme osmotic condition tolerance;

KW pathogen resistance; pest resistance; yield; photosynthesis; seed oil;

XX

OS Gossypium hirsutum.

XX

PN US2004181830-A1.

XX

PD 16-SEP-2004.

XX

PF 29-JAN-2004; 2004US-00767795.

XX

PR 07-MAY-2001; 2001US-00849529.

XX

PR 12-DEC-2001; 2001US-00021323.

XX

PA (KOVA/) KOVALIC D K.

PA (ZHOU/) ZHOU Y.

PA (CAOY/) CAO Y.

XX

PI Kovalic DK, Zhou Y, Cao Y;

XX

DR WPI; 2004-667718/65.

XX

XX New recombinant nucleic acid molecules and polypeptides from Gossypium

PT hirsutum, useful for producing plants with improved biological

PT characteristics (e.g. Improved plant cold or drought tolerance).

XX

PS Claim 1; SEQ ID NO 6095; 14pp; English.

XX

CC The invention relates to a recombinant polynucleotide comprising any of

CC the 58798 Cotton plant cDNA sequences mentioned in the specification.

CC Also a recombinant polypeptide comprising any of the 58798 amino acid

CC sequences mentioned in the specification and producing a plant having an

CC improved property. Producing a plant having an improved property

CC comprises transforming a plant with a recombinant construct comprising a

CC promoter region functional in a plant cell operably joined to a

CC polynucleotide comprising a coding sequence for a polypeptide associated

CC with the property, and growing the transformed plant. The polypeptide is

CC useful for improving plant cold tolerance, manipulating growth rate in

CC plant cells by modification of the cell cycle pathway, improving plant

CC drought tolerance, providing increased resistance to plant disease,

CC producing galactomannan (or lignin or plant growth regulators), improving

CC plant heat tolerance, improving plant tolerance to herbicides, increasing

CC the rate of homologous recombination in plants, improving plant tolerance

CC to extreme osmotic conditions or to pathogens or pests, improving yield

CC by modification of photosynthesis, modifying seed oil or protein yield





US-10-628-525A-35 (1-58) x ADE82003 (1-487)

```
Oy 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 48 ATGGCTCAGATCTTAGCAGCTTCTCCAAACATGTCAGATGAGTGCCTAAACACTCATCA 107
Oy 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 108 GTCATTGCATCA---TCATCCAGTTATGGAGCTCTGTGTGTTGAACAGACGAGCAG 164
Oy 41 ValAlaHisSerAlaLys---PheArgValMetAlaValAenSerGluAenGlyThr 58
Db 165 AGCAACAACAAGTCAGAGGCTTAGAGTTCTTCTCCATCTGATACAGTACT 221
```

## RESULT 9

AAC46992

ID AAC46992 standard; DNA; 1598 BP.

XX AC

AAC46992;

XX AC

XX 18-OCT-2000 (first entry)

XX DE

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 52161.

XX KW

XX Hybridisation assay; genetic mapping; gene expression control;

XX KW

XX protein identification; signal transduction pathway; metabolic pathway;

XX KW

XX promoter; termination sequence; ss.

XX OS

XX Arabidopsis thaliana.

XX PN

XX BP1033405-A2.

XX XX

XX 06-SEP-2000.

XX XX

XX 25-FEB-2000; 2000EP-00301439.

XX PR

XX 25-FEB-1999; 99US-0121825P.

XX PR

XX 05-MAR-1999; 99US-0123380P.

XX PR

XX 09-MAR-1999; 99US-0123348P.

XX PR

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| DB 198    | GTCATGTGCATCA---TCATCCAGTTATGAGACTCTGTGTGTTGAAACAGAGAAGACGAG 254        |                |  |
| QY 41     | ValAlaHisSerAlaLys---PheArgValMetAlaValAsnSerGluHenGlyThr 58            |                |  |
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| XX        | Arabidopsis thaliana DNA fragment SEQ ID NO: 59909.                     |                |  |
| KW        | Hybridisation assay; genetic mapping; gene expression control;          |                |  |
| KW        | protein identification; signal transduction pathway; metabolic pathway; |                |  |
| XX        | promoter; termination sequence; ss.                                     |                |  |
| OS        | Arabidopsis thaliana.                                                   |                |  |
| XX        | EP1033405-A2.                                                           |                |  |
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ID ABL53628 standard; cDNA; 1543 BP.  
XX ABL53628;  
XX 17-JUN-2002 (first entry)  
DE Breast protein-eukaryotic conserved gene 1 (BSTP-ECG1) cDNA.  
XX BSTP-ECG1; breast cancer; diagnosis; gene therapy; antitumour;  
KW cytostatic; differential expression; gene; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 228..1394  
FT /\*tag= a  
FT /\*product= "BSTP-ECG1"  
XX WO200208260-A2.  
XX 31-JAN-2002.  
XX 26-JUL-2001; 2001WO-US023439.  
XX 26-JUL-2000; 2000US-0220967P.  
PR 06-DEC-2000; 2000US-0251669P.  
XX (STRD ) UNIV STANFORD.  
PA (GENO-) APPLIED GENOMICS INC.  
XX Botstein D, Brown PO, Perou C, Ross D, Seitz R;  
XX WPI; 2002-315251/35.  
DR P-PSDB; ABB75677.  
XX Novel substantially purified polypeptide encoded by breast protein-  
PT eukaryotic conserved gene 1, useful for diagnosing, treating or  
PT preventing breast cancer, and for classifying cancer.  
XX Disclosure; Fig 1b; 127pp; English.  
XX The present sequence is that of a BSTP-ECG1 (breast protein-eukaryotic  
CC conserved gene 1) cDNA sequence, encoding a 388-amino acid protein (see  
CC ABB75677). The cDNA corresponds to a 1.5 kb mRNA isoform detected in  
CC liver tumour-derived Hepd2 cells (ATCC HB-8065), colon tumour-derived

CC COLO205 cells (ATCC CCL-222) and breast adenocarcinoma-derived MCF-7  
CC cells (ATCC HTB-22) using Northern blotting. Multiple isoforms of BSTP-  
CC ECG1 mRNA are predicted resulting from alternative 3' processing. BSTP-  
CC ECG1 is differentially expressed among breast tumours, making it useful  
CC for the diagnosis, treatment, prevention, prognosis and classification of  
CC cancer, especially breast cancer, and a target for therapeutic  
CC intervention. The invention provides BSTP-ECG1 polypeptides and  
CC polynucleotides, expression vectors, host cells, antibodies, agonists and  
CC antagonists. It also provides methods for treating or preventing  
CC disorders of cell proliferation, particularly breast cancer, by  
CC administering a polypeptide, polynucleotide or antibody of the invention.  
CC Also provided are methods of classifying diseases, particularly breast  
CC cancer, by detecting expression of BSTP-ECG1 or a polynucleotide encoding  
CC it, and of providing diagnostic, prognostic and/or predictive information  
CC for a patient based on the detection and/or measurement of BSTP-ECG1 or a  
CC polynucleotide encoding BSTP-ECG1. Since BST-ECG1 mRNA can be detected in  
CC a variety of tumour-derived cell lines, these methods may also be  
CC applicable to additional tumour types  
XX Sequence 1543 BP; 321 A; 452 C; 441 G; 329 T; 0 U; 0 Other;  
SQ Alignment Scores:  
Pred. No.: 15.8 Length: 1543  
Score: 73.00 Matches: 19  
Percent Similarity: 43.3% Conservative: 7  
Best Local Similarity: 31.7% Mismatches: 26  
Query Match: 24.6% Indels: 8  
DB: 2  
US-10-628-525A-35 (1-58) x ABL53628 (1-1543)  
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25  
Db 1252 TCACCATCCCAAGCTGGAGACCCCAACCCAGACAGATCCGCTGTACCACCATGT 1311  
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45  
Db 1312 ACATGGAGGCCCTGTGTGAGCTTT---TCGACACAGCACAAGCAAGTTCGGCTCCCG 1368  
QY 46 LysPheArg-----ValMetAlaValAsnSerGluHenglyThr 58  
Db 1369 AGACTGAGGTCCTGGAGGTGAACTGAGCCAGCCTTCGGGGCCAATTCCTCGAGGAACC 1428  
RESULT 12  
ABLS3629  
ID ABL53629 standard; cDNA; 2418 BP.  
XX ABL53629;  
XX 17-JUN-2002 (first entry)  
DE Breast protein-eukaryotic conserved gene 1 (BSTP-ECG1) consensus.  
XX BSTP-ECG1; breast cancer; diagnosis; gene therapy; antitumour;  
KW cytostatic; differential expression; ss.  
OS Homo sapiens.  
XX WO200208260-A2.  
XX 31-JAN-2002.  
XX 26-JUL-2001; 2001WO-US023439.  
PR 26-JUL-2000; 2000US-0220967P.  
PR 06-DEC-2000; 2000US-0251669P.  
XX (STRD ) UNIV STANFORD.  
PA (GENO-) APPLIED GENOMICS INC.  
XX Botstein D, Brown PO, Perou C, Ross D, Seitz R;  
XX WPI; 2002-315251/35.  
DR



XX Novel substantially purified polypeptide encoded by breast protein-  
PT eukaryotic conserved gene 1, useful for diagnosing, treating or  
PT preventing breast cancer, and for classifying cancer.  
XX  
XX Disclosure; Fig 2; 127pp; English.  
XX  
XX The present sequence is that of a consensus of cDNA clones for BStP-ECG1  
CC (breast protein-eukaryotic conserved gene 1). In order to identify genes  
CC that are differentially expressed in breast tumours, cDNA microarrays  
CC were produced, each representing the same set of approximately 8100  
CC different human genes. Variations in patterns of gene expression were  
CC characterised in 62 breast tumour samples from 40 patients, 3 normal  
CC breast tissue samples and 19 samples from 17 human cell lines. IMAGE  
CC clone 161484 was identified based on the expression pattern of its mRNA  
CC among these 84 samples. Overlapping IMAGE clones 48805, 1276329, 1343900  
CC and 1560906 were identified in a database search. The present consensus  
CC sequence was produced from the 5 IMAGE clones, and a coding region (see  
CC ABL53626) was derived. BStP-ECG1 is differentially expressed among breast  
CC tumours, making it useful for the diagnosis, treatment, prevention,  
CC prognosis and classification of cancer, especially breast cancer, and  
CC also a potential therapeutic target. The invention provides BStP-ECG1  
CC polypeptides and polynucleotides, expression vectors, host cells,  
CC antibodies, agonists and antagonists. It also provides methods for  
CC treating or preventing disorders of cell proliferation, particularly  
CC breast cancer, by administering a polypeptide, polynucleotide or antibody  
CC of the invention. Also provided are methods of classifying diseases,  
CC particularly breast cancer by detecting expression of BStP-ECG1 or a  
CC polynucleotide encoding it, and of providing diagnostic, prognostic  
CC and/or predictive information for a patient based on the detection and/or  
CC measurement of BStP-ECG1 or polynucleotide encoding BStP-ECG1  
XX  
SQ Sequence 2418 BP; 590 A; 624 C; 604 G; 582 T; 0 U; 18 Other;

Alignment Scores:  
Pred. No.: 28.7 Length: 2418  
Score: 73.00 Matches: 19  
Percent Similarity: 43.3% Conservative: 7  
Best Local Similarity: 31.7% Mismatches: 26  
Query Match: 24.6% Indels: 8  
DB: Gaps: 2

US-10-628-525A-35 (1-58) x ABL53629 (1-2418)  
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25  
DB 1225 TCACCATCCCAAGCTGGAGACCCCAACCCAGCAGACATCGACCTGTACCACCATGT 1284  
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45  
DB 1285 ACATGGAGGCCCTGGTGAAGCTTT---TCGACAAAGCAGCAAGACCAAGTTCCGGCTCCCGG 1341  
QY 46 LysPheArg-----ValMetAlaValAsnSerGluAsnGlyThr 58  
DB 1342 AGACTGAGGTCTCTGGAGGTGAAGTGAAGCAGCCCTTCGGGGCCCAATTCCTCGGAGGACCC 1401  
RESULT 13  
ABL53627  
ID ABL53627 standard; cDNA; 2445 BP.  
XX  
AC ABL53627;  
XX  
XX 17-JUN-2002 (first entry)  
XX  
XX Breast protein-eukaryotic conserved gene 1 (BStP-ECG1) cDNA.  
XX BStP-ECG1; breast cancer; diagnosis; gene therapy; antitumour;  
KW cytostatic; differential expression; gene; ss.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 228. .1394  
PT CDS

PT /\*tag= a  
XX /product= "BStP-ECG1"  
PN WO200208260-A2.  
XX  
XX 31-JAN-2002.  
XX  
XX 26-JUL-2001; 2001WO-US023439.  
XX  
XX 26-JUL-2000; 2000US-0220967P.  
PR 06-DEC-2000; 2000US-0251669P.  
XX  
XX (STRD ) UNIV STANFORD.  
PA (GENO-) APPLIED GENOMICS INC.  
XX  
XX Botstein D, Brown PO, Perou C, Ross D, Seitz R;  
XX WPI; 2002-315251/35.  
DR P-PSDB; ABB75677.  
XX  
XX Novel substantially purified polypeptide encoded by breast protein-  
PT eukaryotic conserved gene 1, useful for diagnosing, treating or  
PT preventing breast cancer, and for classifying cancer.  
XX  
XX Disclosure; Fig 1C; 127pp; English.

The present sequence is that of a BStP-ECG1 (breast protein-eukaryotic conserved gene 1) cDNA sequence, encoding a 388-amino acid protein (see ABB75677). The cDNA corresponds to a 2.2 kb mRNA isoform detected in liver tumour-derived HepG2 cells (ATCC HB-8065), colon tumour-derived COLO205 cells (ATCC CCL-222) and breast adenocarcinoma-derived MCF-7 cells (ATCC HTB-22) using Northern blotting. Multiple isoforms of BSt-ECG1 mRNA are predicted resulting from alternative 3' processing. BStP-ECG1 is differentially expressed among breast tumours, making it useful for the diagnosis, treatment, prevention, prognosis and classification of cancer, especially breast cancer, and a target for therapeutic intervention. The invention provides BStP-ECG1 polypeptides and polynucleotides, expression vectors, host cells, antibodies, agonists and antagonists. It also provides methods for treating or preventing disorders of cell proliferation, particularly breast cancer, by administering a polypeptide, polynucleotide or antibody of the invention. Also provided are methods of classifying diseases, particularly breast cancer, by detecting expression of BStP-ECG1 or a polynucleotide encoding it, and of providing diagnostic, prognostic and/or predictive information for a patient based on the detection and/or measurement of BStP-ECG1 or a polynucleotide encoding BStP-ECG1. Since BSt-ECG1 mRNA can be detected in a variety of tumour-derived cell lines, these methods may also be applicable to additional tumour types

SQ Sequence 2445 BP; 525 A; 678 C; 676 G; 563 T; 0 U; 3 Other;

Alignment Scores:  
Pred. No.: 29.1 Length: 2445  
Score: 73.00 Matches: 19  
Percent Similarity: 43.3% Conservative: 7  
Best Local Similarity: 31.7% Mismatches: 26  
Query Match: 24.6% Indels: 8  
DB: Gaps: 2

US-10-628-525A-35 (1-58) x ABL53627 (1-2445)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25  
DB 1252 TCACCATCCCAAGCTGGAGACCCCAACCCAGCAGACATCGACCTGTACCACCATGT 1311  
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45  
DB 1312 ACATGGAGGCCCTGGTGAAGCTTT---TCGACAAAGCAGCAAGACCAAGTTCCGGCTCCCGG 1368  
QY 46 LysPheArg-----ValMetAlaValAsnSerGluAsnGlyThr 58  
DB 1369 AGACTGAGGTCTCTGGAGGTGAAGTGAAGCAGCCCTTCGGGGCCCAATTCCTCGGAGGACCC 1428

```
RESULT 14
ADB56392/c
ID ADB56392 standard; DNA; 386 BP.
XX
AC ADB56392;
XX
DT 04-DEC-2003 (first entry)
XX
DE Toxicity-related gene, SEQ ID 1418.
XX
KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;
KW drug screening; toxicity assay; ds.
XX
OS Unidentified.
XX
PN WO2003064624-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-US003194.
XX
PR 31-JAN-2002; 2002US-00060087.
PR 15-MAR-2002; 2002US-0364045P.
PR 15-MAR-2002; 2002US-0364055P.
PR 30-DEC-2002; 2002US-0436643P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;
XX
DR WPI; 2003-689530/65.
XX
PT Predicting a toxic effect of a compound, useful in identifying toxicity
PT markers in liver tissues or cells for drug screening and toxicity assays,
PT comprises preparing gene expression profile of tissue or cells exposed to
PT the compound.
XX
PS Claim 1; SEQ ID NO 1418; 1156pp; English.
XX
RS
XX
CC The present invention relates to a method for predicting a toxic effect
CC of a compound. The method comprises preparing a gene expression profile
CC of a tissue or cell sample exposed to the compound, and comparing the
CC gene expression profile to a database comprising SEQ ID 1-4925, where
CC differential expression of the gene indicates at least one toxic effect.
CC The method is useful for predicting at least one toxic effect of a
CC compound, predicting hepatotoxicity or the progression of a toxic effect
CC of a compound, identifying an agent that modulates the onset or
CC progression of a toxic response, predicting the cellular pathways that a
CC compound modulates in a cell, and identifying an agent that modulates at
CC least one activity of a protein. The method and compositions of the
CC present invention using a database of genes having liver toxin-induced
CC differential expression, are useful in identifying toxicity markers in
CC liver tissues or cells for drug screening and toxicity assays. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 386 BP; 91 A; 98 C; 110 G; 87 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.36 Length: 386
Score: 70.50 Matches: 15
Percent Similarity: 58.1% Conservatives: 3
Best Local Similarity: 48.4% Mismatches: 12
Query Match: 23.7% Indels: 1
DB: 10 Gaps: 1

US-10-628-525A-35 (1-58) x ADB56392 (1-386)

Qy 6 AlaProSerThrGlnTrpGlnMetArgLleThrLysThrSerProCysAlaThrProIle 25
DB ::::|||||
253 TCACCGTCCTTAAGCTGGAGCACCAGCCAGAAAGACATCGACCTGTACACACCATGT 194
```

```
Qy 26 ThrSerLysMetTrp---SerSerLeuValMet 35
DB ::::|||||
193 ACATGGAGGCGCTGGTGAAGCTCTTTGACAAATC 161

RESULT 15
ADB50884/c
ID ADB50884 standard; DNA; 386 BP.
XX
AC ADB50884;
XX
DT 04-DEC-2003 (first entry)
XX
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:1426.
XX
KW toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW toxicity marker; toxicity progression; drug screening;
KW primary rat hepatocyte toxicity modelling; gene; ds.
XX
OS Rattus norvegicus.
XX
PN WO2003065993-A2.
XX
PD 14-AUG-2003.
XX
PF 04-FEB-2003; 2003WO-US003482.
XX
PR 04-FEB-2002; 2002US-0353171P.
PR 13-MAR-2002; 2002US-0363534P.
PR 08-APR-2002; 2002US-0370248P.
PR 10-APR-2002; 2002US-0371134P.
PR 10-APR-2002; 2002US-0371135P.
PR 10-APR-2002; 2002US-0371150P.
PR 11-APR-2002; 2002US-0371413P.
PR 19-APR-2002; 2002US-0373601P.
PR 19-APR-2002; 2002US-0373602P.
PR 22-APR-2002; 2002US-0374139P.
PR 08-MAY-2002; 2002US-0378370P.
PR 09-MAY-2002; 2002US-0378652P.
PR 09-MAY-2002; 2002US-0378653P.
PR 09-MAY-2002; 2002US-0378665P.
PR 09-JUL-2002; 2002US-0394230P.
PR 04-SEP-2002; 2002US-0394253P.
PR 28-JAN-2003; 2003US-0407688P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
PI Elashoff M;
XX
DR WPI; 2003-731472/69.
XX
PT Determining if a compound induces a toxic effect on a tissue or cell, for
PT identifying hepatotoxic compounds, comprises comparing a gene expression
PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
PT mean values.
XX
PS Claim 44; SEQ ID NO 1426; 874pp; English.
XX
CC The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the Tox mean and non-Tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.
```

XX SQ Sequence 386 BP; 91 A; 98 C; 110 G; 87 T; 0 U; 0 Other;

Alignment Scores:

|                        |       |               |     |
|------------------------|-------|---------------|-----|
| Pred. No.:             | 5.36  | Length:       | 386 |
| Score:                 | 70.50 | Matches:      | 15  |
| Percent Similarity:    | 58.1% | Conservative: | 3   |
| Best Local Similarity: | 48.4% | Mismatches:   | 12  |
| Query Match:           | 23.7% | Indels:       | 1   |
| DB:                    | 10    | Gaps:         | 1   |

US-10-628-525A-35 (1-58) x ADB50894 (1-386)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProile 25  
 DB 253 TCACCGGCCCTTAAGCTGGAGCCGCCGAGAAAGACATCGACCTGTACCACCATGT 194

QY 26 ThrSerLysMetTrp---SerSerLeuValMet 35  
 DB 193 ACATGGAGGCCCTGGTGAGCTCTTTGACAATC 161

RESULT 16  
 ADX25897  
 ID ADX25897 standard; DNA; 386 BP.

XX AC ADX25897;

XX DT 05-MAY-2005 (first entry)

XX DE Novel cell pain response detection method-related human gene SeqID243.

XX KW pain; animal disease model; expression; analgesic; antiaddictive;  
 KW nootropic; anticonvulsant; vasotropic; neuroprotective; tranquilizer;  
 KW antiasthmatic; antirheumatic; antiarthritic; osteopathic;  
 KW ophthalmological; antiinflammatory; antipruritic; dermatological;  
 KW antiulcer; gastrointestinal-Gen.; nephrotropic; gynecological;  
 KW hepatotropic; antiparkinsonian; neuroleptic; laxative; gene therapy;  
 KW neuropathic pain; Alzheimers disease; Parkinsons disease;  
 KW motor neurone disease; Huntingtons disease; schizophrenia; gene; ds.

XX OS Homo sapiens.

XX PN WO2005014849-A2.

XX PD 17-FEB-2005.

XX PF 06-JUL-2004; 2004WO-US023166.

XX PR 03-JUL-2003; 2003US-0485101P.

XX PA (EURO-) EUROCELTIQUE SA.

XX PI Tong J, Jin G, Ji R, Xu Y, Chiang LW, Lavery DJ;  
 WPI; 2005-163258/17.

XX DR Detecting pain responses in a cell, useful in identifying potential  
 XX therapeutic and diagnostic candidates for treating pain, by identifying  
 XX genes that are differentially expressed in a model of neuropathic pain.

XX PS Claim 1; SEQ ID NO 243; 173pp; English.

XX CC This invention relates to a novel method of detecting a pain response in  
 CC a cell which comprises determining the expression level in a test cell of  
 CC at least one nucleic acid molecule and comparing the expression level to  
 CC a level in an animal model of pain, where similar or identical expression  
 CC levels indicate a pain response in the test cell. The invention may be  
 CC useful for the development of compounds with an analgesic, antiaddictive,  
 CC nootropic, anticonvulsant, vasotropic, neuroprotective, tranquilizer,  
 CC antiasthmatic, antirheumatic, antiarthritic, osteopathic,  
 CC ophthalmological, antiinflammatory, antipruritic, dermatological,  
 CC antiulcer, gastrointestinal-Gen., nephrotropic, gynecological,  
 CC hepatotropic, antiparkinsonian, neuroleptic or laxative activity whilst

the disclosed sequences may prove useful for gene therapy. The methods  
 and compositions of the present invention are useful for identifying  
 agonists and antagonists for the gene or gene products as potential  
 therapeutic and diagnostic candidates for treating pain, including  
 neuropathic pain, nociceptive pain, chronic pain, inflammatory pain, pain  
 associated with cancer, and pain associated with rheumatic disease, and  
 also for addiction, seizure, stroke, ischemia, a neurodegenerative  
 disorder, anxiety, depression, headache, asthma, rheumatic disease,  
 osteoarthritis, retinopathy, inflammatory eye disorders, pruritus, ulcer,  
 gastric lesions, uncontrollable urination, an inflammatory or unstable  
 bladder disorder, inflammatory bowel disease, irritable bowel syndrome  
 (IBS), irritable bowel disease (IBD), gastroesophageal reflux disease  
 (GERD), functional dyspepsia, functional chest pain of presumed  
 esophageal origin, functional dysphagia, non-cardiac chest pain,  
 symptomatic gastroesophageal disease, gastritis, aerophagia, functional  
 constipation, functional diarrhea, borbulence, chronic functional  
 abdominal pain, recurrent abdominal pain (RAP), function abdominal  
 bloating, functional biliary pain, functional incontinence, functional  
 ano-rectal disorder, cholecystalgia, interstitial cystitis, dysmenorrhea,  
 or dyspareunia. They can also be used diagnosing or treating Alzheimer's  
 disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's  
 disease and schizophrenia. The present sequence is that of a human gene  
 whose expression level analysed in the method of the invention.

XX SQ Sequence 386 BP; 87 A; 110 C; 98 G; 91 T; 0 U; 0 Other;

Alignment Scores:

|                        |       |               |     |
|------------------------|-------|---------------|-----|
| Pred. No.:             | 5.36  | Length:       | 386 |
| Score:                 | 70.50 | Matches:      | 15  |
| Percent Similarity:    | 58.1% | Conservative: | 3   |
| Best Local Similarity: | 48.4% | Mismatches:   | 12  |
| Query Match:           | 23.7% | Indels:       | 1   |
| DB:                    | 14    | Gaps:         | 1   |

US-10-628-525A-35 (1-58) x ADX25897 (1-386)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProile 25  
 DB 134 TCACCGGCCCTTAAGCTGGAGCCGCCGAGAAAGACATCGACCTGTACCACCATGT 193

QY 26 ThrSerLysMetTrp---SerSerLeuValMet 35  
 DB 194 ACATGGAGGCCCTGGTGAGCTCTTTGACAATC 226

RESULT 17  
 ADE58674/c  
 ID ADE58674 standard; DNA; 460 BP.

XX AC ADE58674;

XX DT 29-JAN-2004 (first entry)

XX DE Rat gene AA799889, SEQ ID NO 4550.

XX KW Rat; ds; gene; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO ) GEN HOSPITAL CORP.  
 XX (FARB ) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX WPI; 2003-268312/26.  
 DR GENBANK; AA799889.  
 XX  
 XX New composition comprising two or more isolated polypeptides, useful for  
 FT preparing a medicament for treating pain in an animal.  
 XX  
 XX Claim 1; Page; 1017pp; English.  
 XX  
 CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat DNA (shown in Table 2 of the  
 CC specification) which encodes one of the polypeptides of the invention  
 CC which is differentially expressed during pain. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 460 BP; 155 A; 87 C; 86 G; 131 T; 0 U; 1 Other;

Alignment Scores:  
 Pred. No.: 6.78 Length: 460  
 Score: 70.50 Matches: 16  
 Percent Similarity: 55.6% Conservative: 9  
 Best Local Similarity: 35.6% Mismatches: 19  
 Query Match: 23.7% Indels: 1  
 DB: 10 Gaps: 1

US-10-628-525A-35 (1-58) x ADE58674 (1-460)

QY 11 TrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrp 30  
 Db 352 TGGCAGGTTCGGGGATTAGATAGGAGAGAGAGGGGATCACCCTACCTACTCCCATGTGG 293  
 QY 31 SerSerLeuValMetLysGlnThrLysLysValAlaHisSerAlaLysPheArgValMet 50  
 Db 292 ACAGGTTTAACCTTACCAGACGCGCTCATATCAGT--AGTGCAGCCTTGCTTATAC 236

QY 51 AlaValAsnSerGlu 55  
 Db 235 CAAGTGAACCTCAGAA 221

RESULT 18  
 ADE58670/c  
 ID ADE58670 standard; DNA; 460 BP.  
 XX  
 AC ADE58670;  
 XX

DT 29-JAN-2004 (first entry)  
 XX  
 DE Rat gene AA799889, SEQ ID NO 4546.  
 XX

KW Rat; ds; gene; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNI; Chung.  
 XX  
 OS Rattus norvegicus.  
 XX  
 PN WO2003016475-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 XX 14-AUG-2002; 2002WO-US025765.  
 PF  
 XX 14-AUG-2001; 2001US-0312147P.  
 PR  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX  
 XX Woolf C, D'urso D, Befort K, Costigan M;  
 XX  
 DR WPI; 2003-268312/26.  
 DR GENBANK; AA799889.  
 XX  
 XX New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX  
 XX Claim 1; Page; 1017pp; English.  
 XX  
 CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat DNA (shown in Table 2 of the  
 CC specification) which encodes one of the polypeptides of the invention  
 CC which is differentially expressed during pain. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 460 BP; 155 A; 87 C; 86 G; 131 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 6.78 Length: 460  
 Score: 70.50 Matches: 16  
 Percent Similarity: 55.6% Conservative: 9  
 Best Local Similarity: 35.6% Mismatches: 19  
 Query Match: 23.7% Indels: 1  
 DB: 10 Gaps: 1

US-10-628-525A-35 (1-58) x ADE58670 (1-460)

QY 11 TrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrp 30  
 Db 352 TGGCAGGTTCGGGGATTAGATAGGAGAGAGGGGATCACCCTACCTACTCCCATGTGG 293



CC acids, nucleic acids, vitamins, saccharides and organic acids,  
 CC particularly L-lysine. The present sequence is a nucleic acid described  
 CC in the exemplification of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from the European Patent Office

XX  
 SQ Sequence 1062 BP; 271 A; 266 C; 255 G; 270 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 28.1 Length: 1062  
 Score: 69.50 Matches: 17  
 Percent Similarity: 49.0% Conservatives: 7  
 Best Local Similarity: 34.7% Mismatches: 16  
 Query Match: 23.4% Indels: 9  
 DB: 5 Gaps: 2

US-10-628-525A-35 (1-58) x AAH6383 (1-1062)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 DB 296 ATGTCATCCTTTTGGCGGATTCA-----ATGGACTCAAGCGCGCT 255  
 QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 DB 254 TGTACAGATCCGACTACT-----TGGAGCTCAATGTTGTTCAAAATACCCAAAGCGCA 204  
 QY 41 ValAlaHisSerAlaLysPheArgVal 49  
 DB 203 ACTGCTAATTCACGAGTTTAGATTG 177

RESULT 21

ID ADL65758/c  
 ID ADL65758 standard; DNA; 1192 BP.  
 XX  
 AC ADL65758;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE C. glutamicum RXA-associated DNA #58.  
 XX  
 KW fine chemical production; lysine production; nucleotide; nucleoside;  
 KW lipid; fatty acid; diol; carbohydrate; aromatic compound; vitamin;  
 KW co-factor; enzyme; food; animal feed; cosmetic; pharmaceutical; gene; ds.  
 XX  
 OS Corynebacterium glutamicum.  
 XX  
 PN DE10154177-A1.

PD 08-MAY-2003.

PF 05-NOV-2001; 2001DE-01054177.

PR 05-NOV-2001; 2001DE-01054177.

XX (BADI ) BASF AG.

XX Zelder O, Pompejus M, Schroeder H, Kroeger B, Klopprogge C;  
 PI Habershauer G;

XX WPI; 2003-431900/41.

DR P-PSDB; ADL65759.

PT New nucleic acid encoding variant forms of marker and fine chemical-  
 PT production proteins, useful for production of fine chemicals,  
 PT specifically lysine, in microorganisms.

XX Claim 1; Page; 20pp; German.

XX This invention describes novel polynucleotides that encode protein  
 CC markers and fine chemical-production proteins from Corynebacterium  
 CC glutamicum. The polynucleotides are isolated from a nucleic acid library  
 CC of C. glutamicum then mutated at the specified positions, cloned and  
 CC expressed by standard methods. Cells, especially Corynebacterium

CC glutamicum, containing vectors that express the polynucleotides are used  
 CC for production of fine chemicals, preferably amino acids and specifically  
 CC lysine, but more generally nucleotides, nucleosides, lipids, fatty acids,  
 CC diols, carbohydrates, aromatic compounds, vitamins, co-factors and  
 CC enzymes. These are useful in the food, animal feed, cosmetics and  
 CC pharmaceutical industries. The polynucleotides, optionally as primers and  
 CC probes, can also be used for identification and classification of C.  
 CC glutamicum and related species, e.g. for diagnosis, for genomic mapping,  
 CC functional or evolutionary studies, gene manipulation and modulation of  
 CC metabolic activity. Cells that containing the polynucleotides of the  
 CC invention may produce fine chemicals in better yields, with higher  
 CC productivity and/or more efficiently. NOTE: This sequence is not  
 CC represented in the printed specification but is available in electronic  
 CC format. The sequence represented in this record has been obtained from  
 CC WO2003046123.

XX  
 SQ Sequence 1192 BP; 323 A; 283 C; 285 G; 301 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 32.8 Length: 1192  
 Score: 69.50 Matches: 17  
 Percent Similarity: 49.0% Conservatives: 7  
 Best Local Similarity: 34.7% Mismatches: 16  
 Query Match: 23.4% Indels: 9  
 DB: 11 Gaps: 2

US-10-628-525A-35 (1-58) x ADL65758 (1-1192)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 DB 396 ATGTCATCCTTTTGGCGGATTCA-----ATGGACTCAAGCGCGCT 355  
 QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 DB 354 TGTACAGATCCGACTACT-----TGGAGCTCAATGTTGTTCAAAATACCCAAAGCGCA 304  
 QY 41 ValAlaHisSerAlaLysPheArgVal 49  
 DB 303 ACTGCTAATTCACGAGTTTAGATTG 277

RESULT 22

AAAF71202  
 ID AAFA71202 standard; DNA; 1539 BP.  
 XX  
 AC AAFA71202;  
 XX  
 DT 30-APR-2001 (first entry)  
 XX  
 DE Corynebacterium glutamicum HA protein nucleotide sequence SEQ ID NO:129.  
 KW Corynebacterium glutamicum; homeostasis; adaptation; HA protein;  
 KW fine chemical production; organic acid; proteinogenic amino acid;  
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;  
 KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;  
 KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;  
 KW diagnosis; Corynebacterium diphtheriae; genetic engineering;  
 KW Brevibacterium; environmental condition; ds.  
 XX  
 OS Corynebacterium glutamicum.  
 XX  
 PN WO200100842-A2.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 23-JUN-2000; 2000WO-IB000911.  
 XX  
 XX 25-JUN-1999; 99US-0141031P.  
 PR 08-JUL-1999; 99DE-01031636.  
 PR 09-JUL-1999; 99DE-0103125.  
 PR 09-JUL-1999; 99DE-0103126.  
 PR 09-JUL-1999; 99DE-0103127.  
 PR 09-JUL-1999; 99DE-0103128.  
 PR 09-JUL-1999; 99DE-0103129.









PT identifying nucleic acid sequences comprising methylated CpG site and  
PT down-regulated in diseased cells and comparing its expression level with  
XX demethylated nucleic acid.

PS Claim 11; SEQ ID NO 34; 27bp; English.

XX The invention relates to a method (M1) for identifying one or more  
CC nucleic acid sequences useful as a biomarker for a disease to be  
CC detected. (M1) involves identifying nucleic acid sequences comprising  
CC methylated CpG site in promoter-first exon region and that are down-  
CC regulated in diseased cells, comparing expression level of nucleic acid  
CC sequences with that of demethylated nucleic acid sequences and  
CC identifying nucleic acid sequences exhibiting increase in expression  
CC after demethylation. Also described: (1) detecting (M2) the presence or  
CC stage of a disease in a subject, which involves determining the degree of  
CC methylation of one or more CpG sites on nucleic acid sequences in a  
CC biological sample obtained from the subject, and determining the presence  
CC of, predisposition to, or stage of the disease in the subject based on  
CC the degree of methylation; (2) monitoring the onset, progression, or  
CC regression of a disease in a subject; (3) determining the efficacy of a  
CC test compound for inhibiting a disease in a subject; and (4) a kit (I)  
CC useful for diagnosis, prognosis, staging, monitoring, and therapeutic  
CC treatment of a disease. (M1) is useful for identifying one or more  
CC nucleic acid sequences useful as a biomarker for a disease to be  
CC detected, where the nucleic acid sequences are useful for detecting, the  
CC presence or stage of a disease such as cancer e.g. colorectal cancer in a  
CC subject. The present sequence represents a specifically claimed human  
CC genomic sequence for use in the method of the invention. Note - The  
CC sequence data for this patent is not represented in the printed  
CC specification but was obtained in electronic format from the USPTO web  
CC site.

SQ Sequence 383432 BP; 113010 A; 69169 C; 74959 G; 126294 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 2.18e+04 Length: 110000  
Score: 68.00 Matches: 14  
Percent Similarity: 60.0% Conservative: 7  
Best Local Similarity: 40.0% Mismatches: 14  
Query Match: 22.9% Indels: 0  
DB: 14 Gaps: 0

US-10-628-525A-35 (1-58) x AEA61124\_0 (1-110000)

QY 14 ArgilleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSerSerLeu 33  
Db 72417 CGTATTATATTCTCCCTGCCCTCTTCTCCCTTGGCACAATAAATCTGGCTT 72476

QY 34 ValMetLysGlnThrLysLysValAlaHisSerAlaLysPheArg 48  
Db 72477 TTAATTATCCACTTGGAAAGTGCTCATATTATTGTCTATCGC 72521

RESULT 28  
ACH47744  
ID ACH47744 standard; cDNA; 421 BP.

XX ACH47744;

XX 13-OCT-2003 (first entry)

XX Human infant brain cDNA #1807.

XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
KW Genome mapping; biodiversity; genetic disorder.

XX Homo sapiens.

XX US2003073623-A1.

XX 17-APR-2003.

XX 30-JUL-2001; 2001US-00918995.

XX

PR 30-JUL-2001; 2001US-00918995.

XX (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.

XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

XX WPI; 2003-615964/58.

XX New polynucleotide sequences obtained from various cDNA libraries, useful  
PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
PT mapping, in the recombinant production of protein, or in generating  
PT antisense DNA or RNA.

XX Claim 1; SEQ ID NO 34956; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of  
CC 38043 cDNA sequences, appearing as ACH2789-ACH50831, whose sequence was  
CC determined by the technique of SBH (sequencing by hybridisation). Also  
CC included is a purified polypeptide comprising a sequence corresponding to  
CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
CC are useful in diagnostics as expressed sequence tags (EST) for  
CC identifying expressed genes or for physical mapping of the human genome,  
CC in forensics, in assessing biodiversity, or in identifying mutations  
CC responsible for genetic disorders and other traits. The nucleotide  
CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
CC for chromosome and gene mapping, in the recombinant production of  
CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
CC is useful for generating antibodies specific for it. The present sequence  
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030073623

SQ Sequence 421 BP; 120 A; 98 C; 92 G; 111 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 15.2 Length: 421  
Score: 67.50 Matches: 15  
Percent Similarity: 49.1% Conservative: 11  
Best Local Similarity: 28.3% Mismatches: 18  
Query Match: 22.7% Indels: 9  
DB: 9 Gaps: 1

US-10-628-525A-35 (1-58) x ACH47744 (1-421)

QY 1 MetAlaGlnIleLeuAla-----ProSerThrGlnTrp 11

Db 261 ATGGGAGAGATCTTTCCACCTCTTAATGAACCCGACGCTGTGCCAAAGTTTGTGTGG 320

QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSer 31

Db 321 AAAATGCCAAGAACTTCCCTCAGTGTGTCTAGATAATCTCTGCCAAGAGTGTGGAT 380

QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44

Db 381 GGTATACTGCTAAAGACTTCATTGTTGGAGAGTCACTCA 419

# RESULT 29

AAI63931

ID AAI63931 standard; cDNA; 939 BP.

XX AAI63931;

XX 22-OCT-2001 (first entry)

XX Human polynucleotide SEQ ID NO 139.

XX Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;  
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;

fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;  
neuroprotective; antiallergic; hepatotropic; antidiabetic;  
antiinflammatory; antituberc; vulnerary; anticonvulsant; antibacterial;  
antiparasitic; cardiant; gene therapy; cancer; immune disorder;  
cardiovascular disorder; neurological disease; infection; human; ss.

Homo sapiens.

W0200155308-A2.

02-AUG-2001.

17-JAN-2001; 2001WO-US001309.

31-JAN-2000; 2000US-0179065P.

04-FEB-2000; 2000US-0180628P.

24-FEB-2000; 2000US-0184664P.

02-MAR-2000; 2000US-0186350P.

16-MAR-2000; 2000US-0189874P.

17-MAR-2000; 2000US-0190076P.

18-APR-2000; 2000US-0198123P.

19-MAY-2000; 2000US-0205515P.

07-JUN-2000; 2000US-0209467P.

28-JUN-2000; 2000US-0214886P.

30-JUN-2000; 2000US-0215135P.

07-JUL-2000; 2000US-0216647P.

07-JUL-2000; 2000US-0216880P.

11-JUL-2000; 2000US-0217487P.

11-JUL-2000; 2000US-0217496P.

14-JUL-2000; 2000US-0218290P.

26-JUL-2000; 2000US-0220963P.

26-JUL-2000; 2000US-0220964P.

14-AUG-2000; 2000US-0224518P.

14-AUG-2000; 2000US-0224519P.

14-AUG-2000; 2000US-0225213P.

14-AUG-2000; 2000US-0225214P.

14-AUG-2000; 2000US-0225266P.

14-AUG-2000; 2000US-0225267P.

14-AUG-2000; 2000US-0225268P.

14-AUG-2000; 2000US-0225270P.

14-AUG-2000; 2000US-0225447P.

14-AUG-2000; 2000US-0225757P.

14-AUG-2000; 2000US-0225758P.

14-AUG-2000; 2000US-0225759P.

18-AUG-2000; 2000US-0226279P.

22-AUG-2000; 2000US-0226681P.

22-AUG-2000; 2000US-0226686P.

22-AUG-2000; 2000US-0227182P.

23-AUG-2000; 2000US-0227009P.

30-AUG-2000; 2000US-0228242P.

01-SEP-2000; 2000US-0229287P.

01-SEP-2000; 2000US-0229343P.

01-SEP-2000; 2000US-0229344P.

01-SEP-2000; 2000US-0229345P.

05-SEP-2000; 2000US-0229509P.

05-SEP-2000; 2000US-0229513P.

06-SEP-2000; 2000US-0230437P.

06-SEP-2000; 2000US-0230438P.

08-SEP-2000; 2000US-0231242P.

08-SEP-2000; 2000US-0231243P.

08-SEP-2000; 2000US-0231244P.

08-SEP-2000; 2000US-0231413P.

08-SEP-2000; 2000US-0231414P.

08-SEP-2000; 2000US-0232080P.

12-SEP-2000; 2000US-0231968P.

14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236377P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239335P.  
PR 13-OCT-2000; 2000US-0239337P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 01-NOV-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 01-DEC-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 06-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.

PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-488781/53.  
XX P-PSDB; AAM43625.  
DR  
XX New isolated nucleic acids and polypeptides, useful for diagnosing,  
PT treating and/or preventing human diseases and disorders.  
XX  
XX Claim 1; SEQ ID NO 139; 664pp + Sequence Listing; English.  
PS  
XX The invention relates to human polynucleotides (AAI63803-AAI64012) and  
CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating  
CC or ameliorating medical conditions e.g. by protein or gene therapy. The  
CC genes were isolated from a range of human tissues disclosed in the  
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists  
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,  
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,  
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or  
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,  
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,  
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d)  
CC wound healing; (e) neurological diseases e.g. cerebral anoxia and  
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
CC and parasitic infections. Note: The sequence data for this patent did not  
CC form part of the printed specification, but was obtained in electronic  
CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 939 BP; 246 A; 199 C; 216 G; 273 T; 0 U; 5 Other;

Alignment Scores:  
Pred. No.: 44.2 Length: 939  
Score: 67.50 Matches: 15  
Percent Similarity: 49.1% Conservative: 11  
Best Local Similarity: 28.3% Mismatches: 18  
Query Match: 22.7% Indels: 29  
DB: 4 Gaps: 1

US-10-628-525A-35 (1-58) x AAI63931 (1-939)

QY 1 MetAlaGlnIleLeuAla-----ProSerThrGlnTrp 11  
Db 159 ATGGGAGAGATCCTTCCCACTCTTAATGAACCGCGGTGTGCCAAAGTTTGGTGG 218  
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSer 31  
Db 219 AAATATGCAAGAACATCTCCCTCAGTGTGTGCTAGAATCTTGACCAAGAGTGTGGAT 278  
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44  
Db 279 GTATACCTGCTAAGAACTTCATTTGGGAAGTCACTCA 317

RESULT 30  
AAS31627  
ID AAS31627 standard; cDNA; 939 BP.  
XX  
AC AAS31627;  
XX  
DT 04-DEC-2001 (first entry)  
XX  
DE cDNA encoding novel human calcium-binding protein #51.  
KW Human; calcium-binding protein; calcium flux; neurological disease;  
KW immune dysfunction; digestive disorder; neoplastic disease;  
KW blood disorder; infectious disease; gene therapy; immunosuppressive;  
KW antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;

KW virucide; ss.  
XX  
OS Homo sapiens.  
XX WO200155304-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US001302.  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
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(HUMA-) HUMAN GENOME SCI INC.  
Rosen CA, Barash SC, Ruben SM;  
WPI; 2001-465568/50.  
P-PSDB; AAU19942.

Isolated nucleic acid molecule encoding a calcium-binding protein is used in preventing, treating or ameliorating a medical condition.

Claim 4; SEQ ID NO 61; 542pp; English.

The present invention relates to the isolation of novel human calcium-binding proteins (AAU19892-AAU19969), and cDNA and genomic sequences encoding for these proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases associated with aberrant calcium flux. Such disorders include neurological diseases (e.g. amyotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe combined immunodeficiency, SCID), digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit activities mediated by calcium-binding proteins. The polynucleotides of the invention are also useful in gene therapy. AAS31577-AAS31654 represent cDNA sequences encoding for the novel human calcium-binding proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

XX SQ Sequence 939 BP; 246 A; 199 C; 216 G; 273 T; 0 U; 5 Other;

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US-10-628-525A-35 (1-58) x AAS31627 (1-939)

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Search completed: April 1, 2006, 04:28:41  
Job time : 176.553 secs

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 15:18:57 ; Search time 935.32 Seconds  
(without alignments)  
2901.306 Million cell updates/sec

Title: US-10-628-525a-35

Perfect score: 297

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Searched: 41078325 seqs, 23393541228 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Database :

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2: gb.est2:\*  
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6: gb.est5:\*  
7: gb.est6:\*  
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11: gb.gss3:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 1

BE317833

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

ORIGIN

Alignment Scores

Qy

Db

Qy

Db

Qy

Db

RESULT 2

BE323583

LOCUS

DEFINITION

258 bp

mRNA

linear

EST 21-DEC-2000

NF059C04LF1022

Developing leaf

Medicago truncatula

cDNA clone

BE317833

BE317833

BE317833.2

GI:11960923

EST

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 258)

Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

Medicago truncatula leaf library

Unpublished (2000)

On Jul 14, 2000 this sequence version replaced gi:9191610.

Contact: May GD

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 224 6650

Fax: 580 224 6692

Email: gdmay@noble.org

Medicago Genome Initiative accession: MGI:S:21920

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/note="Vector: Lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."

2.11e-18

Length: 258

Matches: 47

Score: 223.00

Percent Similarity: 88.9%

Conservative: 1

Best Local Similarity: 87.0%

Mismatches: 6

Query Match: 75.1%

Indels: 0

DB: 2

Gaps: 0

US-10-628-525A-35 (1-58) x BE317833 (1-258)

1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20

3 ATGGCACAGATTTTGGCTCTTACAAAGTCTCAGGACAGAGTCAAAAATCTCTCCC 62

21 CysAlaThrProIleThrSerIysMetTrpSerSerLeuValMetLysGlnThrLysLys 40

63 GTTGCACTCCAACTCATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAA 122

41 ValAlaHisSerAlaLysPheArgValMetAlaValAenSer 54

123 GTCGCACCTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 164

BE323583

393 bp

mRNA

linear

EST 21-DEC-2000

NF016C08PL1F1055

Phosphate starved leaf

Medicago truncatula

cdna clone

NF016C08PL 5', mRNA sequence.

ACCESSION BE323583  
 VERSION BE323583.2 GI:11965726  
 KEYWORDS EST.  
 SOURCE Medicago truncatula  
 ORGANISM Medicago truncatula (barrel medic)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.  
 REFERENCE 1 (bases 1 to 393)  
 AUTHORS Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W., May, G.D., and Harrison, M.J.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library  
 JOURNAL Unpublished (2000)  
 COMMENT On Jul 14, 2000 this sequence version replaced gi:9197360.  
 Contact: Harrison MJ  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7325  
 Fax: 580 221 7380  
 Email: mjharrison@noble.org  
 Medicago Genome Initiative accession: MGI:S:22731  
 Insert Length: 792 Std Error: 0.00  
 Plate: 016 row: C column: 08  
 Seq primer: TCACACGAGAAACAGCTATGAC.  
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 Location/Qualifiers  
 /organism="Medicago truncatula"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3880"  
 /clone="NF016C08PL"  
 /tissue\_type="leaf"  
 /dev\_stage="trifoliolate"  
 /clone\_lib="Phosphate starved leaf"  
 /notes="Vector: Lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.69e-18 Length: 393  
 Score: 223.00 Matches: 47  
 Percent Similarity: 88.9% Conservative: 1  
 Best Local Similarity: 87.0% Mismatches: 6  
 Query Match: 75.1% Indels: 0  
 DB: 2 Gaps: 0  
 US-10-628-525A-35 (1-58) x BE323583 (1-393)  
 QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
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 Db 92 ATGGCACAGATTTGGCTCCTTCTACACAATGTGCGCAAGAAATCAGAAAATCTCTCCC 151  
 QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 |||||  
 Db 152 GTTGCACACTCATCTCATCAAGATGTGGAGTTCTTTGTTATGAACAACAAGAA 211  
 QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
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 Db 212 GTCGCAGTTCTGCTAAATTCAGAGTAATGCGAGTCAACTCT 253  
 RESULT 3  
 BQ140352  
 LOCUS NF034F04PHIP1043 Phoma-infected Medicago truncatula cdna clone  
 DEFINITION NF034F04PH 5', mRNA sequence.  
 ACCESSION BQ140352  
 VERSION BQ140352.1 GI:20276478

KEYWORDS EST.  
 SOURCE Medicago truncatula (barrel medic)  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.  
 REFERENCE 1 (bases 1 to 399)  
 AUTHORS Watson, B.S., Shin, H.-S., Lopez-Meyer, M., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Imman, J.T., Waugh, M.E., Sullivan, J.P., May, G.D., and Paiva, N.L.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula Phoma-infected library  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Paiva NL  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7317  
 Fax: 580 221 7380  
 Email: nlpaiva@noble.org  
 Insert Length: 399 Std Error: 0.00  
 Plate: 034 row: F column: 04  
 Seq primer: TCACACGAGAAACAGCTATGAC.  
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 Location/Qualifiers  
 /organism="Medicago truncatula"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3880"  
 /clone="NF034F04PH"  
 /tissue\_type="leaf"  
 /dev\_stage="Pathogen-induced, young trifoliolate"  
 /clone\_lib="Phoma-infected"  
 /notes="Vector: pBluescript SK(-); Young trifoliolate leaves of Medicago truncatula were excised and dip-inoculated in a spore suspension of Phoma medicaginis, and incubated in humid dishes. Pools of leaves were harvested at 0, 15, and 30 minutes and 1, 2, 3, 6, 14, 24, 48, 72, and 96 hours, and used to prepare total RNA. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using ExAest helper phage and the E. coli strain XL1-Blue MRP' (Stratagene). Excised plasmids were plated using SOLR cells."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.77e-18 Length: 399  
 Score: 223.00 Matches: 47  
 Percent Similarity: 88.9% Conservative: 1  
 Best Local Similarity: 87.0% Mismatches: 6  
 Query Match: 75.1% Indels: 0  
 DB: 3 Gaps: 0  
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 QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
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 Db 97 ATGGCACAGATTTGGCTCCTTCTACACAATGTGCGCAAGAAATCAGAAAATCTCTCCC 156  
 QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 |||||  
 Db 157 GTTGCACACTCATCTCATCAAGATGTGGAGTTCTTTGTTATGAACAACAAGAA 216  
 QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
 |||||  
 Db 217 GTCGCAGTTCTGCTAAATTCAGAGTAATGCGAGTCAACTCT 258  
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BE323195
LOCUS       BE323195               428 bp     mRNA     linear     EST 21-DEC-2000
DEFINITION   clone NF001G02PL1F1008 Phosphate starved leaf Medicago truncatula cDNA
ACCESSION   BE323195
VERSION     BE323195
KEYWORDS    Medicago truncatula (barrel medic)
SOURCE      Medicago truncatula
ORGANISM    Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE    1 (bases 1 to 428)
AUTHORS     Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
            Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.
TITLE       Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula phosphate-starved leaf library
JOURNAL     Unpublished (2000)
COMMENT     On Jul 14, 2000 this sequence version replaced gi:9196972.
            Contact: Harrison MJ
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7325
            Fax: 580 221 7380
            Email: mjharrison@noble.org
            Medicago Genome Initiative accession: MGI:S:19371
            Insert length: 701 Std Error: 0.00
            Plate: 001 row: G column: 02
            Seq primer: TCACACAGGAACAGCTATGAC.
            Location/Qualifiers
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        /organism="Medicago truncatula"
        /mol_type="mRNA"
        /db_xref="taxon:3880"
        /clone="NF001G02PL"
        /tissue_type="leaf"
        /dev_stage="trifoliolate"
        /clone_lib="Phosphate starved leaf"
        /note="Vector: Lambda Zap; At the trifoliolate stage, M.
            truncatula plants were transplanted to phosphate-free sand
            and grown for a further 30 days. During this 30 day
            period, the plants were fertilized twice weekly with 1/2
            Hoaglands solution containing only 20uM potassium
            phosphate. RNA was prepared from above ground tissues."
ORIGIN
Alignment Scores:
Pred. No.:      4,14e-18      Length:      428
Score:          223.00      Matches:      47
Percent Similarity: 88.9%      Conservative: 1
Best Local Similarity: 87.0%      Mismatches: 6
Query Match:    75.1%      Indels:      0
DB:             2           Gaps:         0

US-10-628-525A-35 (1-58) x BE323195 (1-428)

QY      1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIlySerPro 20
DB      123 ATGGCACAGATTTGGCTCTTCTACAAATGTCAGGCAAGAATCACAAAAATCTCTCC 182
QY      21 CysAlaThrProIleThrSerIlyMetTrpSerSerLeuValMetIlyGlnThrIlyLys 40
DB      193 GTTGCACCTCCATCTCATCAAGAATGTGGAGTTCTTTGGTTATGAAACAAACAGAAA 242
QY      41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
DB      243 GTGGCAGCTGTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 284

RESULT 5
BF521090
LOCUS       BF521090               447 bp     mRNA     linear     EST 08-DEC-2000
DEFINITION   EST458564 DSIL Medicago truncatula cDNA clone pDSIL-41114, mRNA
sequence.
ACCESSION   BF521090
VERSION     BF521090.1 GI:11609773
KEYWORDS    Medicago truncatula (barrel medic)
SOURCE      Medicago truncatula
ORGANISM    Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE    1 (bases 1 to 447)
AUTHORS     Fedorova, M., Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, G.S.,
            Peng, H., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B.,
            Hansen, T.S., Holt, J.E. and Fraser, C.M.
TITLE       ESTs from leaves of Medicago truncatula after inoculation with
            Colletotrichum trifolii
JOURNAL     Unpublished (2000)
COMMENT     Contact: Deborah A. Samac
            Department of Plant Pathology
            University of Minnesota
            495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
            Tel: 612 625 1243
            Fax: 651 649 5058
            Email: debbys@umn.edu
            University of Minnesota name: M278533e
            TIGR sequence name: MTPDD55TK
            More information is available at: http://chrysis.tamu.edu/medicago
            Seq primer: SKmod (CTA GAA CTA gtg gar cc).
            Location/Qualifiers
FEATURES             source
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        /mol_type="mRNA"
        /cultivar="genotype Al7"
        /db_xref="taxon:3880"
        /clone="pDSIL-41114"
        /tissue_type="leaves infected with Colletotrichum
            trifolii"
        /dev_stage="cotyledons and primary leaves harvested 5 and
            8 days after inoculation with Colletotrichum trifolii"
        /lab_host="E. coli strain XLOLR"
        /clone_lib="DSIL"
        /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
            XhoI; cDNA was prepared from polyA+ enriched RNA from
            cotyledons and primary leaves harvested 5 and 8 days after
            inoculation with Colletotrichum trifolii. The cDNA was
            directionally ligated into the Uni-ZAP XR vector from
            Stratagene and packaged using Gigapack III Gold packaging
            extracts. Plasmids containing cDNA inserts were excised
            from the recombinant lambda-ZAP phage using Ex-Aestit
            helper phage and propagated in XLOLR cells. Note: EST may
            be of fungal origin."
ORIGIN
Alignment Scores:
Pred. No.:      4,38e-18      Length:      447
Score:          223.00      Matches:      47
Percent Similarity: 88.9%      Conservative: 1
Best Local Similarity: 87.0%      Mismatches: 6
Query Match:    75.1%      Indels:      0
DB:             2           Gaps:         0

US-10-628-525A-35 (1-58) x BF521090 (1-447)

QY      1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIlySerPro 20
DB      90 ATGGCACAGATTTGGCTCTTCTACAAATGTCAGGCAAGAATCACAAAAATCTCTCC 149
QY      21 CysAlaThrProIleThrSerIlyMetTrpSerSerLeuValMetIlyGlnThrIlyLys 40
DB      150 GTTGCACCTCCATCTCATCAAGAATGTGGAGTTCTTTGGTTATGAAACAAACAGAAA 209
QY      41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54

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Db      210 GTGCACGTTCTGCTAAATTCAGAGTAATGCAGTCAACTCT 251
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RBSULT 6
BE317419
LOCUS   BE317419
DEFINITION BE317419 454 bp mRNA linear EST 21-DEC-2000
          NF069A11LP.1 Developing leaf Medicago truncatula cDNA clone
          NF069A11LP 5', mRNA sequence.
ACCESSION BE317419
VERSION    BE317419.2 GI:11960851
KEYWORDS   EST.
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula

REFERENCE
AUTHORS   Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
          Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
          Medicago truncatula leaf library
JOURNAL   Unpublished (2000)
COMMENT   On Jul 14, 2000 this sequence version replaced gi:9191196.
          Contact: May GD
          Plant Biology Division
          The Samuel Roberts Noble Foundation
          2510 Sam Noble Parkway, Ardmore, OK 73402, USA
          Tel: 580 224 6650
          Fax: 580 224 6692
          Email: gdmay@noble.org
          Medicago Genome Initiative accession: MGI:S:21261
          Insert Length: 740 Std Error: 0.00
          Plate: 069 row: A column: 11
          Seq primer: TCACACAGGAACAGCTATGAC.
          Location/Qualifiers
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/tissue_type="leaf"
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/clone_lib="Developing leaf"
/notes="Vector: Lambda Zap; Contains a mixture of very
young, developing, mature and senescing leaves."
ORIGIN
Alignment Scores:
Pred. No.: 4,47e-18 Length: 454
Score: 223.00 Matches: 47
Percent Similarity: 88.9% Conservative: 1
Best Local Similarity: 87.0% Mismatches: 6
Query Match: 75.1% Indels: 0
DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BE317419 (1-454)
QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
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Db 72 ATGGCAGAGTTTGGCTCTCTACACAAATGTGAGGAGTCTTTGGTTATGAACAAACAGAGAA 131
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QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
|||||
Db 132 GTTGCAACTCCATCTCATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAGAA 191
|||||
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
|||||
Db 192 GTGCACGTTCTGCTAAATTCAGAGTAATGCAGTCAACTCT 233
|||||
RBSULT 7
AW689288
LOCUS   AW689288
DEFINITION AW689288 477 bp mRNA linear EST 15-JUN-2000
          NF039G07ST.5 Developing stem Medicago truncatula cDNA clone
          NF039G07ST 5', mRNA sequence.
ACCESSION AW689288
VERSION    AW689288.2 GI:11936565
KEYWORDS   EST.
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula

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DEFINITION NF017E08STIF1000 Developing stem Medicago truncatula cDNA clone
ACCESSION AW689288
VERSION    AW689288.1 GI:7564024
KEYWORDS   EST.
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
          Medicago.
REFERENCE   1 (bases 1 to 477)
AUTHORS     He, X.-Z., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A.,
          Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and
          Dixon, R.A.
TITLE       Expressed Sequence Tags from the Samuel Roberts Noble Foundation
          Medicago truncatula stem library
JOURNAL     Unpublished (2000)
COMMENT     Contact: Dixon RA
          Plant Biology Division
          The Samuel Roberts Noble Foundation
          2510 Sam Noble Parkway, Ardmore, OK 73402, USA
          Tel: 580 221 7302
          Fax: 580 221 7380
          Email: radixon@noble.org
          Insert Length: 477 Std Error: 0.00
          Plate: 017 row: E column: 08
          Seq primer: TCACACAGGAACAGCTATGAC.
          Location/Qualifiers
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/tissue_type="stem"
/dev_stage="Pooled developmental"
/clone_lib="Developing stem"
/notes="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"
ORIGIN
Alignment Scores:
Pred. No.: 4,78e-18 Length: 477
Score: 223.00 Matches: 47
Percent Similarity: 88.9% Conservative: 1
Best Local Similarity: 87.0% Mismatches: 6
Query Match: 75.1% Indels: 0
DB: 1 Gaps: 0

US-10-628-525A-35 (1-58) x AW689288 (1-477)
QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
|||||
Db 62 ATGGCAGAGTTTGGCTCTCTACACAAATGTGAGGAGTCTTTGGTTATGAACAAACAGAGAA 131
|||||
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
|||||
Db 122 GTTGCAACTCCATCTCATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAGAA 191
|||||
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
|||||
Db 182 GTGCACGTTCTGCTAAATTCAGAGTAATGCAGTCAACTCT 233
|||||
RBSULT 8
AW690855
LOCUS   AW690855
DEFINITION AW690855 486 bp mRNA linear EST 21-DEC-2000
          NF039G07STIF1000 Developing stem Medicago truncatula cDNA clone
          NF039G07ST 5', mRNA sequence.
ACCESSION AW690855
VERSION    AW690855.2 GI:11936565
KEYWORDS   EST.
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

REFERENCE 1 (bases 1 to 486)  
AUTHORS He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon,R.A.

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library

JOURNAL Unpublished (2000)  
COMMENT On Apr 14, 2000 this sequence version replaced gi:7565679.

Contact: Dixon RA  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7302  
Fax: 580 221 7380  
Email: radixon@noble.org  
Insert Length: 692 Std Error: 0.00  
Plate: 039 row: G column: 07  
Seq primer: TCACACGAGAAACAGCTATGAC.

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/note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"

ORIGIN

Alignment Scores:  
Pred. No.: 4,9e-18 Length: 486  
Score: 223.00 Matches: 47  
Percent Similarity: 88.9% Conservative: 1  
Best Local Similarity: 87.0% Mismatches: 6  
Query Match: 75.1% Indels: 0  
DB: 1 Gaps: 0

US-10-628-525A-35 (1-58) x AW690855 (1-486)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20  
Db 66 ATGGCACAGATTGGCTCTTACACAATGTCAGGCAAGAAATCACAAAAATCTCTCCC 125  
QY 21 CysAlaThrProIleThrSerIysMetTrpSerSerLeuValMetIysGlnThrIysLys 40  
Db 126 GTTGCACACTCCAAATCTCATCAAGATGTGGAGTTCTTTGGTTATGAAACAAACAGAAA 185  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
Db 186 GTTCGACGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 227

RESULT 9  
BQ140918  
LOCUS BQ140918 488 bp mRNA linear EST 26-APR-2002  
DEFINITION NF055A10PH1F1081 Phoma-infected Medicago truncatula cDNA clone  
ACCESSION BQ140918  
VERSION BQ140918.1 GI:20277044  
KEYWORDS EST.  
SOURCE Medicago truncatula (barrel medic)  
ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

REFERENCE 1 (bases 1 to 488)  
AUTHORS Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,

TITLE

JOURNAL  
COMMENT

Gonzales,R.A., Bell,C.J., Inman,J.T., Waugh,M.E., Sullivan,J.P., May,G.D. and Paiva,N.L.  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula Phoma-infected library  
Unpublished (2002)  
Contact: Paiva NL  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7317  
Fax: 580 221 7380  
Email: nlpaiva@noble.org  
Insert Length: 488 Std Error: 0.00  
Plate: 055 row: A column: 10  
Seq primer: TCACACGAGAAACAGCTATGAC.

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/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"  
/clone="NF055A10PH"  
/tissue\_type="leaf"  
/dev\_stage="Pathogen-induced, young trifoliolate"  
/clone\_lib="Phoma-infected"  
/note="Vector: pBluescript SK(-); Young trifoliolate leaves of Medicago truncatula were excised and dip-inoculated in a spore suspension of Phoma medicaginis, and incubated in humid dishes. Pools of leaves were harvested at 0, 15, and 30 minutes and 1, 2, 3, 6, 14, 24, 48, 72, and 96, hours, and used to prepare total RNA. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using ExAssist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

ORIGIN

Alignment Scores:  
Pred. No.: 4,92e-18 Length: 488  
Score: 223.00 Matches: 47  
Percent Similarity: 88.9% Conservative: 1  
Best Local Similarity: 87.0% Mismatches: 6  
Query Match: 75.1% Indels: 0  
DB: 3 Gaps: 0

US-10-628-525A-35 (1-58) x BQ140918 (1-488)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20  
Db 88 ATGGCACAGATTGGCTCTTACACAATGTCAGGCAAGAAATCACAAAAATCTCTCCC 147  
QY 21 CysAlaThrProIleThrSerIysMetTrpSerSerLeuValMetIysGlnThrIysLys 40  
Db 148 GTTGCACACTCCAAATCTCATCAAGATGTGGAGTTCTTTGGTTATGAAACAAACAGAAA 207  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
Db 208 GTTCGACGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 249

RESULT 10  
BE323101  
LOCUS BE323101 492 bp mRNA linear EST 21-DEC-2000  
DEFINITION NF004A10PL1F1069 Phosphate starved leaf Medicago truncatula cDNA clone NF004A10PL 5', mRNA sequence.  
ACCESSION BE323101  
VERSION BE323101.2 GI:11967028  
KEYWORDS EST.  
SOURCE Medicago truncatula (barrel medic)  
ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 492)  
 REFERENCE  
 AUTHORS Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library  
 JOURNAL Medicago truncatula leaf library  
 COMMENT Unpublished (2000)  
 On Jul 14, 2000 this sequence version replaced gi:9196794.

Contact: Harrison MJ

Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7325  
 Fax: 580 221 7380

Email: mjharrison@noble.org

Medicago Genome Initiative accession: MGI:S:20027

Insert Length: 693 Std Error: 0.00

Plate: 004 row: A column: 10

Seq primer: TCACACGAGAAACAGCTATGAC.

Location/Qualifiers

1..492

/organism="Medicago truncatula"

/mol\_type="mRNA"

/db\_xref="taxon:3880"

/clone="NF004A10PL"

/tissue\_type="leaf"

/dev\_stage="trifoliolate"

/clone\_lib="phosphate starved leaf"

/notes="Vector: Lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues."

ORIGIN

Alignment Scores:

Pred. No.: 4,98e-18 Length: 492

Score: 223.00 Matches: 47

Percent Similarity: 88.9% Conservatives: 1

Best Local Similarity: 87.0% Mismatches: 6

Query Match: 75.1% Indels: 0

DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BE323101 (1-492)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20

DB 75 ATGGCAGAGATTTGGCTCTTCTACACAATGTGCGCAAGATCACAAAAATCTCTCCC 134

QY 21 CyeAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40

DB 135 GTTGCAGCTCCAAATCTCATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAA 194

QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54

DB 195 GTGCGAGTTCTGCTAAATTCAGAGTAATGCGAGTCACTCT 236

RESULT 11

BE316885

LOCUS

DEFINITION

NP056F08L1F1063 Developing leaf Medicago truncatula cDNA clone

ACCESSION

BE316885

VERSION

BE316885.2 GI:11960466

KEYWORDS

EST.

ORGANISM

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 541)

REFERENCE

AUTHORS Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library

JOURNAL Medicago truncatula leaf library

COMMENT Unpublished (2000)

On Jul 14, 2000 this sequence version replaced gi:9190662.

Contact: May GD

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

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Fax: 580 224 6692

Email: gdmay@noble.org

Medicago Genome Initiative accession: MGI:S:21086

Insert Length: 697 Std Error: 0.00

Plate: 056 row: F column: 08

Seq primer: TCACACGAGAAACAGCTATGAC.

Location/Qualifiers

1..541

/organism="Medicago truncatula"

/mol\_type="mRNA"

/db\_xref="taxon:3880"

/clone="NF056F08LP"

/tissue\_type="leaf"

/dev\_stage="Pooled developmental"

/clone\_lib="Developing leaf"

/note="Vector: Lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."

ORIGIN

Alignment Scores:

Pred. No.: 5,64e-18 Length: 541

Score: 223.00 Matches: 47

Percent Similarity: 88.9% Conservatives: 1

Best Local Similarity: 87.0% Mismatches: 6

Query Match: 75.1% Indels: 0

DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BE316885 (1-541)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20

DB 135 ATGGCAGAGATTTGGCTCTTCTACACAATGTGCGCAAGATCACAAAAATCTCTCCC 194

QY 21 CyeAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40

DB 195 GTTGCAGCTCCAAATCTCATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAA 254

QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54

DB 255 GTGCGAGTTCTGCTAAATTCAGAGTAATGCGAGTCACTCT 296

RESULT 12

BE319151

LOCUS

DEFINITION

NP045C12LF1087 Developing leaf Medicago truncatula cDNA clone

ACCESSION

BE319151

VERSION

BE319151.2 GI:11962557

KEYWORDS

EST.

ORGANISM

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 553)

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation



JOURNAL  
COMMENT

Medicago truncatula leaf library  
Unpublished (2000)  
On Jul 14, 2000 this sequence version replaced gi:9192928.  
Contact: May GD  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 224 6650  
Fax: 580 224 6692  
Email: gdmay@noble.org  
Medicago Genome Initiative accession: MGI:S:27435  
Insert Length: 719 Std Error: 0.00  
Plate: 045 row: C column: 12  
Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES  
source  
1..553  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"  
/clone="NF045C12LP"  
/tissue\_type="leaf"  
/dev\_stage="Pooled developmental"  
/clone\_lib="Developing leaf"  
/note="Vector: Lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."

ORIGIN  
Alignment Scores:  
Pred. No.: 5,81e-18 Length: 553  
Score: 223.00 Matches: 47  
Percent Similarity: 88.9% Conservative: 1  
Best Local Similarity: 87.0% Mismatches: 6  
Query Match: 75.1% Indels: 0  
DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BE319151 (1-553)  
QY 1 MetAlaGInileLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20  
Db 38 ATGGCACAGATTGGCTCTTCTACAAATGTCAGGCAAGATCACAATAATCTCTCCC 97  
QY 21 CysAlaThrProIleThrSerIysMetTrpSerSerLeuValMetIysGlnThrIysLys 40  
Db 98 GTTGCAACTCCAAATCTCATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAA 157  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
Db 158 GTGCGACGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 199

RESULT 13  
BE321453  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BE321453 562 bp mRNA linear EST 21-DEC-2000  
NF025E10IN1P1071 Insect herbivory Medicago truncatula cDNA clone  
BE321453  
BE321453 GI:11963305  
EST  
Medicago truncatula (barrel medic)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
1 (bases 1 to 562)  
Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,  
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Medicago truncatula insect herbivory library  
Unpublished (2000)  
On Jul 14, 2000 this sequence version replaced gi:9195146.  
Contact: Korth K  
Dept. of Plant Pathology  
University of Arkansas

217 Plant Science Building, Fayetteville, AR 72701, USA  
Tel: 501 575 5191  
Fax: 501 575 7601  
Email: kkorthe@comp.uark.edu  
Medicago Genome Initiative accession: MGI:S:20109  
Insert Length: 680 Std Error: 0.00  
Plate: 025 row: E column: 10  
Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES  
source  
1..562  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"  
/clone="NF025E10IN"  
/tissue\_type="local and systemic leaves"  
/dev\_stage="mature"  
/clone\_lib="Insect herbivory"  
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

ORIGIN  
Alignment Scores:  
Pred. No.: 5,94e-18 Length: 562  
Score: 223.00 Matches: 47  
Percent Similarity: 88.9% Conservative: 1  
Best Local Similarity: 87.0% Mismatches: 6  
Query Match: 75.1% Indels: 0  
DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BE321453 (1-562)  
QY 1 MetAlaGInileLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20  
Db 40 ATGGCACAGATTGGCTCTTCTACAAATGTCAGGCAAGATCACAATAATCTCTCCC 99  
QY 21 CysAlaThrProIleThrSerIysMetTrpSerSerLeuValMetIysGlnThrIysLys 40  
Db 100 GTTGCAACTCCAAATCTCATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAA 159  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
Db 160 GTGCGACGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 201

RESULT 14  
BF638827  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BF638827 570 bp mRNA linear EST 19-DEC-2000  
NF079C04PL1F1024 Phosphate starved leaf Medicago truncatula cDNA  
BF638827  
BF638827.1 GI:11902985  
EST  
Medicago truncatula (barrel medic)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
1 (bases 1 to 570)  
Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,  
Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Medicago truncatula phosphate-starved leaf library  
Unpublished (2000)  
Contact: Harrison MJ  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7325  
Fax: 580 221 7380  
Email: mjharrison@noble.org

Insert Length: 570 Std Error: 0.00  
 Plate: 079 row: C column: 04  
 Seq primer: TCACACGAAACAGCTATGAC.  
 Location/Qualifiers  
 1. .570  
 /organism="Medicago truncatula"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3880"  
 /clone="NF079C04Pl"  
 /tissue\_type="leaf"  
 /dev\_stage="trifoliolate"  
 /clone\_lib="Phosphate starved leaf"  
 /notes="Vector: Lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues."

## FEATURES

source

## ORIGIN

Alignment Scores:  
 Pred. No.: 6.05e-18 Length: 570  
 Score: 223.00 Matches: 47  
 Percent Similarity: 88.9% Conservative: 1  
 Best Local Similarity: 87.0% Mismatches: 6  
 Query Match: 75.1% Indels: 0  
 DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BF638827 (1-570)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 |||||  
 Db 45 ATGGCACAGATTTGGCTCTCTTACACAAATGTCAGGCAAGATCAAAAATCTCTCCC 104  
 |||||  
 QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 |||||  
 Db 105 GTTGCACCTCAATCTCATCAAGATGTGGAGTCTTTGGTTATGAACAACAAGAA 164  
 |||||  
 QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
 |||||  
 Db 165 GTGGCAGTTCGTCTAAATTCAGAGTAATGGCAGTCAACTCT 206  
 |||||

## RESULT 15

CX526728

LOCUS s13dNF26A05AT037.513968 Aphid-Infected Shoots Medicago truncatula  
 DEFINITION cDNA, mRNA sequence.

CX526728

CX526728.1 GI:57495447

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Medicago truncatula (barrel medic)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Medicago.

1 (bases 1 to 580)

Zhang, Y., Chekhovskiy, K., Scott, A.D., May, G.D. and Mian, M.A.R.

Medicago truncatula Aphid-Infected Shoot Expressed Sequence Tags  
 from the Samuel Roberts Noble Foundation - Center for Medicago  
 Genomics Research

Unpublished (2005)

Contact: May GD

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 224 6650

Fax: 580 224 6692

Email: gdmay@noble.org.

Location/Qualifiers

1. .580

/organism="Medicago truncatula"

/mol\_type="mRNA"

## FEATURES

source

/db\_xref="taxon:3880"  
 /tissue\_type="Aphid-Infected shoots"  
 /dev\_stage="harvested after 12, 24, 48, 72 and 96 hours of infestation"  
 /clone\_lib="Aphid-Infected Shoots"  
 /notes="Vector: Lambda Zap; Medicago truncatula plants were infested with 300 spotted-aphids each. Tissue samples were collected by harvesting the entire shoots from 13 plants after 12, 24, 48, 72 and 96 hours of infestation. Total RNA was extracted from each sampling time and equal amounts of total RNA were pooled together for mRNA purification for cDNA library construction. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the E. coli strain Xli-Blue MRF<sup>+</sup> (Stratagene). Excised plasmids were plated using SOLR cells."

## ORIGIN

Alignment Scores:  
 Pred. No.: 6.19e-18 Length: 580  
 Score: 223.00 Matches: 47  
 Percent Similarity: 88.9% Conservative: 1  
 Best Local Similarity: 87.0% Mismatches: 6  
 Query Match: 75.1% Indels: 0  
 DB: 8 Gaps: 0

US-10-628-525A-35 (1-58) x CX526728 (1-580)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 |||||  
 Db 97 ATGGCACAGATTTGGCTCTCTTACACAAATGTCAGGCAAGATCAAAAATCTCTCCC 156  
 |||||  
 QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 |||||  
 Db 157 GTTGCACCTCAATCTCATCAAGATGTGGAGTCTTTGGTTATGAACAACAAGAA 216  
 |||||  
 QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
 |||||  
 Db 217 GTGGCAGTTCGTCTAAATTCAGAGTAATGGCAGTCAACTCT 258  
 |||||

## RESULT 16

AW688380

LOCUS

DEFINITION

NF006G01STIF1000 Developing stem Medicago truncatula cDNA clone

NF006G01ST 5', mRNA sequence.

AW688380

AW688380.1 GI:7563116

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Medicago truncatula (barrel medic)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Medicago.

1 (bases 1 to 582)

He, X.-Z., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A.,  
 Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and  
 Dixon, R.A.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

Medicago truncatula stem library

Unpublished (2000)

Contact: Dixon RA

Plant Biology Division

The Samuel Roberts Noble Foundation

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Tel: 580 221 7302

Fax: 580 221 7380

Email: radixon@noble.org

Insert Length: 582 Std Error: 0.00

Plate: 006 row: G column: 01

Seq primer: TCACACAGGAACAGCTATGAC.

# FEATURES

Location/Qualifiers  
1..582  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"  
/clone="NF006G01ST"  
/issue\_type="stem"  
/dev\_stage="Pooled developmental"  
/clone\_lib="Developing stem"  
/note="Vector: Lambda Zap; Contains a mixture of  
internodal stem segments"

## ORIGIN

Alignment Scores:  
Pred. No.: 6,22e-18 Length: 582  
Score: 223.00 Matches: 47  
Percent Similarity: 88.9% Conservative: 1  
Best Local Similarity: 87.0% Mismatches: 6  
Query Match: 75.1% Indels: 0  
DB: 1 Gaps: 0

US-10-628-525A-35 (1-58) x AM688380 (1-582)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
DB 175 ATGGCACAGATTTGGCTCTCTACACAATGTCAGGCAAGATCAAAAATCTCTCCC 234  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
|||||  
DB 235 GTTGCACATCCCAATCTCATCAAGATGTGGAGTCTCTTTGGTTATGAAACAAACAGAA 294  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
|||||  
DB 295 GTTCGACGTTCTGCTAAATTCAGATTAATGGCAGTCAACTCT 336

## RESULT 17

BE321399  
LOCUS NF024E10IN1F1071 Insect herbivory Medicago truncatula cDNA clone  
DEFINITION NF024E10IN 5', mRNA sequence.

## ACCESSION

BE321399  
VERSION BE321399.2 GI:11963972  
KEYWORDS EST.  
SOURCE Medicago truncatula (barrel medic)  
ORGANISM Medicago truncatula

## REFERENCE

AUTHORS Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,  
Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.  
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
JOURNAL Medicago truncatula insect herbivory library  
COMMENT Unpublished (2000)

On Jul 14, 2000 this sequence version replaced gi:9195092.

## CONTACT

Contact: Korth K  
Dept. of Plant Pathology  
University of Arkansas  
217 Plant Science Building, Fayetteville, AR 72701, USA  
Tel: 501 575 5191  
Fax: 501 575 7601  
Email: korthcomp.uark.edu  
Medicago Genome Initiative accession: MGI:S:19989  
Insert Length: 678 Std Error: 0.00  
Plate: 024 row: E column: 10  
Seq primer: TCACACAGGAACAGCTATGAC.

## FEATURES

Location/Qualifiers  
1..597  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"

/clone="NF024E10IN"  
/tissue\_type="local and systemic leaves"  
/dev\_stage="mature"  
/clone\_lib="Insect herbivory"

/note="Vector: Lambda Zap; Library was produced from fully  
expanded M. truncatula leaves of plants fed upon by  
Spodoptera exigua (beet armyworm) for 24 hours. Systemic  
(undamaged leaves from injured plants) and wounded leaves  
were harvested and pooled."

## ORIGIN

Alignment Scores:  
Pred. No.: 6,43e-18 Length: 597  
Score: 223.00 Matches: 47  
Percent Similarity: 88.9% Conservative: 1  
Best Local Similarity: 87.0% Mismatches: 6  
Query Match: 75.1% Indels: 0  
DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BE321399 (1-597)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
DB 40 ATGGCACAGATTTGGCTCTCTACACAATGTCAGGCAAGATCAAAAATCTCTCCC 99  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
|||||  
DB 100 GTTGCACATCCCAATCTCATCAAGATGTGGAGTCTCTTTGGTTATGAAACAAACAGAA 159  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
|||||  
DB 160 GTTCGACGTTCTGCTAAATTCAGATTAATGGCAGTCAACTCT 201

## RESULT 18

BE3268095  
LOCUS NF117F10IN1F1091 Insect herbivory Medicago truncatula cDNA clone  
DEFINITION NF117F10IN 5', mRNA sequence.

## ACCESSION

BE3268095  
VERSION BE3268095.1 GI:14873701  
KEYWORDS EST.  
SOURCE Medicago truncatula (barrel medic)  
ORGANISM Medicago truncatula

## REFERENCE

AUTHORS Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,  
Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.  
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
JOURNAL Medicago truncatula insect herbivory library  
COMMENT Unpublished (2000)

## CONTACT

Dept. of Plant Pathology  
University of Arkansas  
217 Plant Science Building, Fayetteville, AR 72701, USA  
Tel: 501 575 5191  
Fax: 501 575 7601  
Email: korthcomp.uark.edu  
Insert Length: 614 Std Error: 0.00  
Plate: 117 row: F column: 10  
Seq primer: TCACACAGGAACAGCTATGAC.

## FEATURES

Location/Qualifiers  
1..614  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"  
/clone="NF117F10IN"  
/tissue\_type="local and systemic leaves"  
/dev\_stage="mature"  
/clone\_lib="Insect herbivory"  
/note="Vector: Lambda Zap; Library was produced from fully

expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

## ORIGIN

Alignment Scores:  
 Pred. No.: 6,67e-18 Length: 614  
 Score: 223.00 Matches: 47  
 Percent Similarity: 88.9% Conservative: 1  
 Best Local Similarity: 87.0% Mismatches: 6  
 Query Match: 75.1% Indels: 0  
 DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BI268095 (1-614)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 |||||  
 Db 88 ATGGCAGAGTTTGGCTCTTCTACACATGTGAGCAGAGATCAGAAAATCTCTCCC 147  
 |||||  
 QY 21 CyAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 |||||  
 Db 148 GTTGCACACTCCATCTCATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAA 207  
 |||||  
 QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
 |||||  
 Db 208 GTCGCAGTTCGTCTAAATTTCAGAGTAATGGCAGTCAACTCT 249  
 |||||

RESULT 19  
 AW696250

LOCUS  
 DEFINITION NF104E11STP1086 Developing stem Medicago truncatula cDNA clone  
 NF104E11ST 5', mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE

ORGANISM  
 Medicago truncatula (barrel medic)

Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Medicago.

REFERENCE  
 1 (bases 1 to 628)

AUTHORS  
 He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A.,  
 Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and  
 Dixon,R.A.

TITLE  
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
 Medicago truncatula stem library

JOURNAL  
 COMMENT On Apr 14, 2000 this sequence version replaced gi:7571012.

Unpublished (2000)

Contact: Dixon RA  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7302

Fax: 580 221 7380

Email: radixon@noble.org

Insert Length: 668 Std Error: 0.00

Plate: 104 row: E column: 11

Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES  
 source

1. .628  
 /organism="Medicago truncatula"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3880"  
 /clone="NF104E11ST"  
 /tissue\_type="stem"  
 /dev\_stage="Pooled developmental"  
 /clone\_lib="Developing stem"  
 /notes="Vector: Lambda Zap; Contains a mixture of  
 internodal stem segments"

## ORIGIN

Alignment Scores:  
 Pred. No.: 7,08e-18 Length: 642  
 Score: 223.00 Matches: 47  
 Percent Similarity: 88.9% Conservative: 1  
 Best Local Similarity: 87.0% Mismatches: 6

## Alignment Scores:

Pred. No.: 6,88e-18 Length: 628  
 Score: 223.00 Matches: 47  
 Percent Similarity: 88.9% Conservative: 1  
 Best Local Similarity: 87.0% Mismatches: 6  
 Query Match: 75.1% Indels: 0  
 DB: 1 Gaps: 0

US-10-628-525A-35 (1-58) x AW696250 (1-628)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 |||||  
 Db 121 ATGGCAGAGTTTGGCTCTTCTACACATGTGAGCAGAGATCAGAAAATCTCTCCC 180  
 |||||  
 QY 21 CyAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 |||||  
 Db 181 GTTGCACACTCCATCTCATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAA 240  
 |||||  
 QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
 |||||  
 Db 241 GTCGCAGTTCGTCTAAATTTCAGAGTAATGGCAGTCAACTCT 282  
 |||||

RESULT 20

BF642149

LOCUS

DEFINITION NF058D06IN1057 Insect herbivory Medicago truncatula cDNA clone  
 NF058D06IN 5', mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE

ORGANISM  
 Medicago truncatula (barrel medic)

Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Medicago.

REFERENCE  
 1 (bases 1 to 642)

AUTHORS  
 Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,  
 Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.

TITLE  
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation

Medicago truncatula insect herbivory library

JOURNAL  
 COMMENT Unpublished (2000)

Contact: Korth K

Dept. of Plant Pathology

University of Arkansas

217 Plant Science Building, Fayetteville, AR 72701, USA

Tel: 501 575 5191

Fax: 501 575 7601

Email: kkorthe@comp.uark.edu

Insert Length: 642 Std Error: 0.00

Plate: 058 row: D column: 06

Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES  
 source

1. .642  
 /organism="Medicago truncatula"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3880"  
 /clone="NF058D06IN"  
 /tissue\_type="local and systemic leaves"  
 /dev\_stage="mature"  
 /clone\_lib="Insect herbivory"

/note="Vector: Lambda Zap; Library was produced from fully  
 expanded M. truncatula leaves of plants fed upon by  
 Spodoptera exigua (beet armyworm) for 24 hours. Systemic  
 (undamaged leaves from injured plants) and wounded leaves  
 were harvested and pooled."

## ORIGIN

Alignment Scores:  
 Pred. No.: 7,08e-18 Length: 642  
 Score: 223.00 Matches: 47  
 Percent Similarity: 88.9% Conservative: 1  
 Best Local Similarity: 87.0% Mismatches: 6

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Query Match: 75.1% Indels: 0
DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BF642149 (1-642)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
   |||||
Db 103 ATGGCACAGATTTGGCTCCTTCTACACAATGTCAGGCAAGAATCACAAAATCTCTCCC 162
   |||||

QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
   |||||
Db 163 GTTGCAACTCCCAATCTCATCAAGATGTGGAGTCTCTTGGTTATGAAACAAACAGAAA 222
   |||||

QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
   |||||
Db 223 GTGCGACGTTCTGCTAATTCAGATTAATGGCAGTCACTCT 264
   |||||

RESULT 21
AW693739 649 bp mRNA linear EST 15-JUN-2000
LOCUS
DEFINITION
NF068E07ST1054 Developing stem Medicago truncatula cDNA clone
ACCESSION
AW693739
VERSION
AW693739.1 GI:7568476
KEYWORDS
SOURCE
Medicago truncatula (barrel medic)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 649)
AUTHORS
He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A.,
Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and
Dixon,R.A.
TITLE
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula stem library
JOURNAL
Unpublished (2000)
COMMENT
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 649 Std Error: 0.00
Plate: 068 row: E column: 07
Seq primer: TCACACAGGAAACAGCTATGAC.

FEATURES
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1..649
Location/Qualifiers
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    /mol_type="mRNA"
    /db_xref="taxon:3880"
    /clone="NF068E07ST"
    /tissue_type="stem"
    /dev_stage="Pooled developmental"
    /clone_lib="Developing stem"
    /note="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"

ORIGIN
Alignment Scores:
Pred. No.: 7,18e-18 Length: 649
Score: 223.00 Matches: 47
Percent Similarity: 88.9% Conservative: 1
Best Local Similarity: 87.0% Mismatches: 6
Query Match: 75.1% Indels: 0
DB: 1 Gaps: 0

US-10-628-525A-35 (1-58) x AW693739 (1-649)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
   |||||

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Db 88 ATGGCACAGATTTGGCTCCTTCTACACAATGTCAGGCAAGAATCACAAAATCTCTCCC 147
   |||||
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
   |||||
Db 148 GTTGCAACTCCCAATCTCATCAAGATGTGGAGTCTCTTGGTTATGAAACAAACAGAAA 207
   |||||

QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
   |||||
Db 208 GTGCGACGTTCTGCTAATTCAGATTAATGGCAGTCACTCT 249
   |||||

RESULT 22
BE325326 650 bp mRNA linear EST 14-JUL-2000
LOCUS
DEFINITION
NF120H12ST1103 Developing stem Medicago truncatula cDNA clone
ACCESSION
BE325326
VERSION
BE325326.1 GI:9199103
KEYWORDS
SOURCE
Medicago truncatula (barrel medic)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 650)
AUTHORS
He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A.,
Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and
Dixon,R.A.
TITLE
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula stem library
JOURNAL
Unpublished (2000)
COMMENT
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 650 Std Error: 0.00
Plate: 120 row: H column: 12
Seq primer: TCACACAGGAAACAGCTATGAC.

FEATURES
source
1..650
Location/Qualifiers
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    /mol_type="mRNA"
    /db_xref="taxon:3880"
    /clone="NF120H12ST"
    /tissue_type="stem"
    /dev_stage="Pooled developmental"
    /clone_lib="Developing stem"
    /note="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"

ORIGIN
Alignment Scores:
Pred. No.: 7,2e-18 Length: 650
Score: 223.00 Matches: 47
Percent Similarity: 88.9% Conservative: 1
Best Local Similarity: 87.0% Mismatches: 6
Query Match: 75.1% Indels: 0
DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BE325326 (1-650)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
   |||||
Db 110 ATGGCACAGATTTGGCTCCTTCTACACAATGTCAGGCAAGAATCACAAAATCTCTCCC 169
   |||||

QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
   |||||
Db 170 GTTGCAACTCCCAATCTCATCAAGATGTGGAGTCTCTTGGTTATGAAACAAACAGAAA 229
   |||||

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QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
BQ139196
Db 230 GTGCACAGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 271

RESULT 23
BQ139196
LOCUS BQ139196 651 bp mRNA linear EST 26-APR-2002
DEFINITION N7012P06PH1F1048 Phoma-infected Medicago truncatula cDNA clone
ACCESSION BQ139196
VERSION BQ139196.1 GI:20275322
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula

REFERENCE
1 (bases 1 to 651)
AUTHORS Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,
Gonzales,R.A., Bell,C.J., Inman,J.T., Waugh,M.E., Sullivan,J.P.,
May,G.D. and Paiva,N.L.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
JOURNAL Medicago truncatula Phoma-infected library
COMMENT Unpublished (2002)
Contact: Paiva NL
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7317
Fax: 580 221 7380
Email: nipaiva@noble.org
Insert Length: 651 Std Error: 0.00
Plate: 012 row: F column: 06
Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES
source
1..651
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF012P06PH"
/tissue_type="leaf"
/dev_stage="Pathogen-induced, young trifoliolate"
/notes="Vector: pBluescript SK(-); Young trifoliolate leaves
of Medicago truncatula were excised and dip-inoculated in
a spore suspension of Phoma medicaginis, and incubated in
humid dishes. Pools of leaves were harvested at 0, 15, and
30 minutes and 1, 2, 3, 6, 14, 24, 48, 72, and 96 hours,
and used to prepare total RNA. cDNA was prepared from
polyA+ enriched, pooled samples of equivalent amounts of
total RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap XR vector (Stratagene) and
packaged using the Gigapack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-Zap XR vector using Exaestit
helper phage and the E. coli strain XL1-Blue MRF'
(Stratagene). Excised plasmids were plated using SOLR
cells."

ORIGIN
Alignment Scores:
Pred. No.: 7,21e-18 Length: 651
Score: 223.00 Matches: 47
Percent Similarity: 88.9% Conservative: 1
Best Local Similarity: 87.0% Mismatches: 6
Query Match: 75.1% Indels: 0
DB: 3 Gaps: 0

US-10-628-525A-35 (1-58) x BQ139196 (1-651)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
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Db 68 ATGGCAGAGATTTGGCTCTCTTACACAATGTTCAGGCAAGAAATCACAAAAATCTCTCCC 127
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
|||||
Db 128 GTTGCACACTCCAACTCTCATCAAGAATGTGGAGTCTTTGGTTATGAACAACAAACAGAAA 187
|||||
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
|||||
Db 188 GTGCACAGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 229
|||||

RESULT 24
BQ1391414
LOCUS BQ1391414 656 bp mRNA linear EST 15-JUN-2000
DEFINITION NF044E06ST1F1000 Developing stem Medicago truncatula cDNA clone
ACCESSION BQ1391414
VERSION BQ1391414.1 GI:7566150
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula

REFERENCE
1 (bases 1 to 656)
AUTHORS He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A.,
Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and
Dixon,R.A.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
JOURNAL Medicago truncatula stem library
COMMENT Unpublished (2000)
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 656 Std Error: 0.00
Plate: 044 row: E column: 06
Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES
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/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF044E06ST"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/clone_lib="Developing stem"
/notes="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"

ORIGIN
Alignment Scores:
Pred. No.: 7,29e-18 Length: 656
Score: 223.00 Matches: 47
Percent Similarity: 88.9% Conservative: 1
Best Local Similarity: 87.0% Mismatches: 6
Query Match: 75.1% Indels: 0
DB: 1 Gaps: 0

US-10-628-525A-35 (1-58) x BQ1391414 (1-656)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
|||||
Db 97 ATGGCAGAGATTTGGCTCTCTTACACAATGTTCAGGCAAGAAATCACAAAAATCTCTCCC 156
|||||
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
|||||
Db 157 GTTGCACACTCCAACTCTCATCAAGAATGTGGAGTCTTTGGTTATGAACAACAAACAGAAA 216
|||||
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
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```







```

truncatula
JOURNAL
COMMENT
Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058
Email: vance004@maroon.tc.umn.edu
Minnesota EST name: M252574e
TIGR sequence name: MTCAB61TK
More information is available at:
'http://chrysis.tamu.edu/medicago/'
Seq primer: SKmod (CTA gAA CTA gTg gAT CC).
FEATURES
Location/Qualifiers
1..630
/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pGVN-47L2"
/tissue_type="N2-fixing root nodules"
/dev_stage="effective root nodules harvested one month
post inoculation with Sinorhizobium meliloti"
/lab_host="E. coli strain XL0LR"
/clone_lib="GVN"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
inoculation with Sinorhizobium meliloti. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XL0LR cells."
ORIGIN
Alignment Scores:
Pred. No.: 2,23e-17 Length: 630
Score: 219.00 Matches: 46
Percent Similarity: 87.0% Conservative: 1
Best Local Similarity: 85.2% Mismatches: 7
Query Match: 73.7% Indels: 0
DB: 1 Gaps: 0
US-10-628-525A-35 (1-58) x AM573676 (1-630)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 17 ATGGCACAGATTTTGCTCTCTACCAATGTCAGGCAAGAATCACAAAATCTCTCCC 76
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 77 GTTGCAACTCCCAATCTCATCAAGATGTGGAGTCTTTGGTTATGAAACAAACAGAAA 136
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
Db 137 GTCCGACGTTCTGCTAATTCAGATATGGCAGTCAACTCT 178
RESULT 30
AL372792/c
LOCUS
DEFINITION
MTCAB53F02R1 McBA Medicago truncatula cDNA clone MTCAB53F02 T7, mRNA
sequence.
ACCESSION
AL372792
VERSION
AL372792.1 GI:9672545
KEYWORDS
EST.
SOURCE
Medicago truncatula (barrel medic)
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

```

```

REFERENCE
1 (bases 1 to 457)
Journet.E.P., Crespeau.H., van-Tuinen.D., Gouzy,J., Jaillon.O.,
Niebel.A., Carreau.V., Chatagnier.O., Kahn.D.,
Gianinazzi-Pearson,V., and Gamas,P.
Medicago truncatula ESTs from nitrogen-starved roots
Unpublished (2000)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
Mt-est@toulouse.inra.fr Website :
http://sequence.toulouse.inra.fr/Mtruncatula.html).
FEATURES
Location/Qualifiers
1..457
/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MTCAB53F02"
/tissue_type="root tips"
/dev_stage="harvested after 3 days of N-starvation"
/clone_lib="McBA"
/note="Vector: pBluescript pSK; Site 1: EcoRI; Site 2:
XhoI; Plants were grown in an aeroponic chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). cDNA
was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zapXR vector from
Stratagene and packaged using Gigapack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using ExAssist helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."
ORIGIN
Alignment Scores:
Pred. No.: 1,96e-17 Length: 457
Score: 218.00 Matches: 46
Percent Similarity: 87.0% Conservative: 1
Best Local Similarity: 85.2% Mismatches: 7
Query Match: 73.4% Indels: 0
DB: 1 Gaps: 0
US-10-628-525A-35 (1-58) x AL372792 (1-457)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 400 ATGGCACAGATTTTGCTCTCTCTACCAATGTCAGGCAAGAATCACAAAATCTCTCCC 341
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 340 GTTGGCGGCTCCAATCTCATCAAGATGTGGAGTCTTTGGTTATGAAACAAACAGAAA 281
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
Db 280 GTCCGACGTTCTGCTAATTCAGATATGGCAGTCAACTCT 239
Search completed: April 1, 2006, 19:23:30
Job time : 936.32 secs

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c 84 60 20.2 3368 3 US-09-710-279-4169 Sequence 4169, Ap
c 85 60 20.2 162025 3 US-09-834-700-13 Sequence 13, Appl
c 86 60 20.2 162025 3 US-09-834-700-14 Sequence 14, Appl
c 87 60 20.2 162025 3 US-09-834-700-17 Sequence 17, Appl
c 88 60 20.2 162025 3 US-09-834-700-18 Sequence 18, Appl
c 89 59.5 20.0 651 3 US-09-583-110-1895 Sequence 1895, Ap
c 90 59.5 20.0 699 3 US-09-107-433-936 Sequence 936, App
c 91 59.5 20.0 707 3 US-09-270-767-28551 Sequence 28551, A
c 92 59.5 20.0 1012 3 US-09-270-767-12735 Sequence 12735, A
c 93 59.5 20.0 1512 3 US-09-999-833A-161 Sequence 161, App
c 94 59.5 20.0 1512 3 US-10-020-445A-161 Sequence 161, App
c 95 59.5 20.0 18157 3 US-09-949-016-16193 Sequence 16193, A
c 96 59.5 20.0 106256 3 US-09-949-016-16858 Sequence 16858, A
c 97 59 931 3 US-09-270-767-10987 Sequence 10987, A
c 98 59 969 2 US-08-700-637-1 Sequence 1, Appl
c 99 59 1859 3 US-08-894-818B-15 Sequence 15, Appl
c 100 59 1859 3 US-09-841-553-15 Sequence 15, Appl
c 101 59 1977 3 US-08-894-818B-2 Sequence 2, Appl
c 102 59 1977 3 US-08-894-818B-6 Sequence 6, Appl
c 103 59 1977 3 US-09-227-357-83 Sequence 83, Appl
c 104 59 1977 3 US-09-445-472-11 Sequence 11, Appl
c 105 59 1977 3 US-10-090-624-11 Sequence 11, Appl
c 106 59 1977 3 US-09-841-553-2 Sequence 2, Appl
c 107 59 1977 3 US-09-841-553-6 Sequence 6, Appl
c 108 59 1977 3 US-09-973-278-125 Sequence 125, App
c 109 59 1992 3 US-09-252-991A-6684 Sequence 6684, Ap
c 110 59 2028 3 US-09-252-991A-6614 Sequence 6614, Ap
c 111 59 2361 2 US-08-769-309A-4 Sequence 4, Appl
c 112 59 6605 2 US-08-994-570-4 Sequence 4, Appl
c 113 59 6608 3 US-09-220-132-58 Sequence 58, Appl
c 114 59 11601 2 US-08-222-617A-3 Sequence 3, Appl
c 115 59 11601 2 US-08-222-617A-24 Sequence 24, Appl
c 116 59 42325 3 US-08-311-731A-131 Sequence 131, App
c 117 59 42923 3 US-09-949-016-17307 Sequence 17307, A
c 118 59 69737 3 US-09-949-016-15140 Sequence 15140, A
c 119 59 69737 3 US-09-949-016-15140 Sequence 15140, A
c 120 59 116652 3 US-09-949-016-13413 Sequence 13413, A
c 121 58.5 19.7 601 3 US-09-949-016-108061 Sequence 108061,
c 122 58.5 19.7 601 3 US-09-949-016-108062 Sequence 108062,
c 123 58.5 19.7 601 3 US-09-949-016-108063 Sequence 108063,
c 124 58.5 19.7 708 3 US-09-902-540-8467 Sequence 8467, Ap
c 125 58.5 19.7 882 3 US-09-252-991A-12972 Sequence 12972, A
c 126 58.5 19.7 1137 3 US-09-579-383-1 Sequence 1, Appl
c 127 58.5 19.7 1206 3 US-09-252-991A-13133 Sequence 13133, A
c 128 58.5 19.7 1312 3 US-09-252-991A-12808 Sequence 12808, A
c 129 58.5 19.7 1359 3 US-09-252-991A-11454 Sequence 11454, A
c 130 58.5 19.7 1395 3 US-09-252-991A-11477 Sequence 11477, A
c 131 58.5 19.7 1449 3 US-09-695-458-1 Sequence 1, Appl
c 132 58.5 19.7 1452 3 US-09-252-991A-11417 Sequence 11417, A
c 133 58.5 19.7 1488 3 US-09-902-540-4238 Sequence 4238, Ap
c 134 58.5 19.7 2311 3 US-09-949-016-1552 Sequence 1552, Ap
c 135 58.5 19.7 2550 2 US-08-188-228-53 Sequence 53, Appl
c 136 58.5 19.7 2550 2 US-08-332-643-47 Sequence 47, Appl
c 137 58.5 19.7 2550 2 US-08-332-638-53 Sequence 53, Appl
c 138 58.5 19.7 5610 3 US-09-262-537-57 Sequence 57, Appl
c 139 58.5 19.7 12955 3 US-09-902-540-1068 Sequence 1068, Ap
c 140 58.5 19.7 17966 3 US-09-949-016-11986 Sequence 11986, A
c 141 58.5 19.7 18343 3 US-09-949-016-16413 Sequence 16413, A
c 142 58.5 19.7 24791 3 US-09-902-540-1211 Sequence 1211, Ap
c 143 58.5 19.7 250352 3 US-09-949-016-14724 Sequence 14724, A
c 144 58.5 19.7 250715 3 US-09-949-016-13294 Sequence 13294, A
c 145 58 444 3 US-09-397-787-152 Sequence 152, App
c 146 58 601 3 US-09-949-016-160183 Sequence 160183,
c 147 58 601 3 US-09-949-016-201932 Sequence 201932,
c 148 58 861 3 US-09-533-559-801 Sequence 801, App
c 149 58 931 2 US-08-203-905B-4 Sequence 4, Appl
c 150 58 1068 3 US-09-328-352-434 Sequence 434, App
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## ALIGNMENTS

RESULT 1

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US-07-715-751B-1
; Sequence 1, Application US/07715751B
; Patent No. 5391725
; GENERAL INFORMATION:
; APPLICANT: CORUZZI, GLORIA M
; APPLICANT: EDWARDS, JANICE W
; APPLICANT: WALKER, ELSBETH L
; APPLICANT: BREARS, TIMOTHY B
; TITLE OF INVENTION: NOVEL ORGAN-SPECIFIC PLANT PROMOTER
; TITLE OF INVENTION: SEQUENCES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: N.Y.
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/715,751B
; FILING DATE: 19910613
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 3288-017-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1601 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-715-751B-1
Alignment Scores:
Pred. No.: 18-27 Length: 1601
Score: 271.00 Matches: 53
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 91.2% Indels: 0
DB: 2 Gaps: 0
US-10-628-525A-35 (1-58) x US-07-715-751B-1 (1-1601)
QY 1 MetalAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
|||||
Db 1443 ATGGCGCAGATTTCGACCTTCGACGCAATGCGCAGATGAGATCACAAAACCTCTCT 1502
|||||
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
|||||
Db 1503 TGTGCAACTCCCAATCACATCAATCAAAAGATGTGGAGTTCTTTGGTTATGAAACAAACTAAGAAA 1562
|||||
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAen 53
|||||
Db 1563 GTTGGCATTTCGTAATTTAGATTATGCGATGCGATCAAC 1601
|||||
RESULT 2
US-09-605-703B-499/c
; Sequence 499, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejeu, Markus
; APPLICANT: Kroger, Burkhard
```

```
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberkauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; PRIOR FILING DATE: 2000-06-27, 764
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 499
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1114)
; OTHER INFORMATION: RXN01128
US-09-605-703B-499

Alignment Scores:
Pred. No.: 5.07 Length: 1137
Score: 69.50 Matches: 17
Percent Similarity: 49.0% Conservative: 7
Best Local Similarity: 34.7% Mismatches: 16
Query Match: 23.4% Indels: 9
DB: 4 Gaps: 2

US-10-628-525A-35 (1-58) x US-09-605-703B-499 (1-1137)
QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db 348 ATGTCATCCTTTTGGCGGATTCA-----ATGGACTCAACGCGCGCT 307

QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 306 TGTACAGATCCGACTACT-----TGGAGCTCAATGTTGTTCAATAATACCAACGCGCA 256

QY 41 ValAlaHisSerAlaLysPheArgVal 49
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db 255 ACTGCTAATCCAGGATTGATTG 229

RESULT 3
US-09-605-703B-501/c
; Sequence 501, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberkauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 501
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1114)
; OTHER INFORMATION: FRXA01128
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US-09-605-703B-501
Alignment Scores:
Pred. No.: 5.07 Length: 1137
Score: 69.50 Matches: 17
Percent Similarity: 49.0% Conservative: 7
Best Local Similarity: 34.7% Mismatches: 16
Query Match: 23.4% Indels: 9
DB: 4 Gaps: 2

US-10-628-525A-35 (1-58) x US-09-605-703B-501 (1-1137)
QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db 348 ATGTCATCCTTTTGGCGGATTCA-----ATGGACTCAACGCGCGCT 307

QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 306 TGTACAGATCCGACTACT-----TGGAGCTCAATGTTGTTCAATAATACCAACGCGCA 256

QY 41 ValAlaHisSerAlaLysPheArgVal 49
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db 255 ACTGCTAATCCAGGATTGATTG 229

RESULT 4
US-09-602-777A-129
; Sequence 129, Application US/09602777A
; Patent No. 6831165
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberkauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; FILE REFERENCE: BGI-128CP
; CURRENT APPLICATION NUMBER: US/09/602,777A
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932924.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932928.1
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932930.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932933.8
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932935.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932973.7
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933002.6
; PRIOR FILING DATE: 1999-07-14
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/ PRIOR APPLICATION NUMBER: DE 19933003.4
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19933005.0
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19933006.9
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19941378.9
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: DE 19941379.7
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: DE 19941390.8
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: DE 19941391.6
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: DE 19942088.2
/ PRIOR FILING DATE: 1999-09-03
/ NUMBER OF SEQ ID NOS: 442
/ SEQ ID NO 129
/ LENGTH: 1539
/ TYPE: DNA
/ ORGANISM: Corynebacterium glutamicum
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (101)..(1516)
/ OTHER INFORMATION: RXN00622
US-09-602-777A-129
Alignment Scores:
Pred. No.: 7.7 Length: 1539
Score: 69.50 Matches: 19
Percent Similarity: 50.8% Conservative: 14
Best Local Similarity: 29.2% Mismatches: 21
Query Match: 23.4% Indels: 11
DB: 3 Gaps: 3
US-10-628-525A-35 (1-58) x US-09-602-777A-129 (1-1539)
QY 3 Gln1LeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAla 22
DB 32 CAGATACTGTGGCGCCACAGGTGGGTACCCCGTTGAAGAACGCTGTGGTGATCC 91
QY 23 ThrProIleThrSerLysMet-----TrpSerSerLeuValMetLysGln----- 37
DB 92 ACCGAGCTGATGACGCTATTATCCACTGGGTGGGCACCACTCGTTCAGAAAAAGTTTCATC 151
QY 38 -----ThrLysLysValAlaHisSerAlaLysPheArgValMetAlaValAsn 53
DB 152 CTTTGTGGTGGCGCTCCAGATC-----ACCTCTGAAGTACGCGTCTCTTCGAC 205
QY 54 SerGluAsnGlyThr 58
DB 206 CAGCCAGAGGGCACC 220
RESULT 5
US-09-602-777A-131
/ Sequence 131, Application US/09602777A
/ Patent No. 6831165
/ GENERAL INFORMATION:
/ APPLICANT: Pompejus, Markus
/ APPLICANT: Kroeger, Burkhard
/ APPLICANT: Schroeder, Hartwig
/ APPLICANT: Zelder, Oskar
/ APPLICANT: Haberhauer, Gregor
/ TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
/ TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
/ FILE REFERENCE: BGI-128CP
/ CURRENT APPLICATION NUMBER: US/09/602,777A
/ CURRENT FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 60/141031
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: DE 19931636.8
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19932125.6
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/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932126.4
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932127.2
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932128.0
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932129.9
/ PRIOR FILING DATE: 1999-07-19
/ PRIOR APPLICATION NUMBER: DE 19932226.0
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932920.6
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19932922.2
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19932924.9
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19932928.1
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19932930.3
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19932933.8
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19932935.4
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19932973.7
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19933002.6
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19933003.4
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19933005.0
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19933006.9
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19941378.9
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: DE 19941379.7
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: DE 19941390.8
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: DE 19941391.6
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: DE 19942088.2
/ PRIOR FILING DATE: 1999-09-03
/ NUMBER OF SEQ ID NOS: 442
/ SEQ ID NO 131
/ LENGTH: 1539
/ TYPE: DNA
/ ORGANISM: Corynebacterium glutamicum
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (101)..(1516)
/ OTHER INFORMATION: FRXA00622
US-09-602-777A-131
Alignment Scores:
Pred. No.: 7.7 Length: 1539
Score: 69.50 Matches: 19
Percent Similarity: 50.8% Conservative: 14
Best Local Similarity: 29.2% Mismatches: 21
Query Match: 23.4% Indels: 11
DB: 3 Gaps: 3
US-10-628-525A-35 (1-58) x US-09-602-777A-131 (1-1539)
QY 3 Gln1LeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAla 22
DB 32 CAGATACTGTGGCGCCACAGGTGGGTACCCCGTTGAAGAACGCTGTGGTGATCC 91
QY 23 ThrProIleThrSerLysMet-----TrpSerSerLeuValMetLysGln----- 37
DB 92 ACCGAGCTGATGACGCTATTATCCACTGGGTGGGCACCACTCGTTCAGAAAAAGTTTCATC 151
QY 38 -----ThrLysLysValAlaHisSerAlaLysPheArgValMetAlaValAsn 53
DB 152 CTTTGTGGTGGCGCTCCAGATC-----ACCTCTGAAGTACGCGTCTCTTCGAC 205
QY 54 SerGluAsnGlyThr 58
DB 206 CAGCCAGAGGGCACC 220
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QY 38 -----ThrLysLysValAlaHisSerAlaLysPheArgValMetAlaValAen 53
Db 152 CTTTGTGTCGCGCTCCAGATC-----ACCTCTGAAGTACGCGTCTTCCTTCGAC 205
QY 54 SerGluAenGlyThr 58
Db 206 CAGCCAGAGGGCACC 220

RESULT 6
US-09-949-002-1185/c
; Sequence 1185, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1185
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-1185

Alignment Scores:
Pred. No.: 3.4 Length: 601
Score: 68.00 Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9% Indels: 0
DB: 3 Gaps: 0

US-10-628-525A-35 (1-58) x US-09-949-002-1185 (1-601)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 573 GCCCGCGACTCCACCATGGTAGATGAATATACTGGAGACCCCTGTTCCAGCCTCAGAGATT 514
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 513 TGGCAGAGCCCATGGGGCAGAGTGGAGATGGTGGGACAACTGGATGGTCCCTCAGGG 454
QY 46 LysPheArgValMetAlaValAenSerGluAenGlyThr 58
Db 453 AGATTTCAGCGAGCTCAACGAGGAACCTGGAGAAAGGCACT 415

RESULT 7
US-09-949-002-1186/c
; Sequence 1186, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1186
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-1186

Alignment Scores:
Pred. No.: 3.4 Length: 601
Score: 68.00 Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9% Indels: 0
DB: 3 Gaps: 0

US-10-628-525A-35 (1-58) x US-09-949-002-1186 (1-601)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 573 GCCCGCGACTCCACCATGGTAGATGAATATACTGGAGACCCCTGTTCCAGCCTCAGAGATT 514
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 513 TGGCAGAGCCCATGGGGCAGAGTGGAGATGGTGGGACAACTGGATGGTCCCTCAGGG 454
QY 46 LysPheArgValMetAlaValAenSerGluAenGlyThr 58
Db 453 AGATTTCAGCGAGCTCAACGAGGAACCTGGAGAAAGGCACT 415

RESULT 8
US-09-949-002-1187/c
; Sequence 1187, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1187
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-1187

Alignment Scores:
Pred. No.: 3.4 Length: 601
Score: 68.00 Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9% Indels: 0
DB: 3 Gaps: 0

US-10-628-525A-35 (1-58) x US-09-949-002-1187 (1-601)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 290 GCCCGCGACTCCACCATGGTAGATGAATATACTGGAGACCCCTGTTCCAGCCTCAGAGATT 231
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 230 TGGCAGAGCCCATGGGGCAGAGTGGAGATGGTGGGACAACTGGATGGTCCCTCAGGG 171
QY 46 LysPheArgValMetAlaValAenSerGluAenGlyThr 58
Db 170 AGATTTCAGCGAGCTCAACGAGGAACCTGGAGAAAGGCACT 132

RESULT 9
US-09-949-002-9808/c
; Sequence 9808, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
```

```
US-09-949-002-1186
Alignment Scores:
Pred. No.: 3.4 Length: 601
Score: 68.00 Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9% Indels: 0
DB: 3 Gaps: 0
```

```
US-10-628-525A-35 (1-58) x US-09-949-002-1186 (1-601)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 543 GCCCGCGACTCCACCATGGTAGATGAATATACTGGAGACCCCTGTTCCAGCCTCAGAGATT 484
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 483 TGGCAGAGCCCATGGGGCAGAGTGGAGATGGTGGGACAACTGGATGGTCCCTCAGGG 424
QY 46 LysPheArgValMetAlaValAenSerGluAenGlyThr 58
Db 423 AGATTTCAGCGAGCTCAACGAGGAACCTGGAGAAAGGCACT 385
```

```
RESULT 8
US-09-949-002-1187/c
; Sequence 1187, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1187
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-1187
```

```
Alignment Scores:
Pred. No.: 3.4 Length: 601
Score: 68.00 Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9% Indels: 0
DB: 3 Gaps: 0
```

```
US-10-628-525A-35 (1-58) x US-09-949-002-1187 (1-601)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 290 GCCCGCGACTCCACCATGGTAGATGAATATACTGGAGACCCCTGTTCCAGCCTCAGAGATT 231
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 230 TGGCAGAGCCCATGGGGCAGAGTGGAGATGGTGGGACAACTGGATGGTCCCTCAGGG 171
QY 46 LysPheArgValMetAlaValAenSerGluAenGlyThr 58
Db 170 AGATTTCAGCGAGCTCAACGAGGAACCTGGAGAAAGGCACT 132
```

```
RESULT 9
US-09-949-002-9808/c
; Sequence 9808, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
```



```
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9808
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-9808

Alignment Scores:
Pred. No.: 3.4 Length: 601
Score: 68.00 Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9% Indels: 0
DB: 3 Gaps: 0

US-10-628-525A-35 (1-58) x US-09-949-002-9808 (1-601)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
DB 573 GCGCCGCACTCCACATGGTAGATGAATATCTGGAGACCCCTGTTCCAGCCTCAGAGATT 514
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysValAlaHisSerAla 45
DB 513 TGCCAGAGCCCATGGGCGAGAGTGGAGTGGGGGACAACTGGATGGTCCCTCAGGG 454
QY 46 LysPheArgValMetAlaValAsnSerGluAenGlyThr 58
DB 453 AGATTTCAGGCAGCTCAACAGGAGAACTGGAGAAAGGCACT 415

RESULT 10
US-09-949-002-9809/c
; Sequence 9809, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9809
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-9809

Alignment Scores:
Pred. No.: 3.4 Length: 601
Score: 68.00 Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9% Indels: 0
DB: 3 Gaps: 0

US-10-628-525A-35 (1-58) x US-09-949-002-9809 (1-601)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
DB 573 GCGCCGCACTCCACATGGTAGATGAATATCTGGAGACCCCTGTTCCAGCCTCAGAGATT 514
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysValAlaHisSerAla 45
DB 513 TGCCAGAGCCCATGGGCGAGAGTGGAGTGGGGGACAACTGGATGGTCCCTCAGGG 454
QY 46 LysPheArgValMetAlaValAsnSerGluAenGlyThr 58
DB 453 AGATTTCAGGCAGCTCAACAGGAGAACTGGAGAAAGGCACT 415

RESULT 11
US-09-949-002-9810/c
; Sequence 9810, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9810
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-9810

Alignment Scores:
Pred. No.: 3.4 Length: 601
Score: 68.00 Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9% Indels: 0
DB: 3 Gaps: 0

US-10-628-525A-35 (1-58) x US-09-949-002-9810 (1-601)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
DB 573 GCGCCGCACTCCACATGGTAGATGAATATCTGGAGACCCCTGTTCCAGCCTCAGAGATT 514
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysValAlaHisSerAla 45
DB 513 TGCCAGAGCCCATGGGCGAGAGTGGAGTGGGGGACAACTGGATGGTCCCTCAGGG 454
QY 46 LysPheArgValMetAlaValAsnSerGluAenGlyThr 58
DB 453 AGATTTCAGGCAGCTCAACAGGAGAACTGGAGAAAGGCACT 415

RESULT 12
US-09-949-002-836/c
; Sequence 836, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 836
; LENGTH: 34589
; TYPE: DNA
```

```
Db 543 GCGCCGCACTCCACATGGTAGATGAATATCTGGAGACCCCTGTTCCAGCCTCAGAGATT 484
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysValAlaHisSerAla 45
Db 483 TGCCAGAGCCCATGGGCGAGAGTGGAGTGGGGGACAACTGGATGGTCCCTCAGGG 424
QY 46 LysPheArgValMetAlaValAsnSerGluAenGlyThr 58
Db 423 AGATTTCAGGCAGCTCAACAGGAGAACTGGAGAAAGGCACT 385

RESULT 11
US-09-949-002-9810/c
; Sequence 9810, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9810
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-9810

Alignment Scores:
Pred. No.: 3.4 Length: 601
Score: 68.00 Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9% Indels: 0
DB: 3 Gaps: 0

US-10-628-525A-35 (1-58) x US-09-949-002-9810 (1-601)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 290 GCGCCGCACTCCACATGGTAGATGAATATCTGGAGACCCCTGTTCCAGCCTCAGAGATT 231
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysValAlaHisSerAla 45
Db 230 TGCCAGAGCCCATGGGCGAGAGTGGAGTGGGGGACAACTGGATGGTCCCTCAGGG 171
QY 46 LysPheArgValMetAlaValAsnSerGluAenGlyThr 58
Db 170 AGATTTCAGGCAGCTCAACAGGAGAACTGGAGAAAGGCACT 132

RESULT 12
US-09-949-002-836/c
; Sequence 836, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 836
; LENGTH: 34589
; TYPE: DNA
```

```
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(34589)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-002-836

Alignment Scores:
Pred. No.: 911          Length: 34589
Score: 68.00           Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9%      Indels: 0
DB: 3                  Gaps: 0

US-10-628-525A-35 (1-58) x US-09-949-002-836 (1-34589)

Qy 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 9692 GCCCGGCACTACCATGGTAGATGAATATACGTGGAGACCCCTGTTCCAGCCTCAGAGATT 9633

Qy 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 9632 TGCAGAGCCCATGGGSCAGAGTGGAGATGGTGGGACAACTGGATGGTCCCTCAGGG 9573

Qy 46 LysPheArgValMetAlaValaAenSerGluAenGlyThr 58
Db 9572 AGATTGAGGAGCTCAACGAGGAACCTGGAGAAAGGCACT 9534

RESULT 13
US-09-949-002-581/c
; Sequence 581, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 581
; LENGTH: 59258
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(59258)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-002-581

Alignment Scores:
Pred. No.: 1,92e+03      Length: 59258
Score: 68.00           Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9%      Indels: 0
DB: 3                  Gaps: 0

US-10-628-525A-35 (1-58) x US-09-949-002-581 (1-59258)

Qy 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 27787 GCCCGGCACTACCATGGTAGATGAATATACGTGGAGACCCCTGTTCCAGCCTCAGAGATT 27728

Qy 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 27727 TGCAGAGCCCATGGGSCAGAGTGGAGATGGTGGGACAACTGGATGGTCCCTCAGGG 27668

Qy 46 LysPheArgValMetAlaValaAenSerGluAenGlyThr 58
Db 27667 AGATTGAGGAGCTCAACGAGGAACCTGGAGAAAGGCACT 27629

RESULT 14
US-09-949-016-11976
; Sequence 11976, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11976
; LENGTH: 22874
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11976

Alignment Scores:
Pred. No.: 604          Length: 22874
Score: 67.50           Matches: 19
Percent Similarity: 54.5% Conservative: 11
Best Local Similarity: 34.5% Mismatches: 19
Query Match: 22.7%      Indels: 6
DB: 3                  Gaps: 2

US-10-628-525A-35 (1-58) x US-09-949-016-11976 (1-22874)

Qy 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSer-----ProCysAlaThr 23
Db 14553 CCCCCCTCCCTTGGCCCTTCTCTGACTTGGACTTCTCTCCCTCCCTGTCCTCCCTGTCCTCC 14612

Qy 23 rProLerThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHi 43
Db 14613 ACCTCTTACCACCTGGTGGTCTCTCTCTGAGGGTGAACAGACTCTGTGAGGCGGACACT 14672

Qy 43 sSerAlaLysPheArgValMetAlaValaAenSerGluAenGly 57
Db 14673 GCAGGCCCTGTCTGAGGTGGTGGCC-----TCGGATGACGGG 14709

RESULT 15
US-09-949-016-16363
; Sequence 16363, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16363
; LENGTH: 22875
; TYPE: DNA
```

; ORGANISM: Human  
US-09-949-016-16363

Alignment Scores: 604 Length: 22875  
Pred. No.: 67.50 Matches: 19  
Score: 54.5% Conservative: 11  
Percent Similarity: 34.5% Mismatches: 19  
Best Local Similarity: 22.7% Indels: 6  
Query Match: 3 Gaps: 2  
DB:

US-10-628-525A-35 (1-58) x US-09-949-016-16363 (1-22875)

QY 7 ProSerThrGlnTrpGlnMet-ArgfileThrLysThrSer-----ProCysAlaTh 23  
Db 14553 CCCCCCTCCCTTGGCCCTCTCTGACTGGACTTCTGTCTCCCTCCCTGTCCCCC 14612  
QY 23 rProleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHi 43  
Db 14613 ACCTCTACACCCCTGGTGTCTCTCTGAGGTGAACAAGACTCTGAAGCGGACACT 14672  
QY 43 sSerAlaLysPheArgValMetAlaValAsnSerGluAangly 57  
Db 14673 GCAGGCCCTGCTGAGGTGGTGC-----TCGGATGACGG 14709

RESULT 16

US-09-761-534A-11/c  
; Sequence 11, Application US/09761534A  
; Patent No. 6875435  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Qian  
; APPLICANT: Richmond, Joan F.L.  
; APPLICANT: Cho, Bryan K.  
; APPLICANT: Palliser, Deborah  
; APPLICANT: Chen, Jianzhu  
; APPLICANT: Eissen, Herman N.  
; APPLICANT: Young, Richard A.  
; TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock  
; TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is  
; TITLE OF INVENTION: CD4+T Cell-Independent  
; FILE REFERENCE: 0399.2006-003  
; CURRENT APPLICATION NUMBER: US/09/761,534A  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: PCT/US00/32831  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: US 60/176,143  
; PRIOR FILING DATE: 2000-01-14  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 627  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Murine hsp70 -Segment II  
; NAME/KEY: CDS  
; LOCATION: (1)...(627)  
; OTHER INFORMATION: Murine hsp70 -Segment II

US-09-761-534A-11  
Alignment Scores: 4.95 Length: 627  
Pred. No.: 67.00 Matches: 19  
Score: 59.1% Conservative: 7  
Percent Similarity: 43.2% Mismatches: 12  
Best Local Similarity: 22.6% Indels: 6  
Query Match: 3 Gaps: 3  
DB:

US-10-628-525A-35 (1-58) x US-09-761-534A-11 (1-627)

QY 4 lleLeuAlaProSerThrGlnTrp---GlnMetArgIleThrLysThrSerPro----- 20  
Db 173 CTCCTTGAACCTCTCCACGAAGTGGCTCACCAGCGGTGTTCGAGTCTCCCTCCCGAGG 114

QY 21 CysAlaThrPro-----lleThrSerLysMetTrpSerSerLeuValMetLysGln 37  
Db 113 TCGGTGTGCGCCCGCGGTGGCCCTTCACCTCGAAGATGCCGCTCGTGCATCGTCAGGATGGAC 54  
QY 38 ThrLysLysVal 41  
Db 53 ACGTCGAACGTG 42  
RESULT 17  
US-09-761-534A-9/c  
; Sequence 9, Application US/09761534A  
; Patent No. 6875435  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Qian  
; APPLICANT: Richmond, Joan F.L.  
; APPLICANT: Cho, Bryan K.  
; APPLICANT: Palliser, Deborah  
; APPLICANT: Chen, Jianzhu  
; APPLICANT: Eissen, Herman N.  
; APPLICANT: Young, Richard A.  
; TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock  
; TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is  
; TITLE OF INVENTION: CD4+T Cell-Independent  
; FILE REFERENCE: 0399.2006-003  
; CURRENT APPLICATION NUMBER: US/09/761,534A  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: PCT/US00/32831  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: US 60/176,143  
; PRIOR FILING DATE: 2000-01-14  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 1929  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Murine hsp70  
; NAME/KEY: CDS  
; LOCATION: (1)...(1929)  
; OTHER INFORMATION: Murine hsp70

US-09-761-534A-9

Alignment Scores: 23.4 Length: 1929  
Pred. No.: 67.00 Matches: 19  
Score: 59.1% Conservative: 7  
Percent Similarity: 43.2% Mismatches: 12  
Best Local Similarity: 22.6% Indels: 6  
Query Match: 3 Gaps: 3  
DB:

US-10-628-525A-35 (1-58) x US-09-761-534A-9 (1-1929)

QY 4 lleLeuAlaProSerThrGlnTrp---GlnMetArgIleThrLysThrSerPro----- 20  
Db 740 CTCCTTGAACCTCTCCACGAAGTGGCTCACCAGCGGTGTTCGAGTCTCCCTCCCGAGG 681  
QY 21 CysAlaThrPro-----lleThrSerLysMetTrpSerSerLeuValMetLysGln 37  
Db 680 TCGGTGTGCGCCCGCGGTGGCCCTTCACCTCGAAGATGCCGCTCGTGCATCGTCAGGATGGAC 621  
QY 38 ThrLysLysVal 41  
Db 620 ACGTCGAACGTG 609

RESULT 18

US-09-949-016-40647/c  
; Sequence 40647, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

```

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40647
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-40647

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Best Local Similarity: 29.5% Mismatches: 24  
Query Match: 22.2% Indels: 0  
DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x US-08-824-707-1 (1-1459)

QY 1 MetAlaGlnIleuAlaProSerThrGlnMetArgIleThrLysThrSerPro 20  
Db 822 GTGGCCAGGCACTGCTGCTCGCTTCTGGATGTCGGAGCGAACCTGCCGACACCCCT 881

QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db 882 GGCCTACCTCCGCTGAGATCGACATCGAGAACCTGGGCAATCGGCCACAGGCTCC 941

QY 41 ValAlaHisSer 44  
Db 942 ACGGCACGGTCC 953

RESULT 21  
US-10-012-231A-291  
; Sequence 291, Application US/10012231A  
; Patent No. 6924355  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan l.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC48  
; CURRENT APPLICATION NUMBER: US/10/012,231A  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 291  
; LENGTH: 1570  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-012-231A-291

Alignment Scores:  
Pred. No.: 24.2 Length: 1570  
Score: 66.00 Matches: 19  
Percent Similarity: 45.3% Conservative: 5  
Best Local Similarity: 35.8% Mismatches: 18  
Query Match: 22.2% Indels: 12  
DB: 3 Gaps: 2

US-10-628-525A-35 (1-58) x US-10-012-231A-291 (1-1570)  
; Sequence 291, Application US/10012231A  
; Patent No. 6924355  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan l.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC23  
; CURRENT APPLICATION NUMBER: US/10/012,231A  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 291  
; LENGTH: 1570  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-012-231A-291

Alignment Scores:  
Pred. No.: 24.2 Length: 1570  
Score: 66.00 Matches: 19  
Percent Similarity: 45.3% Conservative: 5  
Best Local Similarity: 35.8% Mismatches: 18  
Query Match: 22.2% Indels: 12  
DB: 3 Gaps: 2

US-10-628-525A-35 (1-58) x US-10-012-231A-291 (1-1570)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25  
Db 1209 TCACCATCCCCAAGCTGGAGCACCCCAACCCAGACATCGACCTGTACACCATCT 1268

QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45  
Db 1269 ACATGGAGGCCCTGGTG-AAGCTCTTCGACAAG-----CACAGAGCC 1309

QY 46 LysPhe-----ArgValMetAlaValAsn 53  
Db 1310 AAGTTGGGCTCCCGGAGACTGAGGTCTCTGGAGGTGAAC 1348

RESULT 22  
US-10-006-768A-291  
; Sequence 291, Application US/10006768A  
; Patent No. 6936697  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan l.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC10
; CURRENT APPLICATION NUMBER: US/10/006,768A
; CURRENT FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 291
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-768A-291

Alignment Scores:
Pred. No.: 24.2 Length: 1570
Score: 66.00 Matches: 19
Percent Similarity: 45.3% Conservative: 5
Best Local Similarity: 35.8% Mismatches: 18
Query Match: 22.2% Indels: 12
DB: 2 Gaps: 2

US-10-628-525A-35 (1-58) x US-10-006-768A-291 (1-1570)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 1209 TCACCATCCCAAGCTGGAGCACCACCCAGCAGACATCGACCTGTACCACCATGT 1268
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 1269 ACATGGAGGCCCTGGTG-AAGCTCTTCGACAAG-----CACAGACC 1309
QY 46 LysPhe-----ArgValMetAlaValAen 53
Db 1310 AAGTTCGGCCTCCGGAGACTGAGGTCTCTGGAGGTGAAC 1348
RESULT 24
US-10-015-671A-291
; Sequence 291, Application US/10015671A
; Patent No. 694263
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 291
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-393A-291

Alignment Scores:
Pred. No.: 24.2 Length: 1570
Score: 66.00 Matches: 19
Percent Similarity: 45.3% Conservative: 5
Best Local Similarity: 35.8% Mismatches: 18
Query Match: 22.2% Indels: 12
DB: 2 Gaps: 2

US-10-628-525A-35 (1-58) x US-10-015-393A-291 (1-1570)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 1209 TCACCATCCCAAGCTGGAGCACCACCCAGCAGACATCGACCTGTACCACCATGT 1268
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 1269 ACATGGAGGCCCTGGTG-AAGCTCTTCGACAAG-----CACAGACC 1309
QY 46 LysPhe-----ArgValMetAlaValAen 53
Db 1310 AAGTTCGGCCTCCGGAGACTGAGGTCTCTGGAGGTGAAC 1348
RESULT 26
US-10-011-833A-291
; Sequence 291, Application US/10011833A
; Patent No. 6951920
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; PRIOR APPLICATION NUMBER: 60/099598  
; PRIOR FILING DATE: 1998-09-09  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 291  
; LENGTH: 1570  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-012-064A-291

Alignment Scores:  
Pred. No.: 24.2 Length: 1570  
Score: 66.00 Matches: 19  
Percent Similarity: 45.3% Conservative: 5  
Best Local Similarity: 35.8% Mismatches: 18  
Query Match: 22.2% Indels: 12  
DB: 3 Gaps: 2

US-10-628-525A-35 (1-58) x US-10-012-064A-291 (1-1570)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 1209 TCACCATCCCAAGCTGGAGCACCACCAACCCAGCAGACATCGACCTGTACCACCATGT 1268  
QY 26 ThrSerLysMetTrpSerSerIleValMetLysGlnThrLysLysValAlaHisSerAla 45  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 1269 ACATGGAGGCCCTGGTG-AAGCTCTTCGACAG-----CACAAAGACC 1309  
QY 46 LysPhe-----ArgValMetAlaValAsn 53  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 1310 AAGTTCGGCTCCCGGAGACTGAGTCTCGAGGTGAAC 1348

RESULT 29

US-09-625-188-1

; Sequence 1, Application US/09625188

; Patent No. 6307037

; GENERAL INFORMATION:

; APPLICANT: No. 6307037artis AG

; TITLE OF INVENTION: Fungal Target Genes and Methods

; FILE REFERENCE: PB/5-31285P1

; CURRENT APPLICATION NUMBER: US/09/625,188

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1575

; TYPE: DNA

; ORGANISM: Ashbya gossypii

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1575)

US-09-625-188-1

Alignment Scores:  
Pred. No.: 24.3 Length: 1575  
Score: 66.00 Matches: 12  
Percent Similarity: 63.3% Conservative: 7  
Best Local Similarity: 40.0% Mismatches: 11  
Query Match: 22.2% Indels: 0  
DB: 3 Gaps: 0

US-10-628-525A-35 (1-58) x US-09-625-188-1 (1-1575)

QY 3 GlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAla 22  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 1187 CGTTACTGGCACCTCGTACTACATAGCGCGCGGAGCGATCGAGGCCAGCTTACAGCG 1246  
QY 23 ThrProIleThrSerLysMetTrpSerSer 32  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 1247 TCACCAAGCGACGTCTGGTGGCTGCTCA 1276

RESULT 30

US-09-949-016-2306/c

; Sequence 2306, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2306  
; LENGTH: 2464  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-2306

Alignment Scores:  
Pred. No.: 45 Length: 2464  
Score: 66.00 Matches: 21  
Percent Similarity: 50.0% Conservative: 7  
Best Local Similarity: 37.5% Mismatches: 12  
Query Match: 22.2% Indels: 16  
DB: 3 Gaps: 3

US-10-628-525A-35 (1-58) x US-09-949-016-2306 (1-2464)

QY 2 AlaGlnIleLeuAlaPro-----SerThrGlnTrp 11  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 861 GCGCGCTTGTGGGCCCAATGCTTCTTGTGCTTGAATCTCTCCGCCAGGTGG 802  
QY 12 ---GlnMetArgIleThrLysThrSerPro-----CysAlaThrProIle 25  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 801 CTCACCATGCGGTGTGCGAAGTCTCACCGCCCGGCGGTGTCGCGCGCTTC 742  
QY 26 ThrSerLysMetTrpSerSerIleValMetLysGlnThrLysLysVal 41  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 741 ACCTCGAAGATGCCATCTCTCGATGTCAGGATGGACACGTCGAAAGTG 694

Search completed: March 31, 2006, 23:22:52

Job time : 99.568 secs

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 2, 2006, 00:58:46 ; Search time 274.022 Seconds  
(without alignments)  
1750.313 Million cell updates/sec

Title: US-10-628-525A-35

Perfect score: 297

Sequence: 1 MAQILAPSTQWQRITKSP.....KKVAHSKPRVMAVNSNGT 58

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Database :

Published Applications NA Main:

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- 10: /cgn2\_6/prodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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| 3          | 197   | 66.3        | 2124   | 7  | US-10-424-599-3238 |
| 4          | 174.5 | 58.8        | 1508   | 8  | US-10-767-795-6095 |
| 5          | 155.5 | 52.4        | 3895   | 7  | US-10-487-901-5832 |
| 6          | 137   | 46.1        | 382    | 7  | US-10-424-599-465  |
| 7          | 115   | 38.7        | 487    | 3  | US-09-770-961-774  |
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|            |       |             |        |    | Sequence 5829, Ap  |
|            |       |             |        |    | Sequence 3238, Ap  |
|            |       |             |        |    | Sequence 6095, Ap  |
|            |       |             |        |    | Sequence 5832, Ap  |
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|            |       |             |        |    | Sequence 774, App  |

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Sequence 291, App

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143 66 22.2 1570 5 US-10-184-614-335 Sequence 335, App
144 66 22.2 1570 5 US-10-184-623-335 Sequence 335, App
145 66 22.2 1570 5 US-10-184-633-335 Sequence 335, App
146 66 22.2 1570 5 US-10-184-637-335 Sequence 335, App
147 66 22.2 1570 5 US-10-184-646-335 Sequence 335, App
148 66 22.2 1570 5 US-10-184-647-335 Sequence 335, App
149 66 22.2 1570 5 US-10-184-652-335 Sequence 335, App
150 66 22.2 1570 5 US-10-187-594-335 Sequence 335, App
```

## ALIGNMENTS

```
RESULT 1
US-10-487-901-1682
; Sequence 1682, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutula
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1682
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-1682

Alignment Scores:
Pred. No.: 2,2e-19 Length: 589
Score: 199.00 Matches: 40
Conservative: 10
Best Local Similarity: 66.7% Mismatches: 8
Query Match: 67.0% Indels: 2
DB: 9 Gaps: 1

US-10-628-525A-35 (1-58) x US-10-487-901-1682 (1-589)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20
60 ATGGCTCAGATCTTGCTCCATCTCGCAATGGCAGATGAGATGACAAAGAGCTCAACA 119
21 CysAlaThrProIleThrSerIysMetTrpSerSerLeuValMetIysGlnThrIysLys 40
120 GATGCTAAATCCCTTGACTTCAAGATGTGGAGTTCTGTGGTGTGAAGCAGATAAAGA 179
41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
180 CTGCTGTATAAGCTCTGCCAATTAGTCTTTGCTCTCCAATCTGATAGTGGCACT 239

RESULT 2
US-10-487-901-5829
; Sequence 5829, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutula
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
```

; NUMBER OF SEQ ID NOS: 7560  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5829  
; LENGTH: 1633  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-487-901-5829

Alignment Scores:  
Pred. No.: 8.44e-19 Length: 1633  
Score: 199.00 Matches: 40  
Percent Similarity: 83.3% Conservative: 10  
Best Local Similarity: 66.7% Mismatches: 8  
Query Match: 67.0% Indels: 2  
DB: 9 Gaps: 1

US-10-628-525A-35 (1-58) x US-10-487-901-5829 (1-1633)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
DB 74 ATGGCTCAGATCTTGGCTCCATCTGCGCAATGGCAGATGAGATGACAAAGAGCTCAACA 133  
QY 21 CyAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
DB 134 GATGCTAATCCCTTGACTTCAGAGATGTGGAGTTCTGTGGTGTGAAGCAGATAAAGA 193  
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAAsnSerGluAAsnGlyThr 58  
DB 194 CTTCGCTGTTAAAGCTCTGCCAAATTCGAGTCTTGCTCTCCAACTGATGTGGCACT 253

## RESULT 3

US-10-424-599-3238  
; Sequence 3238, Application US/10424599  
; Publication No. US20040031072A1

; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 3238  
; LENGTH: 2124  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_102929C.1  
US-10-424-599-3238

Alignment Scores:  
Pred. No.: 2.36e-18 Length: 2124  
Score: 197.00 Matches: 43  
Percent Similarity: 84.7% Conservative: 7  
Best Local Similarity: 72.9% Mismatches: 6  
Query Match: 66.3% Indels: 3  
DB: 7 Gaps: 1

US-10-628-525A-35 (1-58) x US-10-424-599-3238 (1-2124)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPr 20  
DB 480 ATGGCAGATTTGGCTCCCTCTACGCAATGGCAGATGAGATCTCCAAATCCCTCTCC 539  
QY 20 CyAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
DB 540 CAATGCAAGTCCCATACATCAACATGTGGAGTTCTTTATTGTGGAAACAAATAGAA 599

QY 40 sValAla-----HisSerAlaLysPheArgValMetAlaValAAsnSerGluAAsn 56  
DB 600 AGTTTCCACCACCAAGTTCTCTCTAAATTTAGAGTATGCAATTAAGTCTGCAAT 654

## RESULT 4

US-10-767-795-6095  
; Sequence 6095, Application US/10767795  
; Publication No. US2004018130A1

; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Zhou, Yihua  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53534)B  
; CURRENT APPLICATION NUMBER: US/10/767,795  
; CURRENT FILING DATE: 2004-01-30  
; NUMBER OF SEQ ID NOS: 117596  
; SEQ ID NO 6095  
; LENGTH: 1508  
; TYPE: DNA  
; ORGANISM: Gossypium hirsutum  
; FEATURE:  
; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C6662\_1  
US-10-767-795-6095

Alignment Scores:  
Pred. No.: 3.29e-15 Length: 1508  
Score: 174.50 Matches: 38  
Percent Similarity: 76.7% Conservative: 8  
Best Local Similarity: 63.3% Mismatches: 11  
Query Match: 58.8% Indels: 3  
DB: 8 Gaps: 2

US-10-628-525A-35 (1-58) x US-10-767-795-6095 (1-1508)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
DB 135 ATGGCAGATCTTTAGCACCTCACTCAATGGCAATGACACTACCAAGAGCTCAACC 194  
QY 21 CyAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
DB 195 TATGGAAGTCCCATTCGACAAATAATGTGGAGTTCTCTGTACTGAAACAGAACAGAA 254  
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAAsnSerGluAAsnGlyThr 58  
DB 255 GGAGCTGTCTAAAGCTCTGGCAAGTTTAAAGTGGTGGCTTG---TCTGAAAAAGCACT 311

## RESULT 5

US-10-487-901-5832  
; Sequence 5832, Application US/10487901  
; Publication No. US20050091708A1

; GENERAL INFORMATION:  
; APPLICANT: Oreido, Jeremiah Vincent  
; APPLICANT: McCrery, David  
; APPLICANT: Fell, Randy  
; APPLICANT: Miller, Barbara  
; APPLICANT: Weglarz, Thaddeus  
; APPLICANT: Gachotte, Daniel  
; APPLICANT: Blakeslee, Beth  
; APPLICANT: Larrinua, Ignacio  
; APPLICANT: Reddy, Avutu  
; APPLICANT: Shukla, Vipula  
; APPLICANT: Croasley, Rodney  
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri  
; FILE REFERENCE: DOW-08552  
; CURRENT APPLICATION NUMBER: US/10/487,901  
; CURRENT FILING DATE: 2004-02-26  
; NUMBER OF SEQ ID NOS: 7560  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5832  
; LENGTH: 3895  
; TYPE: DNA

; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-487-901-5832

## Alignment Scores:

Pred. No.: 7.59e-12 Length: 3895  
Score: 155.50 Matches: 34  
Percent Similarity: 72.1% Conservative: 10  
Best Local Similarity: 55.7% Mismatches: 14  
Query Match: 52.4% Indels: 3  
DB: 9 Gaps: 2

US-10-628-525A-35 (1-58) x US-10-487-901-5832 (1-3895)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
Db 318 ATGGCACAGATTTAGCACCTTCACGCAATGTCAGATGAAGATAACAAATCAACAACA 377  
QY 21 ---CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLys 39  
|||||  
Db 378 AATGCTGCAAGCCCAATTACTACAAGATGTGGGTTCTCTAATGTTTAACCGAAGAAAGA 437  
QY 40 Lys-----ValalaHisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGly 57  
|||||  
Db 438 AGTGGACTTACTAAAAACGCTTCTAAATTCAAAATGTTATGTTGTTAAATCGGAACGCT 497  
QY 58 Thr 58  
|||  
Db 498 ACC 500

## RESULT 6

US-10-424-599-465  
; Sequence 465, Application US/10424599  
; Publication No. US20040031072A1

## GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 465  
; LENGTH: 382  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_10041C.1  
US-10-424-599-465

## Alignment Scores:

Pred. No.: 1.98e-10 Length: 382  
Score: 137.00 Matches: 29  
Percent Similarity: 85.0% Conservative: 5  
Best Local Similarity: 72.5% Mismatches: 6  
Query Match: 46.1% Indels: 1  
DB: 7 Gaps: 0

US-10-628-525A-35 (1-58) x US-10-424-599-465 (1-382)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
Db 263 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGAGAATCTCAAAATCCTCTCCC 322  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLys 40  
|||||  
Db 323 AATGCAACTCCCATTACATCAACATGTGGGT-TCTTTATTGTGGAAACAAATATAGAAAG 381

## RESULT 7

US-09-770-961-774  
; Sequence 774, Application US/09770961  
; Publication No. US20030115639A1  
; GENERAL INFORMATION:

; APPLICANT: Gorlach, Jorn  
; APPLICANT: An, Yong-Qiang  
; APPLICANT: Hamilton, Carol M.  
; APPLICANT: Price, Jennifer L.  
; APPLICANT: Raines, Tracy M.  
; APPLICANT: Yu, Yang  
; APPLICANT: Rameaka, Joshua G.  
; APPLICANT: Page, Amy  
; APPLICANT: Matthew, Abraham V.  
; APPLICANT: Ledford, Brooke L.  
; APPLICANT: Woessner, Jeffrey P.  
; APPLICANT: Haas, William David  
; APPLICANT: Garcia, Carlos A.  
; APPLICANT: Kricker, Maja  
; APPLICANT: Slader, Ted  
; APPLICANT: Davis, Keith R.  
; APPLICANT: Allen, Keith  
; APPLICANT: Hoffman, Neil  
; APPLICANT: Hurban, Patrick  
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
; FILE REFERENCE: 2026 (PARA-015PRV)  
; CURRENT APPLICATION NUMBER: US/09/770,961  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 60/178,466  
; NUMBER OF SEQ ID NOS: 999  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 774  
; LENGTH: 487  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-770-961-774

## Alignment Scores:

Pred. No.: 5.03e-07 Length: 487  
Score: 115.00 Matches: 28  
Percent Similarity: 65.1% Conservative: 11  
Best Local Similarity: 47.5% Mismatches: 18  
Query Match: 38.7% Indels: 2  
DB: 3 Gaps: 2

US-10-628-525A-35 (1-58) x US-09-770-961-774 (1-487)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
Db 48 ATGGCTCAGATCTTAGCAGCTTCTCCACATGTCAGATGAGAGTGCTTAAACACTCATCA 107  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLys 40  
|||||  
Db 108 GTCATTGCATCA---TCATCCAAAGTTATGGAGCTCTGTGTGTTGAAACAGAAAGCAG 164  
QY 41 ValAlaHisSerAlaLys---PheArgValMetAlaValAsnSerGluAsnGlyThr 58  
|||||  
Db 165 AGCAACAACAAAGTCAGAGGCTTTAGAGTTCTTGCTCTCCAAATCTGATAACAGTACT 221

## RESULT 8

US-10-424-599-24764  
; Sequence 24764, Application US/10424599  
; Publication No. US20040031072A1

## GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599





## Alignment Scores:

Pred. No.: 7.96 Length: 1062  
Score: 69.50 Matches: 17  
Percent Similarity: 49.0% Conservative: 7  
Best Local Similarity: 34.7% Mismatches: 16  
Query Match: 23.4% Indels: 9  
DB: 3 Gaps: 2

US-10-628-525A-35 (1-58) x US-09-738-626-1418 (1-1062)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db ATGTCATCTCTTTTGAGCGATTCA-----ATGAGCTCAACGGCGCCT 255  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db TGTACAGATCCGACTACT-----TGGAGCTCAATGTTGTTCAATATACCAAGCGCA 204  
QY 41 ValAlaHisSerAlaLysPheArgVal 49  
Db ACTGCTAATCCACGAAGTTTAGATTG 177

## RESULT 12

US-10-494-672-115/c  
; Sequence 115, Application US/10494672  
; Publication No. US20050003494A1  
; GENERAL INFORMATION:  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Krogger, Burkhard  
; APPLICANT: Klopprogge, Corinna  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: Genes coding for novel proteins  
; FILE REFERENCE: BGI-169US  
; CURRENT APPLICATION NUMBER: US/10/494,672  
; CURRENT FILING DATE: 2004-05-04  
; PRIOR APPLICATION NUMBER: PCT/EP02/12134  
; PRIOR FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: DE 10154177  
; PRIOR FILING DATE: 2001-11-05  
; NUMBER OF SEQ ID NOS: 434  
; SEQ ID NO 115  
; LENGTH: 1192  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (101)..(1162)  
; OTHER INFORMATION: RXA01128

## US-10-494-672-115

Alignment Scores:  
Pred. No.: 9.27 Length: 1192  
Score: 69.50 Matches: 17  
Percent Similarity: 49.0% Conservative: 7  
Best Local Similarity: 34.7% Mismatches: 16  
Query Match: 23.4% Indels: 9  
DB: 8 Gaps: 2

US-10-628-525A-35 (1-58) x US-10-494-672-115 (1-1192)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db ATGTCATCTCTTTTGAGCGATTCA-----ATGAGCTCAACGGCGCCT 355  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db TGTACAGATCCGACTACT-----TGGAGCTCAATGTTGTTCAATATACCAAGCGCA 304  
QY 41 ValAlaHisSerAlaLysPheArgVal 49  
Db ACTGCTAATCCACGAAGTTTAGATTG 277

## RESULT 13

US-10-721-922A-197  
; Sequence 197, Application US/10721922A  
; Publication No. US20050191732A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Krogger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION  
; FILE REFERENCE: BGI-132PCPN  
; CURRENT APPLICATION NUMBER: US/10/721,922A  
; CURRENT FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: 09/6027777  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 09/603124  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 60/143694  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: US 60/151778  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: DE 19931418.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932124.8  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932126.4  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932127.2  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932133.7  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 480  
; SEQ ID NO 197  
; LENGTH: 1539  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (101)..(1516)  
; OTHER INFORMATION: RXN00622

## US-10-721-922A-197

Alignment Scores:  
Pred. No.: 13 Length: 1539  
Score: 69.50 Matches: 19  
Percent Similarity: 50.8% Conservative: 14  
Best Local Similarity: 29.2% Mismatches: 21  
Query Match: 23.4% Indels: 11  
DB: 9 Gaps: 3

US-10-628-525A-35 (1-58) x US-10-721-922A-197 (1-1539)

QY 3 GlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAla 22  
Db CAGATACTGTGTGGCGCCACCAAGTGGGTACCCCGTTGAAGAGACGTTGTTGGTGATCC 91  
QY 23 ThrProIleThrSerLysMet-----TrpSerSerLeuValMetLysGln----- 37  
Db ACGAGCTGTAGTAACGTTATTCCACTGGGTGGGCGCACCTCGTTCAGAAAAGTTTCATC 151  
QY 38 -----ThrLysLysValAlaHisSerAlaLysPheArgValMetAlaValAsn 53  
Db CTTTTTGGTGGCGCTCCAGATC-----ACCTCTGAAGTAGCGGTGCTTCCTTCGAC 205  
QY 54 SerGluAsnGlyThr 58  
Db CAGCCAGAGGGCACC 220





```
QY 1 MetAlaGlnIleuAla-----ProSerThrGlnTrp 11
Db 261 ATGGAGAGATCTTTCCCACTCCTAATGAACCGCCAGCGTGTGCCCAAGATTTTGGTGG 320
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSer 31
Db 321 AAAATGCAAGAACTTCCCTCAGTGTGTGTAGNAATCTCTGACCAAGAAGTGTGGAAAT 380
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
Db 381 GGTATACTGCTAAAGACTTCATTGTTGGGAAGTCACTCA 419
RESULT 20
US-09-764-881-61
; Sequence 61, Application US/09764881
; Publication No. US20020086821A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT207
; CURRENT APPLICATION NUMBER: US/09/764,881
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (873)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (902)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (920)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (936)
; OTHER INFORMATION: n equals a,t,g, or c
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-881-61
Alignment Scores:
Pred. No.: 13.4 Length: 939
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservative: 11
Best Local Similarity: 28.3% Mismatches: 18
Query Match: 22.7% Indels: 9
DB: 3 Gaps: 1
US-10-628-525A-35 (1-58) x US-09-764-881-61 (1-939)
QY 1 MetAlaGlnIleuAla-----ProSerThrGlnTrp 11
Db 159 ATGGAGAGATCTTTCCCACTCCTAATGAACCGCCAGCGTGTGCCCAAGATTTTGGTGG 218
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSer 31
Db 219 AAAATGCAAGAACTTCCCTCAGTGTGTGTAGNAATCTCTGACCAAGAAGTGTGGAAAT 278
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
Db 279 GGTATACTGCTAAAGACTTCATTGTTGGGAAGTCACTCA 317
RESULT 21
US-09-764-881-61
; Sequence 61, Application US/09764881
; Publication No. US20030125246A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
```

```
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT207
; CURRENT APPLICATION NUMBER: US/09/764,881
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (873)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (902)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (920)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (936)
; OTHER INFORMATION: n equals a,t,g, or c
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-881-61
Alignment Scores:
Pred. No.: 13.4 Length: 939
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservative: 11
Best Local Similarity: 28.3% Mismatches: 18
Query Match: 22.7% Indels: 9
DB: 3 Gaps: 1
US-10-628-525A-35 (1-58) x US-09-764-881-61 (1-939)
QY 1 MetAlaGlnIleuAla-----ProSerThrGlnTrp 11
Db 159 ATGGAGAGATCTTTCCCACTCCTAATGAACCGCCAGCGTGTGCCCAAGATTTTGGTGG 218
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSer 31
Db 219 AAAATGCAAGAACTTCCCTCAGTGTGTGTAGNAATCTCTGACCAAGAAGTGTGGAAAT 278
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
Db 279 GGTATACTGCTAAAGACTTCATTGTTGGGAAGTCACTCA 317
RESULT 22
US-09-764-875-496
; Sequence 496, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ202
; CURRENT APPLICATION NUMBER: US/09/764,875
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 496
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (873)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (902)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
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; LOCATION: (920)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (936)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-875-496

Alignment Scores:
Pred. No.: 13.4 Length: 939
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservatives: 11
Best Local Similarity: 28.3% Mismatches: 18
Query Match: 22.7% Indels: 9
DB: 3 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-764-875-496 (1-939)
QY 1 MetAlaGlnIleLeuAla-----ProSerThrGlnTrp 11
Db 159 ATGGGAGAGATCCTTTCCCACTCTAATGAACCGCCAGCGTGTGCCAAAGTTTGGTGG 218
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSer 31
Db 219 AAAATGCAAGAACTTCCCTCAGTGTGCTAGAAATCTCTGACCAAGAAAGTTTGGAAAT 278
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
Db 279 GGTATCTGCTAAGACTTCATTGTTGGGAAGTCACTCA 317

RESULT 23
US-10-242-747-61
; Sequence 61, Application US/10242747
; Publication No. US2004005577A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT207C1
; CURRENT APPLICATION NUMBER: US/10/242,747
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,881
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (873)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (902)
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; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (920)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (936)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-242-747-61

Alignment Scores:
Pred. No.: 13.4 Length: 939
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservatives: 11
Best Local Similarity: 28.3% Mismatches: 18
Query Match: 22.7% Indels: 9
DB: 6 Gaps: 1

US-10-628-525A-35 (1-58) x US-10-242-747-61 (1-939)
QY 1 MetAlaGlnIleLeuAla-----ProSerThrGlnTrp 11
Db 159 ATGGGAGAGATCCTTTCCCACTCTAATGAACCGCCAGCGTGTGCCAAAGTTTGGTGG 218
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSer 31
Db 219 AAAATGCAAGAACTTCCCTCAGTGTGCTAGAAATCTCTGACCAAGAAAGTTTGGAAAT 278
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
Db 279 GGTATCTGCTAAGACTTCATTGTTGGGAAGTCACTCA 317

RESULT 24
US-10-158-057-139
; Sequence 139, Application US/10158057
; Publication No. US20040014039A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ205C1
; CURRENT APPLICATION NUMBER: US/10/158,057
; CURRENT FILING DATE: 2002-06-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (873)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (902)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (920)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (936)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-158-057-139

Alignment Scores:
Pred. No.: 13.4 Length: 939
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservatives: 11
Best Local Similarity: 28.3% Mismatches: 18
```

```
Query Match: 22.7% Indels: 9
DB: 7 Gaps: 1
US-10-628-525A-35 (1-58) x US-10-158-057-139 (1-939)
QY 1 MetAlaGlnIleuAla-----ProSerThrGlnTTP 11
Db 159 ATGGGAGAGATCTTTCCCACTCTAATGACCCGAGCGTGTGCCAAAGTTTGGTGG 218
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTTPSer 31
Db 219 AAAATGCAAGAACTTCCCTCAGTGTGTCTAGAAATCTCTGACCAAGAGTGTGGAAAT 278
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
Db 279 GGTATACTGCTAAAGACTTCATTGTTGGGAAGTCACTCA 317
RESULT 25
US-09-764-875-202
; Sequence 202, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: RJZ02
; CURRENT APPLICATION NUMBER: US/09/764,875
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 202
; LENGTH: 1339
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-875-202
Alignment Scores:
Pred. No.: 21.4 Length: 1339
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservatives: 11
Best Local Similarity: 28.3% Mismatches: 18
Query Match: 22.7% Indels: 9
DB: 3 Gaps: 1
US-10-628-525A-35 (1-58) x US-09-764-875-202 (1-1339)
QY 1 MetAlaGlnIleuAla-----ProSerThrGlnTTP 11
Db 102 ATGGGAGAGATCTTTCCCACTCTAATGACCCGAGCGTGTGCCAAAGTTTGGTGG 161
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTTPSer 31
Db 162 AAAATGCAAGAACTTCCCTCAGTGTGTCTAGAAATCTCTGACCAAGAGTGTGGAAAT 221
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
Db 222 GGTATACTGCTAAAGACTTCATTGTTGGGAAGTCACTCA 260
RESULT 26
US-10-158-057-62
; Sequence 62, Application US/10158057
; Publication No. US20040014039A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: RJZ05C1
; CURRENT APPLICATION NUMBER: US/10/158,057
; CURRENT FILING DATE: 2002-06-12
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-158-057-62
Alignment Scores:
Pred. No.: 21.5 Length: 1346
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservatives: 11
Best Local Similarity: 28.3% Mismatches: 18
Query Match: 22.7% Indels: 9
DB: 7 Gaps: 1
US-10-628-525A-35 (1-58) x US-10-158-057-62 (1-1346)
QY 1 MetAlaGlnIleuAla-----ProSerThrGlnTTP 11
Db 103 ATGGGAGAGATCTTTCCCACTCTAATGACCCGAGCGTGTGCCAAAGTTTGGTGG 162
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTTPSer 31
Db 163 AAAATGCAAGAACTTCCCTCAGTGTGTCTAGAAATCTCTGACCAAGAGTGTGGAAAT 222
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
Db 223 GGTATACTGCTAAAGACTTCATTGTTGGGAAGTCACTCA 261
RESULT 27
US-10-232-484-3
; Sequence 3, Application US/10232484
; Publication No. US20030113847A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: No US20030113847A1a1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 79ICIP2BDIV
; CURRENT APPLICATION NUMBER: US/10/232,484
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 09/695,783
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 09/552,929
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2438
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (205)..(2124)
; OTHER INFORMATION:
US-10-232-484-3
Alignment Scores:
Pred. No.: 47.1 Length: 2438
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservatives: 11
Best Local Similarity: 28.3% Mismatches: 18
Query Match: 22.7% Indels: 9
DB: 5 Gaps: 1
US-10-628-525A-35 (1-58) x US-10-232-484-3 (1-2438)
QY 1 MetAlaGlnIleuAla-----ProSerThrGlnTTP 11
Db 1052 ATGGGAGAGATCTTTCCCACTCTAATGACCCGAGCGTGTGCCAAAGTTTGGTGG 1111
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTTPSer 31
Db 1112 AAAATGCAAGAACTTCCCTCAGTGTGTCTAGAAATCTCTGACCAAGAGTGTGGAAAT 1171
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
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Db 1172 GGTATACGTAAAGACTTCATTGTTGGGAAGTCACTCA 1210  
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RESULT 28  
US-10-972-024-93  
; Sequence 93, Application US/10972024  
; Publication No. US20050221342A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 79ICIP4  
; CURRENT APPLICATION NUMBER: US/10/972,024  
; CURRENT FILING DATE: 2004-10-22  
; PRIOR APPLICATION NUMBER: PCT/US01/08655  
; PRIOR FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: 09/522,929  
; PRIOR FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: 09/770,160  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/668,317  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 09/695,783  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: 09/728,628  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 09/783,066  
; PRIOR FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: 09/816,828  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 584  
; SOFTWARE: Custom  
; SEQ ID NO 93  
; LENGTH: 2438  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (205)..(2124)  
US-10-972-024-93

Alignment Scores:  
Pred. No.: 47.1 Length: 2438  
Score: 67.50 Matches: 15  
Percent Similarity: 49.1% Conservative: 11  
Best Local Similarity: 28.3% Mismatches: 18  
Query Match: 22.7% Indels: 9  
DB: 9 Gaps: 1  
US-10-628-525A-35 (1-58) x US-10-972-024-93 (1-2438)  
QY 1 MetAlaGlnIleuAla-----ProSerThrGlnTTP 11  
Db 1052 ATGGGAGAGATCTTCCCACTCTTAATGAACGCCAGGTGTGCCAAAGTTTGGTGG 1111  
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTTPSer 31  
Db 1112 AAAATGCAAGAACTTCCCTCAGTGTGCTAGAAATCTCTGACCAAGAGTGTGGAT 1171  
QY 32 SerLeuValMetCysGlnThrLysLysValAlaHisSer 44  
Db 1172 GGTATACGTAAAGACTTCATTGTTGGGAAGTCACTCA 1210  
RESULT 29  
US-09-967-768A-314/c  
; Sequence 314, Application US/09967768A  
; Patent No. US20020150877A1  
; GENERAL INFORMATION:  
; APPLICANT: Augustus, Meena  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
; FILE REFERENCE: Seta  
; NAME REFERENCE: 689290-72  
; CURRENT APPLICATION NUMBER: US/09/967,768A  
; CURRENT FILING DATE: 2001-09-28

; PRIOR APPLICATION NUMBER: US/60/236,109  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US/60/236,034  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US/60/236,111  
; PRIOR FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 325  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 314  
; LENGTH: 174424  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-967-768A-314  
Alignment Scores:  
Pred. No.: 1.31e+04 Length: 174424  
Score: 67.50 Matches: 19  
Percent Similarity: 54.5% Conservative: 11  
Best Local Similarity: 34.5% Mismatches: 19  
Query Match: 22.7% Indels: 6  
DB: 3 Gaps: 2  
US-10-628-525A-35 (1-58) x US-09-967-768A-314 (1-174424)  
QY 7 ProSerThrGlnTTPGlnMet-ArgIleThrLysThrSer-----ProCysAlaTh 23  
Db 66631 CCCCCCTCCCTTTGGCCCCCTCTCTGACTTGGACTTCTCTCCCTCTCTGCCCC 66572  
QY 23 rProIleThrSerLysMetTTPSerSerLeuValMetLysGlnThrLysLysValAlaHi 43  
Db 66571 ACCTCTACCACTCTGGTGTGCTCTCTGAGGTGAACAAGACTCTGAGGCGGACACT 66512  
QY 43 sSerAlaLysPheArgValMetAlaValAsnSerGluangly 57  
Db 66511 GCAGGCCCTGCTGGAGGTGGTGGCC-----TCGGATGACGGG 66475

RESULT 30  
US-09-960-706-969/c  
; Sequence 969, Application US/09960706  
; Publication No. US20030134280A1  
; GENERAL INFORMATION:  
; APPLICANT: Munger, William E.  
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasi  
; FILE REFERENCE: 44921-5029-01US  
; CURRENT APPLICATION NUMBER: US/09/960,706  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 60/223,323  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: 09/873,319  
; PRIOR FILING DATE: 2001-06-05  
; NUMBER OF SEQ ID NOS: 1124  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 969  
; LENGTH: 174424  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 U52112  
US-09-960-706-969

Alignment Scores:  
Pred. No.: 1.31e+04 Length: 174424  
Score: 67.50 Matches: 19  
Percent Similarity: 54.5% Conservative: 11  
Best Local Similarity: 34.5% Mismatches: 19  
Query Match: 22.7% Indels: 6  
DB: 3 Gaps: 2  
US-10-628-525A-35 (1-58) x US-09-960-706-969 (1-174424)  
QY 7 ProSerThrGlnTTPGlnMet-ArgIleThrLysThrSer-----ProCysAlaTh 23  
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OM protein - nucleic search, using frame\_plus\_p2n model

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(without alignments)  
1278.753 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

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-MAXLEN=2000000000 -HOST=abs05h  
-USER=US10628525 @CN1\_1\_2249@runat\_31032006\_095139\_17270 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: /SIDSS/ptodata/2/pubnpa/US06\_NEW\_PUB.seq.\*  
3: /SIDSS/ptodata/2/pubnpa/US07\_NEW\_PUB.seq.\*  
4: /SIDSS/ptodata/2/pubnpa/PCT\_NEW\_PUB.seq.\*  
5: /SIDSS/ptodata/2/pubnpa/US05\_NEW\_PUB.seq.\*  
6: /SIDSS/ptodata/2/pubnpa/US09\_NEW\_PUB.seq.\*  
7: /SIDSS/ptodata/2/pubnpa/US10\_NEW\_PUB.seq.\*  
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9: /SIDSS/ptodata/2/pubnpa/US10\_NEW\_PUB.seq.\*  
10: /SIDSS/ptodata/2/pubnpa/US10\_NEW\_PUB.seq.\*  
11: /SIDSS/ptodata/2/pubnpa/US11\_NEW\_PUB.seq.\*  
12: /SIDSS/ptodata/2/pubnpa/US11\_NEW\_PUB.seq.\*  
13: /SIDSS/ptodata/2/pubnpa/US11\_NEW\_PUB.seq.\*  
14: /SIDSS/ptodata/2/pubnpa/US11\_NEW\_PUB.seq.\*  
15: /SIDSS/ptodata/2/pubnpa/US16\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description                         |
|------------|-------|-------|--------|----|-------------------------------------|
| 1          | 115   | 38.7  | 1310   | 11 | US-11-087-099-118 Sequence 118, App |
| 2          | 70.5  | 23.7  | 1367   | 14 | US-11-066-725-412 Sequence 412, App |



Alignment Scores:  
Pred. No.: 53.6 Length: 1367  
Score: 70.50 Matches: 15  
Percent Similarity: 58.1% Conservative: 3  
Best Local Similarity: 48.4% Mismatches: 12  
Query Match: 23.7% Indels: 1  
DB: 1 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-066-725-412 (1-1367)

Qy 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25  
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Db 1225 TCACCGTCCCTAAGCTGGAGCACCACCGACCCAGGAAAGACATGACCTGTACACACCATGT 1284

Qy 26 ThrSerLysMetTrp---SerSerLeuValMet 35  
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Db 1285 ACATGGAGGCCCTGGTGAAGCTCTTTGACAATC 1317

## RESULT 3

US-11-231-243-111  
; Sequence 111, Application US/11231243  
; Publication No. US2006063730A1  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Siwkowski, Andrew M.  
; APPLICANT: Bhanot, Sanjay  
; TITLE OF INVENTION: ENHANCED ANTISENSE OLIGONUCLEOTIDES  
; FILE REFERENCE: CORE0051US  
; CURRENT APPLICATION NUMBER: US/11/231,243  
; CURRENT FILING DATE: 2005-09-19  
; PRIOR APPLICATION NUMBER: 60/611,100  
; PRIOR FILING DATE: 2004-09-17  
; PRIOR APPLICATION NUMBER: 60/663,442  
; PRIOR FILING DATE: 2005-03-18  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 111  
; LENGTH: 31737  
; TYPE: DNA  
; ORGANISM: R. norvegicus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (26994)...(27191)  
; OTHER INFORMATION: n = A,T,C or G  
US-11-231-243-111

Alignment Scores:  
Pred. No.: 2.11e+03 Length: 31737  
Score: 70.50 Matches: 15  
Percent Similarity: 58.1% Conservative: 3  
Best Local Similarity: 48.4% Mismatches: 12  
Query Match: 23.7% Indels: 1  
DB: 1 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-231-243-111 (1-31737)

Qy 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25  
:::|||||  
Db 30208 TCACCGTCCCTAAGCTGGAGCACCACCGACCCAGGAAAGACATGACCTGTACACACCATGT 30267

Qy 26 ThrSerLysMetTrp---SerSerLeuValMet 35  
|||:::|||||  
Db 30268 ACATGGAGGCCCTGGTGAAGCTCTTTGACAATC 30300

## RESULT 4

US-10-454-437-129  
; Sequence 129, Application US/10454437  
; Publication No. US2005027115A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar

; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; FILE REFERENCE: BGI-128CPCN  
; CURRENT APPLICATION NUMBER: US/10/454,437  
; CURRENT FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: US 60/141031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: DE 19931636.8  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932125.6  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932126.4  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932127.2  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932128.0  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932129.9  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: DE 19932226.0  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932920.6  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: DE 19932922.2  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 442  
; SEQ ID NO 129  
; LENGTH: 1539  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (101)...(1516)  
; OTHER INFORMATION: RXN00622  
US-10-454-437-129

Alignment Scores:  
Pred. No.: 83 Length: 1539  
Score: 69.50 Matches: 19  
Percent Similarity: 50.8% Conservative: 14  
Best Local Similarity: 29.2% Mismatches: 21  
Query Match: 23.4% Indels: 11  
DB: 8 Gaps: 3

US-10-628-525A-35 (1-58) x US-10-454-437-129 (1-1539)

Qy 3 GlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAla 22  
|||||  
Db 32 CAGATACTGTGTGGCGCCACAGGTGGGTACCCCGTTTGAAGAGACGTTGGTGTACC 91  
|||||

Qy 23 ThrProIleThrSerLysMet-----TrpSerSerLeuValMetLysGln----- 37  
|||:::|  
Db 92 ACGAGCCTGATGAAGCTTATTCCACCTGGTGGGCACCACTCGTTTCAGAAAAAGTTTCATC 151  
|||||

Qy 38 -----ThrLysLysValAlaHisSerAlaLysPheArgValMetAlaValAsn 53  
|||:::|  
Db 152 CTTTTTGGTGGCGCTCCCAAGATC-----ACCTCTGAAGTAGCGGTCTTCTTTTCGAC 205  
|||||

Qy 54 SerGluAsnGlyThr 58  
|||  
Db 206 CAGCCAGAGGGGCACC 220  
|||||

## RESULT 5

US-10-454-437-131  
; Sequence 131, Application US/10454437  
; Publication No. US2005027115A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar



```
US-10-628-525A-35 (1-58) x US-09-925-065A-864939 (1-682)
Qy 15 lIeThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSerSerLeuVal 34
Db 381 GTGGTTTCAACAGGTCGGCTGCTGCCGCCCAAGCTTGTGGCAAGACCATC 322
Qy 35 MetLysGlnThrLysLeValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
Db 321 ACCGACAGGCCCAAGAGTGGGGGCACCAAGCCAGAGAGGGCTACCTTCATGCTTTAGT 262
Qy 55 GluAsn 56
Db 261 TCCAAC 256

RESULT 8
US-11-231-243-110
; Sequence 110, Application US/11231243
; Publication No. US2006063730A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Siwkowski, Andrew M.
; APPLICANT: Bhanot, Sanjay
; TITLE OF INVENTION: ENHANCED ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: CORE0051US
; CURRENT APPLICATION NUMBER: US/11/231,243
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: 60/611,100
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/663,442
; PRIOR FILING DATE: 2005-03-18
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 2439
; TYPE: DNA
; ORGANISM: H. sapiens
US-11-231-243-110

Alignment Scores:
Pred. No.: 404 Length: 2439
Score: 66.00 Matches: 19
Percent Similarity: 45.3% Conservative: 5
Best Local Similarity: 35.8% Mismatches: 18
Query Match: 22.2% Indels: 12
DB: 11 Gaps: 2

US-10-628-525A-35 (1-58) x US-11-231-243-110 (1-2439)
Qy 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 1255 TCACCATCCCAAGCTGGAGCACCACCCAGCAAGACATCGACCTGTATCACCATGT 1314
Qy 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 1315 ACATGGAGGCCCTGGTG-AAGCTCTTCGACAAAG-----CACAGACC 1355
Qy 46 LysPhe-----ArgValMetAlaValAsn 53
Db 1356 AAGTTCGGCTCCCGGAGACTGAGGTCTCTGGAGGTGAAC 1394

RESULT 9
US-11-066-725-4
; Sequence 4, Application US/11066725
; Publication No. US20050272680A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Kenneth W. Doble
; APPLICANT: Xing-Xian Yu
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
; FILE REFERENCE: RTS-0678US.C1
; CURRENT APPLICATION NUMBER: US/11/066,725

US-10-628-525A-35 (1-58) x US-11-066-725-4 (1-2439)
Qy 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 1255 TCACCATCCCAAGCTGGAGCACCACCCAGCAAGACATCGACCTGTATCACCATGT 1314
Qy 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 1315 ACATGGAGGCCCTGGTG-AAGCTCTTCGACAAAG-----CACAGACC 1355
Qy 46 LysPhe-----ArgValMetAlaValAsn 53
Db 1356 AAGTTCGGCTCCCGGAGACTGAGGTCTCTGGAGGTGAAC 1394

RESULT 10
US-11-072-512-756
; Sequence 756, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOMYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 756
; LENGTH: 2678
```



```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-756

Alignment Scores:
Pred. No.: 450 Length: 2678
Score: 66.00 Matches: 19
Percent Similarity: 45.3% Conservatives: 5
Best Local Similarity: 35.8% Mismatches: 18
Query Match: 22.2% Indels: 12
DB: 11 Gaps: 2

US-10-628-525A-35 (1-58) x US-11-072-512-756 (1-2678)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
   ::::::::::::::::::::
Db 2412 TCACCATCCCCAAGCTGGAGACCCCAACCCAGACATCGACCTGTACCCACACCATGT 2471
   ::::::::::::::::::::

QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
   ::::::::::::::::::::
Db 2472 ACATGGAGGCCCTGGTG-AAGCTCTTCGACAAAG-----CACAGACC 2512
   ::::::::::::::::::::

QY 46 LysPhe-----ArgValMetAlaValAen 53
   ::::::::::::::::::::
Db 2513 AAGTTGGGCTCCCGGAGACTGAGGTCTCTGGAGGTGAAC 2551
   ::::::::::::::::::::

RESULT 11
US-11-066-725-18
; Sequence 18, Application US/11066725
; Publication NO. US20050272680A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Kenneth W. Dobie
; APPLICANT: King-Xian Yu
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
; FILE REFERENCE: RTS-0678US.C1
; CURRENT APPLICATION NUMBER: US/11/066, 725
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: US/10/643, 801
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: PCT/US2004/024384
; PRIOR FILING DATE: 2004-08-18
; NUMBER OF SEQ ID NOS: 492
; SEQ ID NO 18
; LENGTH: 42823
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-11-066-725-18

Alignment Scores:
Pred. No.: 1,14e+04 Length: 42823
Score: 66.00 Matches: 19
Percent Similarity: 45.3% Conservatives: 5
Best Local Similarity: 35.8% Mismatches: 18
Query Match: 22.2% Indels: 12
DB: 14 Gaps: 2

US-10-628-525A-35 (1-58) x US-11-066-725-18 (1-42823)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
   ::::::::::::::::::::
Db 41255 TCACCATCCCCAAGCTGGAGACCCCAACCCAGACATCGACCTGTACCCACACCATGT 41314
   ::::::::::::::::::::

QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
   ::::::::::::::::::::
Db 41315 ACATGGAGGCCCTGGTG-AAGCTCTTCGACAAAG-----CACAGACC 41355
   ::::::::::::::::::::

QY 46 LysPhe-----ArgValMetAlaValAen 53
   ::::::::::::::::::::
Db 41356 AAGTTGGGCTCCCGGAGACTGAGGTCTCTGGAGGTGAAC 41394
   ::::::::::::::::::::
```

```
RESULT 12
US-09-925-065A-651006/c
; Sequence 651006, Application US/09925065A
; Publication NO. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 651006
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-651006

Alignment Scores:
Pred. No.: 76.8 Length: 518
Score: 65.50 Matches: 17
Percent Similarity: 66.7% Conservatives: 9
Best Local Similarity: 43.6% Mismatches: 12
Query Match: 22.1% Indels: 22
DB: 6 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-925-065A-651006 (1-518)

QY 17 LysThrSerProCysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLys 36
   ::::::::::::::::::::
Db 466 AAATCTCTACCATGTGCCAA----CTCTGTGCCAAGGCTGGGATACTCTGGGAATAAAA 411
   ::::::::::::::::::::

QY 37 GlnThrLysLysValAlaHisSerAlaLysPheArgValMetAlaValAenSerGlu 55
   ::::::::::::::::::::
Db 410 AGATRGAGAAAGTCTCTTCTTCTGTGAGTTTCAGGGTCAGTGGGGTGTCAAGTGAG 354
   ::::::::::::::::::::

RESULT 13
US-11-177-506-8/c
; Sequence 8, Application US/11177506
; Publication NO. US20060029956A1
; GENERAL INFORMATION:
; APPLICANT: Beyer, Wayne F.
; APPLICANT: Venetta, Thomas M.
; APPLICANT: Groelke, John W.
; APPLICANT: Blaesius, Rainer H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: DETECTION OF OVARIAN DISEASE
; FILE REFERENCE: 46143/294851
; CURRENT APPLICATION NUMBER: US/11/177,506
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: 60/586,856
; PRIOR FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 5067
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)...(5052)
```

## US-11-177-506-8

Alignment Scores:  
Pred. No.: 1.28e+03 Length: 5067  
Score: 65.00 Matches: 13  
Percent Similarity: 63.0% Conservative: 4  
Best Local Similarity: 48.1% Mismatches: 10  
Query Match: 21.9% Indels: 0  
DB: 11 Gaps: 0

## US-10-628-525A-35 (1-58) x US-11-177-506-8 (1-5067)

QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26  
Db 251 CCTGGGAGTCGTGGACAGTAACAGTCCCTTGGCGGTGGCGCTCC 192  
QY 27 SerLysMetTrpSerSerLeu 33  
Db 191 AGCACCATGGTCTCTCGCTC 171

## RESULT 14

US-11-000-688-83/c  
; Sequence 83, Application US/11000688  
; Publication No. US20050287544A1  
; GENERAL INFORMATION:  
; APPLICANT: BERTUCCI, Francois  
; APPLICANT: HOULGATTE, Remi  
; APPLICANT: BIRNBAUM, Daniel  
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS  
; FILE REFERENCE: 1423-R-03  
; CURRENT APPLICATION NUMBER: US/11/000,688  
; CURRENT FILING DATE: 2004-12-01  
; PRIOR APPLICATION NUMBER: US 60/525,987  
; PRIOR FILING DATE: 2003-12-01  
; NUMBER OF SEQ ID NOS: 1596  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 83  
; LENGTH: 5067  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial sequences: primer  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(5067)  
; OTHER INFORMATION: complement component 3 (C3) gene.  
US-11-000-688-83

Alignment Scores:  
Pred. No.: 1.28e+03 Length: 5067  
Score: 65.00 Matches: 13  
Percent Similarity: 63.0% Conservative: 4  
Best Local Similarity: 48.1% Mismatches: 10  
Query Match: 21.9% Indels: 0  
DB: 14 Gaps: 0

## US-10-628-525A-35 (1-58) x US-11-000-688-83 (1-5067)

QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26  
Db 251 CCTGGGAGTCGTGGACAGTAACAGTCCCTTGGCGGTGGCGCTCC 192  
QY 27 SerLysMetTrpSerSerLeu 33  
Db 191 AGCACCATGGTCTCTCGCTC 171

## RESULT 15

US-10-467-657-2417  
; Sequence 2417, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 2417  
; LENGTH: 1569  
; TYPE: DNA  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2417

Alignment Scores:  
Pred. No.: 377 Length: 1569  
Score: 64.50 Matches: 18  
Percent Similarity: 50.0% Conservative: 2  
Best Local Similarity: 45.0% Mismatches: 13  
Query Match: 21.7% Indels: 7  
DB: 8 Gaps: 2

## US-10-628-525A-35 (1-58) x US-10-467-657-2417 (1-1569)

QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 25  
Db 221 CGTCAACCTCTTGGACACGCCGGGACACCAAGACTTCTCCG---AAGACACCTACCGCG 277  
QY 26 -----ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db 278 TTTTAACCGCAGTGGACAGCGCTTGTGTCATCGACGGCAAGGGCGTGGAGCGC 337

## RESULT 16

US-09-925-065A-261697  
; Sequence 261697, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 261697  
; LENGTH: 562  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-261697

Alignment Scores:  
Pred. No.: 132 Length: 562  
Score: 64.00 Matches: 11  
Percent Similarity: 50.0% Conservative: 8  
Best Local Similarity: 28.9% Mismatches: 19  
Query Match: 21.5% Indels: 0  
DB: 6 Gaps: 0

## US-10-628-525A-35 (1-58) x US-09-925-065A-261697 (1-562)

```
QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 440 CCCACAGTCAGTGGCACTGAGAGTGAAGATAGCTTGCCTTGGAAATCCAACTGAA 499

QY 27 SerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSer 44
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 500 GGGAAATATGGGTTAAAGAAATAGAGGGGGATTGTACACTTAGCACATACT 553

RESULT 17
US-09-925-065A-261698
; Sequence 261698, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261698
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-261698

Alignment Scores:
Pred. No.: 132 Length: 562
Score: 64.00 Matches: 11
Percent Similarity: 50.0% Conservative: 8
Best Local Similarity: 28.9% Mismatches: 19
Query Match: 21.5% Indels: 0
DB: 6 Gaps: 0

US-10-628-525A-35 (1-58) x US-09-925-065A-261698 (1-562)

QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 440 CCCACAGTCAGTGGCACTGAGAGTGAAGATAGCTTGCCTTGGAAATCCAACTGAA 499

QY 27 SerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSer 44
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 500 GGGAAATATGGGTTAAAGAAATAGAGGGGGATTGTACACTTAGCACATACT 553

RESULT 18
US-10-301-480-339963
; Sequence 339963, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 339963
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-339963

Alignment Scores:
Pred. No.: 133 Length: 565
Score: 64.00 Matches: 11
Percent Similarity: 50.0% Conservative: 8
Best Local Similarity: 28.9% Mismatches: 19
Query Match: 21.5% Indels: 0
DB: 10 Gaps: 0

US-10-628-525A-35 (1-58) x US-10-301-480-339963 (1-565)

QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 440 CCCACAGTCAGTGGCACTGAGAGTGAAGATAGCTTGCCTTGGAAATCCAACTGAA 499

QY 27 SerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSer 44
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 500 GGGAAATATGGGTTAAAGAAATAGAGGGGGATTGTACACTTAGCACATACT 553

RESULT 19
US-10-301-480-339964
; Sequence 339964, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339964
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-339964

Alignment Scores:
Pred. No.: 133 Length: 565
Score: 64.00 Matches: 11
Percent Similarity: 50.0% Conservative: 8
Best Local Similarity: 28.9% Mismatches: 19
Query Match: 21.5% Indels: 0
DB: 10 Gaps: 0

US-10-628-525A-35 (1-58) x US-10-301-480-339964 (1-565)

QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 440 CCCACAGTCAGTGGCACTGAGAGTGAAGATAGCTTGCCTTGGAAATCCAACTGAA 499

QY 27 SerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSer 44
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 500 GGGAAATATGGGTTAAAGAAATAGAGGGGGATTGTACACTTAGCACATACT 553

RESULT 20
US-10-301-480-953372
; Sequence 953372, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; in the Human Genome
```

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; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 953372
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-953372

Alignment Scores:
Pred. No.: 133 Length: 565
Score: 64.00 Matches: 11
Percent Similarity: 50.0% Conservative: 8
Best Local Similarity: 28.9% Mismatches: 19
Query Match: 21.5% Indels: 0
DB: 10 Gaps: 0

US-10-628-525A-35 (1-58) x US-10-301-480-953372 (1-565)

QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26
Db 440 CCCACAGTCAGTGGCACTGAGAGTGAAGATAGCTTGCCAAATGGAAATCCCACTGAA 499
QY 27 SerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValalaHisSer 44
Db 500 GGGAAATATGGTTAAAGAAATAGAGGGGGGATTTGTACACTTAGCACATACT 553

RESULT 21
US-10-301-480-953373
; Sequence 953373, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 953373
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-953373

Alignment Scores:
Pred. No.: 133 Length: 565
Score: 64.00 Matches: 11
Percent Similarity: 50.0% Conservative: 8
Best Local Similarity: 28.9% Mismatches: 19
Query Match: 21.5% Indels: 0
DB: 10 Gaps: 0

US-10-628-525A-35 (1-58) x US-10-301-480-953373 (1-565)

QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26
Db 440 CCCACAGTCAGTGGCACTGAGAGTGAAGATAGCTTGCCAAATGGAAATCCCACTGAA 499
QY 27 SerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValalaHisSer 44
Db 500 GGGAAATATGGTTAAAGAAATAGAGGGGGGATTTGTACACTTAGCACATACT 553
```

```

RESULT 22
US-09-925-065A-309283/c
; Sequence 309283, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 309283
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-309283

Alignment Scores:
Pred. No.: 149 Length: 549
Score: 63.50 Matches: 13
Percent Similarity: 63.6% Conservative: 8
Best Local Similarity: 39.4% Mismatches: 11
Query Match: 21.4% Indels: 1
DB: 6 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-925-065A-309283 (1-549)

QY 10 GlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMet 29
Db 416 CAGTGGGAGATG---ATCAAAATGACATCACCTGTTCTAAACCATTAATCTGGTGAGACA 360
QY 30 TrpSerSerLeuValMetLysGlnThrLysLysValala 42
Db 359 TAATATAGCTCTGTATTAGGGACACAAATTTTATCT 321

RESULT 23
US-10-301-480-384895/c
; Sequence 384895, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 384895
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-384895

Alignment Scores:
Pred. No.: 152 Length: 558
```



```
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 127
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(883)
; OTHER INFORMATION: FRXA00621
US-10-454-437-127

Alignment Scores:
Pred. No.: 268 Length: 906
Score: 63.50 Matches: 14
Percent Similarity: 57.9% Conservative: 8
Best Local Similarity: 36.8% Mismatches: 13
Query Match: 21.4% Indels: 3
DB: 8 Gaps: 1

US-10-628-525A-35 (1-58) x US-10-454-437-127 (1-906)

QY 3 GlnleuAlaProSerThrGlnMetArgIleThrLysThrSerProCysAla 22
|||||
Db 735 CAGATCTGTGCGCCACAGTGGTACCGGTTGGAAGAGCGTGTGGTGACC 794
|||||

QY 23 ThrProIleThrSerLysMet-----ThrSerSerLeuValMetLysGln 37
|||||
Db 795 ACGAGCTGTAGTAACGTTATTCACCTGGTGGCGCCACTCGTTCAGAAAG 848
|||||

RESULT 27
US-09-925-065A-278266
; Sequence 278266, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 278266
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-278266

Alignment Scores:
Pred. No.: 162 Length: 518
Score: 63.00 Matches: 17
```

```
Percent Similarity: 50.0% Conservative: 7
Best Local Similarity: 35.4% Mismatches: 15
Query Match: 21.2% Indels: 9
DB: 6 Gaps: 2

US-10-628-525A-35 (1-58) x US-09-925-065A-278266 (1-518)

QY 3 GlnleuAlaProSer-----ThrGlnTrpGlnMetArgIleThr-LysTh 18
|||||
Db 378 CAAAGTCTGTCTCCCTCCAGCGGAGCACTCACACAATGG-----ACTCACTTG 425
|||||

QY 18 rSerProCysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnTh 38
|||||
Db 426 TTTCCCATGCCCTCTCTTGTGACTTCCAGCTTCAGCGAACAACTTGAGCAAGAGTCAAA 485
|||||

QY 38 rLysLysValAlaHisSerAla 45
|||||
Db 486 CAGGAGTCTCTGCCATGGAGCA 507
|||||

RESULT 28
US-09-925-065A-35022/c
; Sequence 35022, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35022
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-35022

Alignment Scores:
Pred. No.: 211 Length: 572
Score: 62.50 Matches: 16
Percent Similarity: 52.9% Conservative: 11
Best Local Similarity: 31.4% Mismatches: 18
Query Match: 21.0% Indels: 6
DB: 6 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-925-065A-35022 (1-572)

QY 11 TrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrp 30
|||||
Db 163 TGGGAAGCAGAGGTTGCAAGCCGATATTGTGCCACTGCATCCAGCCTGGGTGACTG 104
|||||

QY 31 SerSer-LeuValMetLysGlnThrLysLysValAlaHis-----SerAl 45
|||||
Db 103 ACGGAGACTCTCTCTCAAAAACAAACAAATTCGAAATGCGGTAATGCCAATGC 44
|||||

QY 45 aLysPheArgValMetAlaValAsnSerGlu 55
|||||
Db 43 CAAATTCAGGATAATGGTTCATCTCAGGAGAA 13
|||||

RESULT 29
US-10-301-480-136260/c
; Sequence 136260, Application US/10301480
```





GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 20:18:18 ; Search time 1585.5 Seconds  
(without alignments)  
2022.653 Million cell updates/sec

Title: US-10-628-525A-35  
Perfect score: 297  
Sequence: 1 MAQILAPSTQWQRITKTP.....KVAHSAKFRVMAVNSNGT 58

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/abs/ABSSWEB.spool/US10628525/runat\_31032006\_095128\_16978/app\_query.fasta\_1  
-DB=Pending Patents NA.Main -OPMT=fastap -SUPFIX=p2n.rndm -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=150 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR\_MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=200000000 -HOST=abes06h  
-USER=US10628525 @CGN 1.1 19447 @runat\_31032006\_095128\_16978 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA.Main:  
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11: /cgn2\_6/ptodata/1/pna/US081 COMB.seq:  
12: /cgn2\_6/ptodata/1/pna/US082 COMB.seq:  
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25: /cgn2\_6/ptodata/1/pna/US095A COMB.seq:  
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77: /cgn2\_6/ptodata/1/pna/US602B COMB.seq:  
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81: /cgn2\_6/ptodata/1/pna/US605 COMB.seq:  
82: /cgn2\_6/ptodata/1/pna/US606 COMB.seq:  
83: /cgn2\_6/ptodata/1/pna/US607 COMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                            |
|------------|-------|-------------|--------|----|----------------------------------------|
| 1          | 216   | 72.7        | 262    | 23 | US-09-304-517A-184930 Sequence 184930, |
| 2          | 216   | 72.7        | 262    | 23 | US-09-371-146A-184930 Sequence 184930, |
| 3          | 216   | 72.7        | 262    | 39 | US-09-985-678-184930 Sequence 184930,  |
| 4          | 216   | 72.7        | 278    | 23 | US-09-304-517A-106380 Sequence 106380, |
| 5          | 216   | 72.7        | 278    | 23 | US-09-371-146A-106380 Sequence 106380, |
| 6          | 216   | 72.7        | 278    | 39 | US-09-985-678-106380 Sequence 106380,  |
| 7          | 216   | 72.7        | 282    | 22 | US-09-244-000A-9660 Sequence 9660, Ap  |

|    |       |      |      |    |                        |                    |     |       |      |      |    |                       |                    |
|----|-------|------|------|----|------------------------|--------------------|-----|-------|------|------|----|-----------------------|--------------------|
| 8  | 216   | 72.7 | 282  | 38 | US-09-978-703-9660     | Sequence 9660, Ap  | 81  | 199   | 67.0 | 1633 | 1  | PCT-US02-27884-5829   | Sequence 5829, Ap  |
| 9  | 216   | 72.7 | 1299 | 83 | US-60-723-596-48951    | Sequence 48951, A  | 82  | 199   | 67.0 | 1633 | 51 | US-10-487-901-5829    | Sequence 5829, Ap  |
| 10 | 216   | 72.7 | 1808 | 72 | US-11-216-545-8521     | Sequence 8521, Ap  | 83  | 197   | 66.3 | 273  | 22 | US-09-263-191-9119    | Sequence 9119, Ap  |
| 11 | 216   | 72.7 | 1808 | 82 | US-60-606-062-8521     | Sequence 8521, Ap  | 84  | 197   | 66.3 | 273  | 38 | US-09-975-254-3119    | Sequence 9119, Ap  |
| 12 | 215   | 72.4 | 391  | 23 | US-09-304-517A-259355  | Sequence 259355, A | 85  | 197   | 66.3 | 2124 | 51 | US-10-424-599-3238    | Sequence 3238, Ap  |
| 13 | 215   | 72.4 | 391  | 27 | US-09-565-240-11025    | Sequence 11025, A  | 86  | 191   | 64.3 | 284  | 21 | US-09-199-129A-3325   | Sequence 3325, Ap  |
| 14 | 215   | 72.4 | 391  | 39 | US-09-985-678-259955   | Sequence 259955, A | 87  | 191   | 64.3 | 284  | 21 | US-09-304-517A-278407 | Sequence 278407, A |
| 15 | 215   | 72.4 | 415  | 23 | US-09-371-146A-259623  | Sequence 259623, A | 88  | 191   | 64.3 | 284  | 23 | US-09-371-146A-277188 | Sequence 277188, A |
| 16 | 215   | 72.4 | 415  | 75 | US-60-141-137-396      | Sequence 396, App  | 89  | 191   | 64.3 | 284  | 39 | US-09-985-678-278407  | Sequence 278407, A |
| 17 | 211   | 71.0 | 1217 | 29 | US-09-654-617-15751    | Sequence 15751, A  | 90  | 189   | 63.6 | 254  | 39 | US-09-306-349-32955   | Sequence 32955, A  |
| 18 | 211   | 71.0 | 1217 | 29 | US-09-684-016-15751    | Sequence 15751, A  | 91  | 189   | 63.6 | 254  | 38 | US-09-960-481-32955   | Sequence 32955, A  |
| 19 | 210   | 70.7 | 272  | 23 | US-09-304-517A-120859  | Sequence 120859, A | 92  | 183   | 61.6 | 252  | 23 | US-09-304-517A-105868 | Sequence 105868, A |
| 20 | 210   | 70.7 | 272  | 23 | US-09-371-146A-120859  | Sequence 120859, A | 93  | 183   | 61.6 | 252  | 23 | US-09-371-146A-105868 | Sequence 105868, A |
| 21 | 210   | 70.7 | 272  | 39 | US-09-985-678-120859   | Sequence 120859, A | 94  | 183   | 61.6 | 252  | 39 | US-09-985-678-105868  | Sequence 105868, A |
| 22 | 210   | 70.7 | 278  | 21 | US-09-199-129A-1763    | Sequence 1763, Ap  | 95  | 183   | 61.6 | 272  | 21 | US-09-199-129A-2002   | Sequence 2002, Ap  |
| 23 | 210   | 70.7 | 278  | 23 | US-09-304-517A-277899  | Sequence 277899, A | 96  | 183   | 61.6 | 272  | 23 | US-09-304-517A-277974 | Sequence 277974, A |
| 24 | 210   | 70.7 | 278  | 23 | US-09-371-146A-276680  | Sequence 276680, A | 97  | 183   | 61.6 | 272  | 23 | US-09-371-146A-276755 | Sequence 276755, A |
| 25 | 210   | 70.7 | 278  | 39 | US-09-985-678-277899   | Sequence 277899, A | 98  | 183   | 61.6 | 272  | 39 | US-09-985-678-277974  | Sequence 277974, A |
| 26 | 210   | 70.7 | 289  | 21 | US-09-199-129A-1352    | Sequence 1352, Ap  | 99  | 181   | 60.9 | 244  | 22 | US-09-244-000A-31018  | Sequence 31018, A  |
| 27 | 210   | 70.7 | 289  | 23 | US-09-304-517A-277751  | Sequence 277751, A | 100 | 181   | 60.9 | 244  | 38 | US-09-978-703-31018   | Sequence 31018, A  |
| 28 | 210   | 70.7 | 289  | 23 | US-09-371-146A-276532  | Sequence 276532, A | 101 | 180   | 60.6 | 251  | 22 | US-09-244-000A-56980  | Sequence 56980, A  |
| 29 | 210   | 70.7 | 289  | 39 | US-09-985-678-277751   | Sequence 277751, A | 102 | 180   | 60.6 | 251  | 38 | US-09-978-703-56980   | Sequence 56980, A  |
| 30 | 210   | 70.7 | 293  | 22 | US-09-244-000A-60903   | Sequence 60903, A  | 103 | 180   | 60.6 | 270  | 22 | US-09-244-000A-26030  | Sequence 26030, A  |
| 31 | 210   | 70.7 | 293  | 23 | US-09-304-517A-293754  | Sequence 293754, A | 104 | 180   | 60.6 | 270  | 23 | US-09-304-517A-291690 | Sequence 291690, A |
| 32 | 210   | 70.7 | 293  | 23 | US-09-371-146A-292535  | Sequence 292535, A | 105 | 180   | 60.6 | 270  | 23 | US-09-371-146A-291690 | Sequence 291690, A |
| 33 | 210   | 70.7 | 293  | 27 | US-09-552-086-1395     | Sequence 1395, Ap  | 106 | 180   | 60.6 | 270  | 38 | US-09-978-703-26030   | Sequence 26030, A  |
| 34 | 210   | 70.7 | 293  | 38 | US-09-978-703-60903    | Sequence 60903, A  | 107 | 180   | 60.6 | 270  | 38 | US-09-985-678-291690  | Sequence 291690, A |
| 35 | 210   | 70.7 | 293  | 39 | US-09-985-678-293754   | Sequence 293754, A | 108 | 174.5 | 58.8 | 360  | 29 | US-09-637-086A-9120   | Sequence 9120, Ap  |
| 36 | 210   | 70.7 | 297  | 22 | US-09-210-297-945      | Sequence 945, App  | 109 | 174.5 | 58.8 | 360  | 29 | US-09-637-086D-9120   | Sequence 9120, Ap  |
| 37 | 210   | 70.7 | 297  | 23 | US-09-304-517A-279377  | Sequence 279377, A | 110 | 174.5 | 58.8 | 360  | 29 | US-09-654-617-208428  | Sequence 208428, A |
| 38 | 210   | 70.7 | 297  | 23 | US-09-371-146A-278158  | Sequence 278158, A | 111 | 174.5 | 58.8 | 360  | 29 | US-09-684-016-208428  | Sequence 208428, A |
| 39 | 210   | 70.7 | 297  | 39 | US-09-985-678-279377   | Sequence 279377, A | 112 | 174.5 | 58.8 | 380  | 29 | US-09-637-086A-36684  | Sequence 36684, A  |
| 40 | 210   | 70.7 | 372  | 23 | US-09-304-517A-270709  | Sequence 270709, A | 113 | 174.5 | 58.8 | 380  | 29 | US-09-637-086D-36684  | Sequence 36684, A  |
| 41 | 210   | 70.7 | 372  | 23 | US-09-371-146A-269547  | Sequence 269547, A | 114 | 174.5 | 58.8 | 380  | 29 | US-09-654-617-221183  | Sequence 221183, A |
| 42 | 210   | 70.7 | 372  | 27 | US-09-565-240-16542    | Sequence 16542, A  | 115 | 174.5 | 58.8 | 380  | 29 | US-09-684-016-221183  | Sequence 221183, A |
| 43 | 210   | 70.7 | 372  | 39 | US-09-985-678-270709   | Sequence 270709, A | 116 | 174.5 | 58.8 | 401  | 29 | US-09-637-086A-40055  | Sequence 40055, A  |
| 44 | 210   | 70.7 | 401  | 27 | US-09-565-240-30892    | Sequence 30892, A  | 117 | 174.5 | 58.8 | 401  | 29 | US-09-637-086D-40055  | Sequence 40055, A  |
| 45 | 210   | 70.7 | 401  | 75 | US-60-133-691-4992     | Sequence 4992, Ap  | 118 | 174.5 | 58.8 | 401  | 29 | US-09-654-617-223543  | Sequence 223543, A |
| 46 | 210   | 70.7 | 1299 | 83 | US-60-723-596-48481    | Sequence 48481, A  | 119 | 174.5 | 58.8 | 401  | 29 | US-09-684-016-223543  | Sequence 223543, A |
| 47 | 210   | 70.7 | 1299 | 83 | US-60-723-596-48950    | Sequence 48950, A  | 120 | 174.5 | 58.8 | 723  | 29 | US-09-637-086A-36769  | Sequence 36769, A  |
| 48 | 205   | 69.0 | 250  | 22 | US-09-244-000A-8695    | Sequence 8695, Ap  | 121 | 174.5 | 58.8 | 723  | 29 | US-09-637-086D-36769  | Sequence 36769, A  |
| 49 | 205   | 69.0 | 250  | 38 | US-09-978-703-8695     | Sequence 8695, Ap  | 122 | 174.5 | 58.8 | 723  | 29 | US-09-654-617-221248  | Sequence 221248, A |
| 50 | 205   | 69.0 | 255  | 23 | US-09-304-517A-184372  | Sequence 184372, A | 123 | 174.5 | 58.8 | 723  | 29 | US-09-684-016-221248  | Sequence 221248, A |
| 51 | 205   | 69.0 | 255  | 23 | US-09-371-146A-184372  | Sequence 184372, A | 124 | 174.5 | 58.8 | 1500 | 29 | US-09-654-617-194103  | Sequence 194103, A |
| 52 | 205   | 69.0 | 255  | 39 | US-09-985-678-184372   | Sequence 184372, A | 125 | 174.5 | 58.8 | 1500 | 29 | US-09-684-016-194103  | Sequence 194103, A |
| 53 | 205   | 69.0 | 259  | 22 | US-09-244-000A-38225   | Sequence 38225, A  | 126 | 174.5 | 58.8 | 1508 | 61 | US-10-767-795-6095    | Sequence 6095, Ap  |
| 54 | 205   | 69.0 | 259  | 38 | US-09-978-703-38225    | Sequence 38225, A  | 127 | 174   | 58.6 | 258  | 21 | US-09-199-129A-1959   | Sequence 1959, Ap  |
| 55 | 204   | 68.7 | 255  | 23 | US-09-306-349-31878    | Sequence 31878, A  | 128 | 174   | 58.6 | 258  | 23 | US-09-304-517A-277961 | Sequence 277961, A |
| 56 | 204   | 68.7 | 255  | 38 | US-09-960-481-31878    | Sequence 31878, A  | 129 | 174   | 58.6 | 258  | 23 | US-09-371-146A-276742 | Sequence 276742, A |
| 57 | 203   | 68.4 | 252  | 22 | US-09-244-000A-2084    | Sequence 2084, Ap  | 130 | 174   | 58.6 | 258  | 39 | US-09-985-678-277961  | Sequence 277961, A |
| 58 | 203   | 68.4 | 252  | 23 | US-09-304-517A-282763  | Sequence 282763, A | 131 | 171.5 | 57.7 | 340  | 29 | US-09-637-086A-40579  | Sequence 40579, A  |
| 59 | 203   | 68.4 | 252  | 38 | US-09-371-146A-281544  | Sequence 281544, A | 132 | 171.5 | 57.7 | 340  | 29 | US-09-637-086D-40579  | Sequence 40579, A  |
| 60 | 203   | 68.4 | 252  | 38 | US-09-978-703-2084     | Sequence 2084, Ap  | 133 | 171.5 | 57.7 | 340  | 29 | US-09-637-086D-40579  | Sequence 223886, A |
| 61 | 203   | 68.4 | 252  | 39 | US-09-985-678-282763   | Sequence 282763, A | 134 | 171.5 | 57.7 | 340  | 29 | US-09-684-016-223888  | Sequence 223888, A |
| 62 | 201   | 67.2 | 1651 | 31 | US-09-705-926-459      | Sequence 459, App  | 135 | 167.5 | 56.4 | 441  | 29 | US-09-637-086A-7837   | Sequence 7837, Ap  |
| 63 | 199.5 | 67.2 | 1302 | 83 | US-60-723-596-50982    | Sequence 50982, A  | 136 | 167.5 | 56.4 | 441  | 29 | US-09-637-086D-7837   | Sequence 7837, Ap  |
| 64 | 199   | 67.0 | 245  | 23 | US-09-304-517A-127602  | Sequence 127602, A | 137 | 167.5 | 56.4 | 441  | 29 | US-09-654-617-207681  | Sequence 207681, A |
| 65 | 199   | 67.0 | 245  | 23 | US-09-371-146A-127602  | Sequence 127602, A | 138 | 167.5 | 56.4 | 441  | 29 | US-09-684-016-207681  | Sequence 207681, A |
| 66 | 199   | 67.0 | 245  | 39 | US-09-985-678-127602   | Sequence 127602, A | 139 | 167   | 56.2 | 453  | 29 | US-09-637-086D-6654   | Sequence 6654, Ap  |
| 67 | 199   | 67.0 | 248  | 23 | US-09-304-517A-145989  | Sequence 145989, A | 140 | 167   | 56.2 | 453  | 29 | US-09-637-086D-6654   | Sequence 6654, Ap  |
| 68 | 199   | 67.0 | 248  | 23 | US-09-371-146A-145989  | Sequence 145989, A | 141 | 167   | 56.2 | 453  | 29 | US-09-654-617-206921  | Sequence 206921, A |
| 69 | 199   | 67.0 | 248  | 37 | US-09-552-086-20029    | Sequence 20029, A  | 142 | 167   | 56.2 | 453  | 29 | US-09-684-016-206921  | Sequence 206921, A |
| 70 | 199   | 67.0 | 248  | 39 | US-09-985-678-145989   | Sequence 145989, A | 143 | 167   | 56.2 | 453  | 61 | US-10-767-795-31959   | Sequence 31959, A  |
| 71 | 199   | 67.0 | 255  | 23 | US-09-304-517A-115327  | Sequence 115327, A | 144 | 162.5 | 54.7 | 376  | 29 | US-09-637-086A-36617  | Sequence 36617, A  |
| 72 | 199   | 67.0 | 255  | 23 | US-09-371-146A-115327  | Sequence 115327, A | 145 | 162.5 | 54.7 | 376  | 29 | US-09-637-086D-36617  | Sequence 36617, A  |
| 73 | 199   | 67.0 | 261  | 23 | US-09-985-678-115327   | Sequence 115327, A | 146 | 162.5 | 54.7 | 376  | 29 | US-09-654-617-221136  | Sequence 221136, A |
| 74 | 199   | 67.0 | 261  | 38 | US-09-306-349-35700    | Sequence 35700, A  | 147 | 162.5 | 54.7 | 376  | 29 | US-09-684-016-221136  | Sequence 221136, A |
| 75 | 199   | 67.0 | 263  | 23 | US-09-960-481-35700    | Sequence 35700, A  | 148 | 159   | 53.5 | 226  | 23 | US-09-304-517A-114799 | Sequence 114799, A |
| 76 | 199   | 67.0 | 263  | 23 | US-09-304-517A-1866412 | Sequence 186412, A | 149 | 159   | 53.5 | 226  | 23 | US-09-371-146A-114799 | Sequence 114799, A |
| 77 | 199   | 67.0 | 263  | 39 | US-09-371-146A-1866412 | Sequence 186412, A | 150 | 159   | 53.5 | 226  | 39 | US-09-985-678-114799  | Sequence 114799, A |
| 78 | 199   | 67.0 | 589  | 51 | PCT-US02-27884-1682    | Sequence 1682, Ap  |     |       |      |      |    |                       |                    |
| 79 | 199   | 67.0 |      |    |                        |                    |     |       |      |      |    |                       |                    |
| 80 | 199   | 67.0 |      |    |                        |                    |     |       |      |      |    |                       |                    |

```
RESULT 1
US-09-304-517A-184930
; Sequence 184930, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 184930
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Glycine max
US-09-304-517A-184930

Alignment Scores:
Pred. No.: 8.2e-23 Length: 262
Score: 216.00 Matches: 44
Percent Similarity: 85.0% Conservative: 7
Best Local Similarity: 73.3% Mismatches: 7
Query Match: 72.7% Indels: 2
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-304-517A-184930 (1-262)
QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 70 ATGGCACAGATTTGGCTCCCTTACGCAATGCGAGATGAGATCTCAAAATCTCTCCC 129
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40
DB 130 AATGCAACTCCCATACATCAACATGTGGAGTCTTTATTGTGGAACAAATAAGAAA 189
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAlaAsnSerGluAsnGlyThr 58
DB 190 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTGCGCAATTAAGTCTGCAATAGCACT 249

RESULT 2
US-09-371-146A-184930
; Sequence 184930, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE: 38-21(15097)C
; CURRENT APPLICATION NUMBER: US/09/371,146A
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 184930
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Glycine max
US-09-371-146A-184930

Alignment Scores:
Pred. No.: 8.2e-23 Length: 262
Score: 216.00 Matches: 44
Percent Similarity: 85.0% Conservative: 7
Best Local Similarity: 73.3% Mismatches: 7
Query Match: 72.7% Indels: 2
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-371-146A-184930 (1-262)
QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 70 ATGGCACAGATTTGGCTCCCTTACGCAATGCGAGATGAGATCTCAAAATCTCTCCC 129
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40
DB 130 AATGCAACTCCCATACATCAACATGTGGAGTCTTTATTGTGGAACAAATAAGAAA 189
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAlaAsnSerGluAsnGlyThr 58
DB 190 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTGCGCAATTAAGTCTGCAATAGCACT 249

RESULT 3
US-09-985-678-184930
; Sequence 184930, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517.255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 184930
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Glycine max
US-09-985-678-184930

Alignment Scores:
Pred. No.: 8.2e-23 Length: 262
Score: 216.00 Matches: 44
Percent Similarity: 85.0% Conservative: 7
Best Local Similarity: 73.3% Mismatches: 7
Query Match: 72.7% Indels: 2
DB: 39 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-985-678-184930 (1-262)
QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 70 ATGGCACAGATTTGGCTCCCTTACGCAATGCGAGATGAGATCTCAAAATCTCTCCC 129
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40
DB 130 AATGCAACTCCCATACATCAACATGTGGAGTCTTTATTGTGGAACAAATAAGAAA 189
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAlaAsnSerGluAsnGlyThr 58
DB 190 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTGCGCAATTAAGTCTGCAATAGCACT 249

RESULT 4
US-09-304-517A-106380
; Sequence 106380, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 106380
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
US-09-304-517A-106380

Alignment Scores:
Pred. No.: 9e-23 Length: 278
Score: 216.00 Matches: 44
Percent Similarity: 85.0% Conservative: 7
Best Local Similarity: 73.3% Mismatches: 7
Query Match: 72.7% Indels: 2
DB: 23 Gaps: 1
```

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QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40
DB 130 AATGCAACTCCCATACATCAACATGTGGAGTCTTTATTGTGGAACAAATAAGAAA 189
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAlaAsnSerGluAsnGlyThr 58
DB 190 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTGCGCAATTAAGTCTGCAATAGCACT 249

RESULT 3
US-09-985-678-184930
; Sequence 184930, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517.255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 184930
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Glycine max
US-09-985-678-184930

Alignment Scores:
Pred. No.: 8.2e-23 Length: 262
Score: 216.00 Matches: 44
Percent Similarity: 85.0% Conservative: 7
Best Local Similarity: 73.3% Mismatches: 7
Query Match: 72.7% Indels: 2
DB: 39 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-985-678-184930 (1-262)
QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 70 ATGGCACAGATTTGGCTCCCTTACGCAATGCGAGATGAGATCTCAAAATCTCTCCC 129
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40
DB 130 AATGCAACTCCCATACATCAACATGTGGAGTCTTTATTGTGGAACAAATAAGAAA 189
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAlaAsnSerGluAsnGlyThr 58
DB 190 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTGCGCAATTAAGTCTGCAATAGCACT 249

RESULT 4
US-09-304-517A-106380
; Sequence 106380, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 106380
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
US-09-304-517A-106380

Alignment Scores:
Pred. No.: 9e-23 Length: 278
Score: 216.00 Matches: 44
Percent Similarity: 85.0% Conservative: 7
Best Local Similarity: 73.3% Mismatches: 7
Query Match: 72.7% Indels: 2
DB: 23 Gaps: 1
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US-10-628-525A-35 (1-58) x US-09-304-517A-106380 (1-278)

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QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 92 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGAGAATCTCAAAATCCTCTCCC 151
QY 21 CysAlaThrProIleThrSerLysMetTTPSerSerLeuValMetLysGlnThrLysLys 40
Db 152 AATGCAACTCCCATTTACATCAACATGTGGAGTTCTTTATTGTGGAAACAAATAAGAAA 211
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 212 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTGGCAATTAAGTCTGACAAATAGCACC 271
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## RESULT 5

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US-09-371-146A-106380
; Sequence 106380, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE: 38-21(15097)C
; CURRENT APPLICATION NUMBER: US/09/371,146A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 106380
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
US-09-371-146A-106380
```

Alignment Scores:  
Pred. No.: 9e-23 Length: 278  
Score: 216.00 Matches: 44  
Percent Similarity: 85.0% Conservative: 7  
Best Local Similarity: 73.3% Mismatches: 7  
Query Match: 72.7% Indels: 2  
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-371-146A-106380 (1-278)

```
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 92 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGAGAATCTCAAAATCCTCTCCC 151
QY 21 CysAlaThrProIleThrSerLysMetTTPSerSerLeuValMetLysGlnThrLysLys 40
Db 152 AATGCAACTCCCATTTACATCAACATGTGGAGTTCTTTATTGTGGAAACAAATAAGAAA 211
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 212 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTGGCAATTAAGTCTGACAAATAGCACC 271
```

## RESULT 6

```
US-09-985-678-106380
; Sequence 106380, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517.255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 106380
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
```

US-09-985-678-106380

Alignment Scores:  
Pred. No.: 9e-23 Length: 278  
Score: 216.00 Matches: 44  
Percent Similarity: 85.0% Conservative: 7  
Best Local Similarity: 73.3% Mismatches: 7  
Query Match: 72.7% Indels: 2  
DB: 39 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-985-678-106380 (1-278)

```
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 92 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGAGAATCTCAAAATCCTCTCCC 151
QY 21 CysAlaThrProIleThrSerLysMetTTPSerSerLeuValMetLysGlnThrLysLys 40
Db 152 AATGCAACTCCCATTTACATCAACATGTGGAGTTCTTTATTGTGGAAACAAATAAGAAA 211
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 212 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTGGCAATTAAGTCTGACAAATAGCACC 271
```

## RESULT 7

```
US-09-244-000A-9660
; Sequence 9660, Application US/09244000A
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15305)B
; CURRENT APPLICATION NUMBER: US/09/244,000A
; CURRENT FILING DATE: 1999-02-08
; PRIOR APPLICATION DATA removed - refer to PALM or File Wrapper
; NUMBER OF SEQ ID NOS: 101193
; SEQ ID NO 9660
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(282)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 700682115H1
US-09-244-000A-9660
```

Alignment Scores:  
Pred. No.: 9.2e-23 Length: 282  
Score: 216.00 Matches: 44  
Percent Similarity: 85.0% Conservative: 7  
Best Local Similarity: 73.3% Mismatches: 7  
Query Match: 72.7% Indels: 2  
DB: 22 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-244-000A-9660 (1-282)

```
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 92 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGAGAATCTCAAAATCCTCTCCC 151
QY 21 CysAlaThrProIleThrSerLysMetTTPSerSerLeuValMetLysGlnThrLysLys 40
Db 152 AATGCAACTCCCATTTACATCAACATGTGGAGTTCTTTATTGTGGAAACAAATAAGAAA 211
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 212 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTGGCAATTAAGTCTGACAAATAGCACC 271
```

## RESULT 8

US-09-978-703-9660

; Sequence 9660, Application US/09978703  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Thompson, Michael D.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(15305)B  
; CURRENT APPLICATION NUMBER: US/09/978,703  
; CURRENT FILING DATE: 2001-10-18  
; PRIOR APPLICATION NUMBER: US 09/244,000  
; PRIOR FILING DATE: 1999-02-08  
; PRIOR APPLICATION NUMBER: US 60/074201  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074282  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074280  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074281  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074566  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: US 60/074567  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: US 60/074565  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: US 60/075462  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/074789  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/075459  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/075461  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/075464  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/075460  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/075463  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/086183  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: US 60/086188  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: US 09/198779  
; PRIOR FILING DATE: 1998-11-24  
; PRIOR APPLICATION NUMBER: US 60/110108  
; PRIOR FILING DATE: 1998-11-25  
; PRIOR APPLICATION NUMBER: US 60/110109  
; PRIOR FILING DATE: 1998-11-25  
; PRIOR APPLICATION NUMBER: US 60/111033  
; PRIOR FILING DATE: 1998-12-04  
; PRIOR APPLICATION NUMBER: US 60/111742  
; PRIOR FILING DATE: 1998-12-10  
; NUMBER OF SEQ ID NOS: 101193  
; SEQ ID NO 9660  
; LENGTH: 282  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURES:  
; NAME/KEY: unsure  
; LOCATION: (1)..(282)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: 700682115H1  
US-09-978-703-9660

Alignment Scores:  
Pred. No.: 9,2e-23  
Score: 216.00  
Percent Similarity: 85.0%  
Best Local Similarity: 73.3%  
Query Match: 72.7%  
DB: 36  
Length: 282  
Matches: 44  
Conservative: 7  
Mismatch: 7  
Indels: 2  
Gaps: 1

US-10-628-525A-35 (1-58) x US-09-978-703-9660 (1-282)  
QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db 92 ATGGCACAGATTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAATCTCTCCC 151  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40  
Db 152 AATGCAACTCCCATTTACATCAACATGTGCGAGTTCTTTATTGTGGAAACAAATAAGAAA 211  
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAlaSerGluAenGlyThr 58  
Db 212 GTTTCACCTACCAAGTTCTGCTAAATTTAGAGTGTGCGCAATTAAAGTCTGCAATAGCACC 271

## RESULT 9

US-60-723-596-48951  
; Sequence 48951, Application US/60723596  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark et. al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53708)B  
; CURRENT APPLICATION NUMBER: US/60/723,596  
; CURRENT FILING DATE: 2005-10-04  
; NUMBER OF SEQ ID NOS: 58588  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 48951  
; LENGTH: 1299  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-60-723-596-48951

Alignment Scores:  
Pred. No.: 1.01e-21  
Score: 216.00  
Percent Similarity: 85.0%  
Best Local Similarity: 73.3%  
Query Match: 72.7%  
DB: 83  
Length: 1299  
Matches: 44  
Conservative: 7  
Mismatch: 7  
Indels: 2  
Gaps: 1

US-10-628-525A-35 (1-58) x US-60-723-596-48951 (1-1299)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db 1 ATGGCACAGATTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAATCTCTCCC 60  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40  
Db 61 AATGCAACTCCCATTTACATCAACATGTGCGAGTTCTTTATTGTGGAAACAAATAAGAAA 120  
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAlaSerGluAenGlyThr 58  
Db 121 GTTTCACCTACCAAGTTCTGCTAAATTTAGAGTGTGCGCAATTAAAGTCTGCAATAGCACC 180

## RESULT 10

US-11-216-545-8521  
; Sequence 8521, Application US/11216545  
; GENERAL INFORMATION:  
; APPLICANT: MONSANTO Technology, LLC  
; APPLICANT: McLeod, Paul L  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Wu, Kunsheng  
; TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping  
; FILE REFERENCE: 38-21(53659)B  
; CURRENT APPLICATION NUMBER: US/11/216,545  
; CURRENT FILING DATE: 2005-08-31  
; PRIOR APPLICATION NUMBER: US 60/606,062  
; PRIOR FILING DATE: 2004-08-31  
; NUMBER OF SEQ ID NOS: 8783  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8521  
; LENGTH: 1808

```
; TYPE: DNA
; ORGANISM: Glycine max
US-11-216-545-8521

Alignment Scores:
Pred. No.: 1,7e-21 Length: 1808
Score: 216.00 Matches: 44
Percent Similarity: 85.0% Conservative: 7
Best Local Similarity: 73.3% Mismatches: 7
Query Match: 72.7% Indels: 2
DB: 72 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-216-545-8521 (1-1808)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 269 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAATCCTCTCCC 328
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 329 AATGCAACTCCCATACATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 388
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 389 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTCTGCGCAATTAAAGTCTGACAATAGCACC 448

RESULT 11
US-60-606-062-8521
; Sequence 8521, Application US/60606062
; GENERAL INFORMATION:
; APPLICANT: MONSANTO Technology, LLC
; APPLICANT: McLaird, Paul L
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
; FILE REFERENCE: Soybeans.
; CURRENT APPLICATION NUMBER: US/60/606,062
; CURRENT FILING DATE: 2004-08-31
; NUMBER OF SEQ ID NOS: 8783
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8521
; LENGTH: 1808
; TYPE: DNA
; ORGANISM: Glycine max
US-60-606-062-8521

Alignment Scores:
Pred. No.: 1,7e-21 Length: 1808
Score: 216.00 Matches: 44
Percent Similarity: 85.0% Conservative: 7
Best Local Similarity: 73.3% Mismatches: 7
Query Match: 72.7% Indels: 2
DB: 82 Gaps: 1

US-10-628-525A-35 (1-58) x US-60-606-062-8521 (1-1808)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 269 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAATCCTCTCCC 328
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 329 AATGCAACTCCCATACATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 388
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 389 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTCTGCGCAATTAAAGTCTGACAATAGCACC 448

RESULT 12
US-09-304-517A-259955
; Sequence 259955, Application US/09304517A
; GENERAL INFORMATION:
```

```
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong Annotated Plant Genes
; TITLE OF INVENTION: 38-21(15097)B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 259955
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Glycine max
US-09-304-517A-259955

Alignment Scores:
Pred. No.: 2,21e-22 Length: 391
Score: 215.00 Matches: 44
Percent Similarity: 83.3% Conservative: 6
Best Local Similarity: 73.3% Mismatches: 8
Query Match: 72.4% Indels: 2
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-304-517A-259955 (1-391)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 10 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAAGGCTCTCCC 69
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 70 AATGCAACTCCCATACATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 129
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 130 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTGGCAATTAAAGTCTGACAATAGCACC 189

RESULT 13
US-09-565-240-11025
; Sequence 11025, Application US/09565240
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15793)B
; CURRENT APPLICATION NUMBER: US/09/565,240
; CURRENT FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 54005
; SEQ ID NO 11025
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3092-013-Q1-K1-C1
US-09-565-240-11025

Alignment Scores:
Pred. No.: 2,21e-22 Length: 391
Score: 215.00 Matches: 44
Percent Similarity: 83.3% Conservative: 6
Best Local Similarity: 73.3% Mismatches: 8
Query Match: 72.4% Indels: 2
DB: 27 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-565-240-11025 (1-391)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 10 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAAGGCTCTCCC 69
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 70 AATGCAACTCCCATACATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 129
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
```





```
Alignment Scores: 5.56e-21 Length: 1217
Pred. No.: 211.00 Matches: 43
Score: 211.00
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 71.0% Indels: 2
DB: 29 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-654-617-15751 (1-1217)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 265 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGAGAATCTCAAAATCCTCTCCC 324
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 325 AATGCACTCCCATTTACATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAA 384
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db 385 GTTTCACCTACCAGTTCTGCTAAATTAGAGTGTGGCAATTAAAGTCTGACAA 438

RESULT 18
US-09-684-016-15751
; Sequence 15751, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 15751
; LENGTH: 1217
; TYPE: DNA
; ORGANISM: Glycine max
US-09-684-016-15751

Alignment Scores: 5.56e-21 Length: 1217
Pred. No.: 211.00 Matches: 43
Score: 211.00
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 71.0% Indels: 2
DB: 29 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-684-016-15751 (1-1217)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 265 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGAGAATCTCAAAATCCTCTCCC 324
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 325 AATGCACTCCCATTTACATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAA 384
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db 385 GTTTCACCTACCAGTTCTGCTAAATTAGAGTGTGGCAATTAAAGTCTGACAA 438

RESULT 19
US-09-304-517A-120859
; Sequence 120859, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; PRIOR FILING DATE: 1999-05-06
```

```
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 120859
; LENGTH: 272
; TYPE: DNA
; ORGANISM: Glycine max
US-09-304-517A-120859

Alignment Scores: 7.57e-22 Length: 272
Pred. No.: 210.00 Matches: 43
Score: 210.00
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 70.7% Indels: 2
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-304-517A-120859 (1-272)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 87 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGCGAATCTCAAAATCCTCTCCC 146
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 147 AATGCAAGTCCCATTTACATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAA 206
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db 207 GTTTCACCCACAAGTTCTGCTAAATTAGAGTGTGGCAATTAAAGTCTGACAA 260

RESULT 20
US-09-371-146A-120859
; Sequence 120859, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE: 38-21(15097)C
; CURRENT APPLICATION NUMBER: US/09/371,146A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 120859
; LENGTH: 272
; TYPE: DNA
; ORGANISM: Glycine max
US-09-371-146A-120859

Alignment Scores: 7.57e-22 Length: 272
Pred. No.: 210.00 Matches: 43
Score: 210.00
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 70.7% Indels: 2
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-371-146A-120859 (1-272)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 87 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGCGAATCTCAAAATCCTCTCCC 146
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 147 AATGCAAGTCCCATTTACATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAA 206
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db 207 GTTTCACCCACAAGTTCTGCTAAATTAGAGTGTGGCAATTAAAGTCTGACAA 260

RESULT 21
US-09-985-678-120859
; Sequence 120859, Application US/09985678
```

```

; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517.255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985.678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 120859
; LENGTH: 272
; TYPE: DNA
; ORGANISM: Glycine max
US-09-985-678-120859

Alignment Scores:
Pred. No.: 7.84e-22 Length: 272
Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 70.7% Indels: 2
DB: 39 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-985-678-120859 (1-272)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 87 ATGGCACAGATTTTGGCTCCCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 146
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 147 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 206
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAaenSerGluAaen 56
DB 207 GTTTCACCCACAGTTCTGCTAAATTTAGAGTGTGATGCAATTAAGTCTGCAAT 260

RESULT 22
US-09-199-129A-1763
; Sequence 1763, Application US/09199129A
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15075)B
; CURRENT APPLICATION NUMBER: US/09/199,129A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 5521
; SEQ ID NO 1763
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700555550H1
US-09-199-129A-1763

Alignment Scores:
Pred. No.: 7.84e-22 Length: 278
Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 70.7% Indels: 2
DB: 21 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-199-129A-1763 (1-278)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 93 ATGGCACAGATTTTGGCTCCCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 93 ATGGCACAGATTTTGGCTCCCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152

US-10-628-525A-35 (1-58) x US-09-985-678-120859 (1-272)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 93 ATGGCACAGATTTTGGCTCCCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 153 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 212

US-10-628-525A-35 (1-58) x US-09-304-517A-277899 (1-278)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 93 ATGGCACAGATTTTGGCTCCCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 153 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 212

US-10-628-525A-35 (1-58) x US-09-304-517A-277899 (1-278)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 93 ATGGCACAGATTTTGGCTCCCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 153 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 212

US-10-628-525A-35 (1-58) x US-09-371-146A-276680 (1-278)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 93 ATGGCACAGATTTTGGCTCCCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 153 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 212

US-10-628-525A-35 (1-58) x US-09-371-146A-276680 (1-278)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 93 ATGGCACAGATTTTGGCTCCCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 153 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 212
```

```

Db 153 AATGCAAGTCCCATCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 212
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAaenSerGluAaen 56
DB 213 GTTTCACCCACAGTTCTGCTAAATTTAGAGTGTGATGCAATTAAGTCTGCAAT 266

RESULT 23
US-09-304-517A-277899
; Sequence 277899, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 277899
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
US-09-304-517A-277899

Alignment Scores:
Pred. No.: 7.84e-22 Length: 278
Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 70.7% Indels: 2
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-304-517A-277899 (1-278)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 93 ATGGCACAGATTTTGGCTCCCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 153 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 212

US-10-628-525A-35 (1-58) x US-09-304-517A-277899 (1-278)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 93 ATGGCACAGATTTTGGCTCCCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 153 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 212

US-10-628-525A-35 (1-58) x US-09-304-517A-277899 (1-278)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 93 ATGGCACAGATTTTGGCTCCCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 153 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 212

US-10-628-525A-35 (1-58) x US-09-371-146A-276680 (1-278)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 93 ATGGCACAGATTTTGGCTCCCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 153 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 212

US-10-628-525A-35 (1-58) x US-09-371-146A-276680 (1-278)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 93 ATGGCACAGATTTTGGCTCCCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 153 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 212
```

```
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 93 ATGGCACAGATTGGCTCCCTCTAGCAATGGCAGATGAGATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 153 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 212
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db 213 GTTCCACCACCAAGTCTGCTAAATTTAGAGTGTGGCAATTAAAGTCTGACAA 266
```

## RESULT 25

```
US-09-985-678-277899
; Sequence 277899, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517.255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 277899
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
US-09-985-678-277899
```

```
Alignment Scores:
Pred. No.: 7,84e-22 Length: 278
Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 70.7% Indels: 2
DB: 39 Gaps: 1
```

US-10-628-525A-35 (1-58) x US-09-985-678-277899 (1-278)

```
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 93 ATGGCACAGATTGGCTCCCTCTAGCAATGGCAGATGAGATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 153 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 212
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db 213 GTTCCACCACCAAGTCTGCTAAATTTAGAGTGTGGCAATTAAAGTCTGACAA 266
```

## RESULT 26

```
US-09-199-129A-1352
; Sequence 1352, Application US/09199129A
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15075)B
; CURRENT APPLICATION NUMBER: US/09/199,129A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 5521
; SEQ ID NO 1352
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(289)
```

```
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 700555034H1
US-09-199-129A-1352
```

```
Alignment Scores:
Pred. No.: 8,33e-22 Length: 289
Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 70.7% Indels: 2
DB: 21 Gaps: 1
```

US-10-628-525A-35 (1-58) x US-09-199-129A-1352 (1-289)

```
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 28 ATGGCACAGATTGGCTCCCTCTAGCAATGGCAGATGAGATCTCAAAATCCTCTCCC 87
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 88 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 147
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db 148 GTTCCACCACCAAGTCTGCTAAATTTAGAGTGTGGCAATTAAAGTCTGACAA 201
```

## RESULT 27

```
US-09-304-517A-277751
; Sequence 277751, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 277751
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: unsure at all n locations
US-09-304-517A-277751
```

```
Alignment Scores:
Pred. No.: 8,33e-22 Length: 289
Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 70.7% Indels: 2
DB: 23 Gaps: 1
```

US-10-628-525A-35 (1-58) x US-09-304-517A-277751 (1-289)

```
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 28 ATGGCACAGATTGGCTCCCTCTAGCAATGGCAGATGAGATCTCAAAATCCTCTCCC 87
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 88 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 147
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db 148 GTTCCACCACCAAGTCTGCTAAATTTAGAGTGTGGCAATTAAAGTCTGACAA 201
```

## RESULT 28

```
US-09-371-146A-276532
; Sequence 276532, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: ANNOTATED PLANT GENES
```

```

Db      28  ATGCCACAGATTTTGGCTCCCTCTACTACGCAATGGCAGATGAGAATCTCAAAATCCTCTCTCCC 87
Qy      21  CysAlaThrProIleThrSerIysMetTrpSerSerLeuValMetIysGlnThrIysLys 40
Db      88  AATGCAAGTCCCATTACATCAACATGATGGAGTCTTTTATTGTGGAAACAAATAAGAAA 147
Qy      41  ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db      148  GTTTCACCCCAACAGTTCGTCTAAATTTAGAGTGTGGCAATTAAAGTCTGACAAAT 201

RESULT 30
US-09-244-000A-60903
; Sequence 60903, Application US/09244000A
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associ
; FILE REFERENCE: Plants
; FILE REFERENCE: 38-21(15305)B
; CURRENT APPLICATION NUMBER: US/09/244, 000A
; CURRENT FILING DATE: 1999-02-08
; PRIOR APPLICATION DATA removed - refer to PALM or File Wrapper
; NUMBER OF SEQ ID NOS: 101193
; SEQ ID NO 60903
; LENGTH: 293
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700996496H1
US-09-244-000A-60903

Alignment Scores:
Pred. No.: 8,51e-22 Length: 293
Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 70.7% Indels: 2
DB: 22 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-244-000A-60903 (1-293)
Qy      1  MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20
Db      92  ATGGCACAGATTTTGGCTCCCTCTACTACGCAATGGCAGATGAGAATCTCAAAATCCTCTCCC 151
Qy      21  CysAlaThrProIleThrSerIysMetTrpSerSerLeuValMetIysGlnThrIysLys 40
Db      152  AATGCAAGTCCCATTACATCAACATGATGGAGTCTTTTATTGTGGAAACAAATAAGAAA 211
Qy      41  ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db      212  GTTTCACCCCAACAGTTCGTCTAAATTTAGAGTGTGGCAATTAAAGTCTGACAAAT 265

Search completed: April 2, 2006, 03:27:36
Job time : 1590.5 secs

```

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 21:21:57 ; Search time 108.468 Seconds  
(without alignments)  
1603.719 Million cell updates/sec

Title: US-10-628-525a-35

Perfect score: 297

Sequence: 1 MAQILAPSTQWQRIKTSPTSP.....KKVAHSAKFRVMAVNSNGT 58

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 6698573 seqs, 1499593917 residues

Total number of hits satisfying chosen parameters: 13397146

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh

-Q=abas/ABSWEB.spool/US10628525/runat\_31032006\_095132\_17106/app.query.fasta\_1

-DB=Pending Patents NA New -QFMT=fastcap -SUFFIX=p2n.inpn -MINMATCH=0.1

-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62

-TRANS=human40 cdi -LIST=150 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100

-THR MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0

-MAXLEN=2000000000 -HOST=abes06h

-USER=US10628525 @CGN 1.1 1552 @runat\_31032006\_095132\_17106 -NCPU=6 -ICPU=3

-NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120

-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA New:\*

1: /SIDSS/ptodata/2/pna/PCT NEW COMB.seq:\*

2: /SIDSS/ptodata/2/pna/US06 NEW COMB.seq:\*

3: /SIDSS/ptodata/2/pna/US07 NEW COMB.seq:\*

4: /SIDSS/ptodata/2/pna/US08 NEW COMB.seq:\*

5: /SIDSS/ptodata/2/pna/US09 NEW COMB.seq:\*

6: /SIDSS/ptodata/2/pna/US10 NEW COMB.seq:\*

7: /SIDSS/ptodata/2/pna/US11 NEW COMB.seq:\*

8: /SIDSS/ptodata/2/pna/US12 NEW COMB.seq:\*

9: /SIDSS/ptodata/2/pna/US13 NEW COMB.seq:\*

10: /SIDSS/ptodata/2/pna/US14 NEW COMB.seq:\*

11: /SIDSS/ptodata/2/pna/US15 NEW COMB.seq:\*

12: /SIDSS/ptodata/2/pna/US16 NEW COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description          |
|------------|-------|-------------|--------|----|----------------------|
| 1          | 215   | 72.4        | 391    | 8  | US-11-239-610A-11025 |
| 2          | 210   | 70.7        | 293    | 8  | Sequence 11025, A    |
| 3          | 210   | 70.7        | 372    | 8  | US-11-330-082-1395   |
| 4          | 210   | 70.7        | 401    | 8  | Sequence 1395, Ap    |
| 5          | 199   | 67.0        | 248    | 8  | US-11-239-610A-16542 |
|            |       |             |        |    | Sequence 16542, A    |
|            |       |             |        |    | Sequence 30892, A    |
|            |       |             |        |    | Sequence 20029, A    |

|                   |                  |                   |                   |                   |                   |                   |                   |                   |                   |                  |                    |                    |                   |                   |                    |                   |                   |                   |                   |                   |                    |                  |                   |                   |                    |                    |                   |                    |                    |                    |                   |                   |                    |                   |                    |                  |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                    |                    |                    |                    |                    |                    |                    |                   |                   |                    |                   |                   |                   |                   |                    |                    |
|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|------------------|-------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|--------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|
| Sequence 9120, Ap | Sequence 3684, A | Sequence 40055, A | Sequence 36769, A | Sequence 40579, A | Sequence 7837, Ap | Sequence 6654, Ap | Sequence 8967, Ap | Sequence 8122, Ap | Sequence 15715, A | Sequence 8922, A | Sequence 189520, A | Sequence 243182, A | Sequence 45019, A | Sequence 345, App | Sequence 162817, A | Sequence 11005, A | Sequence 254, App | Sequence 11416, A | Sequence 3689, Ap | Sequence 1611, Ap | Sequence 249122, A | Sequence 1, Appl | Sequence 434, App | Sequence 51591, A | Sequence 219252, A | Sequence 418580, A | Sequence 54928, A | Sequence 184821, A | Sequence 192322, A | Sequence 480462, A | Sequence 1655, Ap | Sequence 91047, A | Sequence 143858, A | Sequence 335, App | Sequence 7039, App | Sequence 9, Appl | Sequence 631, App | Sequence 918, App | Sequence 94, Appl | Sequence 30574, A | Sequence 25, Appl | Sequence 1541, Ap | Sequence 22786, A | Sequence 27565, A | Sequence 1730, Ap | Sequence 3910, Ap | Sequence 630, App | Sequence 42, Appl | Sequence 77004, A | Sequence 2675, Ap | Sequence 81680, A | Sequence 17214, A | Sequence 1954, Ap | Sequence 7194, Ap | Sequence 2229, Ap | Sequence 187151, A | Sequence 258017, A | Sequence 278363, A | Sequence 318534, A | Sequence 258016, A | Sequence 278362, A | Sequence 318533, A | Sequence 29769, A | Sequence 832, App | Sequence 1173, App | Sequence 28805, A | Sequence 29054, A | Sequence 1667, Ap | Sequence 2477, Ap | Sequence 408170, A | Sequence 479216, A |
|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|------------------|-------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|--------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|

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82      64      21.5 3720 7 US-10-515-325-1523
83      64      21.5 138837 6 US-10-539-228-146
84      63.5 21.4 441 10 US-11-292-078-3277
85      63.5 21.4 445 10 US-11-266-748A-178801
86      63      21.4 270 8 US-11-239-610A-20443
87      63      21.2 422 8 US-11-353-150-37237
88      63      21.2 439 8 US-11-239-591A-24111
89      63      21.2 445 8 US-11-353-150-37316
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95      63      21.2 4233 10 US-11-266-748A-57283
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98      62.5 21.0 1000 10 US-11-266-748A-117181
99      62.5 21.0 1000 10 US-11-266-748A-159345
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102     62.5 21.0 1000 10 US-11-266-748A-399591
103     62.5 21.0 1109 10 US-11-266-748A-740637
104     62.5 21.0 1109 10 US-11-266-748A-74428
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106     62.5 21.0 1611 10 US-11-266-748A-187292
107     62.5 21.0 1611 10 US-11-266-748A-382872
108     62.5 21.0 1611 10 US-11-266-748A-433728
109     62.5 21.0 2300 12 US-60-762-056-25883
110     62.5 21.0 3944 12 US-60-763-366-800
111     62.5 21.0 3944 12 US-60-763-366-801
112     62.5 21.0 3974 12 US-60-763-366-802
113     62.5 21.0 3974 12 US-60-763-366-803
114     62.5 21.0 4190 1 PC7-US06-05584-102
115     62.5 21.0 4190 1 PC7-US06-05584-102
116     62.5 21.0 4190 7 US-10-917-503B-14679
117     62.5 21.0 89807 10 US-11-266-748A-61887
118     62      20.9 360 8 US-11-352-293-6868
119     62      20.9 384 10 US-11-313-816-660
120     62      20.9 419 10 US-11-313-816-660
121     62      20.9 802 8 US-11-360-355-50381
122     62      20.9 1000 10 US-11-266-748A-195439
123     62      20.9 1000 10 US-11-266-748A-282873
124     62      20.9 1000 10 US-11-266-748A-309513
125     62      20.9 1000 10 US-11-266-748A-392449
126     62      20.9 1000 10 US-11-266-748A-483167
127     62      20.9 1510 7 US-10-953-349-14286
128     62      20.9 1947 12 US-60-772-265-638
129     62      20.9 1947 12 US-60-772-265-960
130     62      20.9 1950 12 US-60-772-265-812
131     62      20.9 1953 12 US-60-772-265-1312
132     62      20.9 2029 8 US-11-360-355-47647
133     62      20.9 2036 12 US-60-772-265-554
134     62      20.9 2092 8 US-11-360-355-48763
135     62      20.9 2094 8 US-11-360-355-50003
136     62      20.9 2097 12 US-60-772-265-1288
137     62      20.9 2882 10 US-11-266-446-7
138     61.5 20.7 248 8 US-11-360-355-58810
139     61.5 20.7 510 8 US-11-360-355-96506
140     61.5 20.7 693 8 US-11-360-355-73204
141     61.5 20.7 721 8 US-11-360-355-95226
142     61.5 20.7 773 8 US-11-360-355-89016
143     61.5 20.7 950 10 US-11-266-748A-381222
144     61.5 20.7 950 10 US-11-266-748A-430978
145     61.5 20.7 1004 10 US-11-266-748A-70999
146     61.5 20.7 1004 10 US-11-266-748A-106371
147     61.5 20.7 1004 10 US-11-266-748A-123810
148     61.5 20.7 1080 10 US-11-266-748A-258185
149     61.5 20.7 1080 10 US-11-266-748A-278448
150     61.5 20.7 1080 10 US-11-266-748A-318702

Sequence 256041,
Sequence 316558,
Sequence 18116, A
Sequence 1523, Ap
Sequence 146, App
Sequence 3277, Ap
Sequence 178801,
Sequence 20443, A
Sequence 37237, A
Sequence 24111, A
Sequence 37316, A
Sequence 38921, A
Sequence 1264, Ap
Sequence 4949, Ap
Sequence 40717, A
Sequence 57283, A
Sequence 15982, A
Sequence 21632, A
Sequence 117181,
Sequence 159345,
Sequence 288683,
Sequence 340112,
Sequence 399591,
Sequence 740637,
Sequence 74428, A
Sequence 127239,
Sequence 187292,
Sequence 350349,
Sequence 382872,
Sequence 433728,
Sequence 25883, A
Sequence 800, App
Sequence 801, App
Sequence 802, App
Sequence 803, App
Sequence 102, App
Sequence 786, App
Sequence 14679, A
Sequence 61887, A
Sequence 6868, Ap
Sequence 1501, Ap
Sequence 50381, A
Sequence 195439,
Sequence 282873,
Sequence 309513,
Sequence 392449,
Sequence 483167,
Sequence 14286, A
Sequence 638, App
Sequence 960, App
Sequence 812, App
Sequence 1512, Ap
Sequence 47647, A
Sequence 554, App
Sequence 48763, A
Sequence 50003, A
Sequence 1288, Ap
Sequence 7, Appli
Sequence 58810, A
Sequence 96506, A
Sequence 73204, A
Sequence 95226, A
Sequence 89016, A
Sequence 381222,
Sequence 430978, A
Sequence 70999, A
Sequence 106371,
Sequence 123810,
Sequence 258185,
Sequence 278448,
Sequence 318702,

ALIGNMENTS

RESULT 1
US-11-239-610A-11025
; Sequence 11025, Application US/11239610A
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 16517.341 - 38-21(15793)C/US
; CURRENT APPLICATION NUMBER: US/11/239,610A
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US 09/565,240
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 54005
; SEQ ID NO 11025
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3092-013-Q1-K1-C1
US-11-239-610A-11025
Alignment Scores:
Pred. No.: 76-21 Length: 391
Score: 215.00 Matches: 44
Percent Similarity: 83.3% Conservative: 6
Best Local Similarity: 73.3% Mismatches: 8
Query Match: 72.4% Indels: 2
DB: 8 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-239-610A-11025 (1-391)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 10 ATGGCACAGATTTCCTCTACGCAATGGCAGATGAGATCTCAAGGCTCTCC 69
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLys 40
Db 70 AATGCAACTCCCATACATCAACATATGAGAGTTCTTTATTGTGGAACAAATAAGAAA 129
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 130 GTTCCCTACCACTTCGTAAATTTAGTGTGGCAATTAAGTCTGCACATAGCACC 189

RESULT 2
US-11-330-082-1395
; Sequence 1395, Application US/113300082
; GENERAL INFORMATION:
; APPLICANT: Buehler, Robert E.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Coombs, Brian E.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 16517.356 - 38-21(15760)C/US
; CURRENT APPLICATION NUMBER: US/11/330,082
; CURRENT FILING DATE: 2006-01-12
; PRIOR APPLICATION NUMBER: US 09/552,086
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 27278
; SEQ ID NO 1395
; LENGTH: 293
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700996496H1
US-11-330-082-1395
Alignment Scores:
Pred. No.: 2.42e-20 Length: 293
```



Score: 210.00 Matches: 43  
Percent Similarity: 86.2% Conservative: 7  
Best Local Similarity: 74.1% Mismatches: 6  
Query Match: 8 Indels: 2  
DB: 1 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-330-082-1395 (1-293)

Qy 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db 92 ATGGCACAGATTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAATCCTCTCCC 151  
Qy 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db 152 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 211  
Qy 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56  
Db 212 GTTTCACCCACAGTTCTGCTAAATTAGATGATGCAATTAAAGTCTGACAAAT 265

RESULT 3  
US-11-239-610A-16542  
; Sequence 16542, Application US/11239610A  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 16517.341 - 38-21(15793)C/US  
; CURRENT FILING DATE: 2005-09-30  
; PRIOR APPLICATION NUMBER: US 09/565,240  
; PRIOR FILING DATE: 2000-05-08  
; NUMBER OF SEQ ID NOS: 54005  
; SEQ ID NO 16542  
; LENGTH: 372  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3106-116-Q1-K1-C5  
US-11-239-610A-16542

Alignment Scores:  
Pred. No.: 3,38e-20 Length: 372  
Score: 210.00 Matches: 43  
Percent Similarity: 86.2% Conservative: 7  
Best Local Similarity: 74.1% Mismatches: 6  
Query Match: 8 Indels: 2  
DB: 1 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-239-610A-16542 (1-372)

Qy 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db 80 ATGGCACAGATTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAATCCTCTCCC 139  
Qy 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db 140 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 199  
Qy 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56  
Db 200 GTTTCACCCACAGTTCTGCTAAATTAGATGATGCAATTAAAGTCTGACAAAT 253

RESULT 4  
US-11-239-610A-30892  
; Sequence 30892, Application US/11239610A  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 16517.341 - 38-21(15793)C/US  
; CURRENT APPLICATION NUMBER: US/11/239,610A  
; CURRENT FILING DATE: 2005-09-30  
; PRIOR APPLICATION NUMBER: US 09/565,240  
; PRIOR FILING DATE: 2000-05-08  
; NUMBER OF SEQ ID NOS: 54005  
; SEQ ID NO 30892  
; LENGTH: 401  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3138-051-Q1-N1-E12  
US-11-239-610A-30892

Alignment Scores:  
Pred. No.: 3,75e-20 Length: 401  
Score: 210.00 Matches: 43  
Percent Similarity: 86.2% Conservative: 7  
Best Local Similarity: 74.1% Mismatches: 6  
Query Match: 8 Indels: 2  
DB: 1 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-239-610A-30892 (1-401)

Qy 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db 89 ATGGCACAGATTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAATCCTCTCCC 148  
Qy 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db 149 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 208  
Qy 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56  
Db 209 GTTTCACCCACAGTTCTGCTAAATTAGATGATGCAATTAAAGTCTGACAAAT 262

RESULT 5  
US-11-330-082-20029  
; Sequence 20029, Application US/11330082  
; GENERAL INFORMATION:  
; APPLICANT: Buehler, Robert E.  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: Coombs, Brian E.  
; APPLICANT: La Rosa, Thomas J.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 16517.356 - 38-21(15760)C/US  
; CURRENT APPLICATION NUMBER: US/11/330,082  
; CURRENT FILING DATE: 2006-01-12  
; PRIOR APPLICATION NUMBER: US 09/552,086  
; PRIOR FILING DATE: 2000-04-19  
; NUMBER OF SEQ ID NOS: 27278  
; SEQ ID NO 20029  
; LENGTH: 248  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700872751H1  
US-11-330-082-20029

Alignment Scores:  
Pred. No.: 7,13e-19 Length: 248  
Score: 199.00 Matches: 41  
Percent Similarity: 87.0% Conservative: 6  
Best Local Similarity: 75.9% Mismatches: 5  
Query Match: 8 Indels: 2  
DB: 1 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-330-082-20029 (1-248)

Qy 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||

```
Db      84  ATGGCAGAGATTTGGCTCCCTCTACGCAATGGCAGATGCGAATCTCAAAATCCTCTCC 143
QY      21  CysAlaThrProIleThrSerIysMetTTPSerSerLeuValMetIysGlnThrIysIys 40
Db      144  ATGCAACTCCCATATACATCAACATGTGGAGTCTCTTATTGTGGAAACAAATAAGAAA 203
QY      41  ValAla-----HisSerAlaIysPheArgValMetAlaVal 52
Db      204  GTTTCACCTACCACTCTCTGTAATTTAGAGTGTGGCAATT 245

RESULT 6
US-11-331-019-9120
; Sequence 9120, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; PRIOR FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 9120
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3120-053-P1-K1-C3
US-11-331-019-9120

Alignment Scores:
Pred. No.:      3-75e-15      Length:      360
Score:          174.50      Matches:      38
Percent Similarity: 76.7%      Conservative: 8
Best Local Similarity: 63.3%      Mismatches: 11
Query Match:    58.8%      Indels:      3
DB:             8          Gaps:      2

US-10-628-525A-35 (1-58) x US-11-331-019-9120 (1-360)
QY      1  MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20
Db      104  ATGGCACAGCTTTTAGCACCTCAACTCAATGGCAATGACACTACCAAGACCTCAACC 163
QY      21  CysAlaThrProIleThrSerIysMetTTPSerSerLeuValMetIysGlnThrIysIys 40
Db      164  TATGGAAGTCCCATTCGCAACAAATGTGGAGTCTCTGGTACTGAAACAGAACAGAAA 223
QY      41  ValAla-----HisSerAlaIysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db      224  GGAGCTGTAAAGCTCTGGCAAGTTAAAGTGTGGCTTG--TCTGAAACAGCACT 280

RESULT 7
US-11-331-019-36684
; Sequence 36684, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; PRIOR FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 36684
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-048-Q1-K1-C1
US-11-331-019-40055

Alignment Scores:
Pred. No.:      4.36e-15      Length:      401
Score:          174.50      Matches:      38
Percent Similarity: 76.7%      Conservative: 8
Best Local Similarity: 63.3%      Mismatches: 11
Query Match:    58.8%      Indels:      3
DB:             8          Gaps:      2

US-10-628-525A-35 (1-58) x US-11-331-019-40055 (1-401)
QY      1  MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20
Db      122  ATGGCACAGCTTTTAGCACCTCAACTCAATGGCAATGACACTACCAAGACCTCAACC 181
```

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; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 36684
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-006-P1-K3-A11
US-11-331-019-36684

Alignment Scores:
Pred. No.:      4.05e-15      Length:      380
Score:          174.50      Matches:      38
Percent Similarity: 76.7%      Conservative: 8
Best Local Similarity: 63.3%      Mismatches: 11
Query Match:    58.8%      Indels:      3
DB:             8          Gaps:      2

US-10-628-525A-35 (1-58) x US-11-331-019-36684 (1-380)
QY      1  MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20
Db      119  ATGGCACAGCTTTTAGCACCTCAACTCAATGGCAATGACACTACCAAGACCTCAACC 178
QY      21  CysAlaThrProIleThrSerIysMetTTPSerSerLeuValMetIysGlnThrIysIys 40
Db      179  TATGGAAGTCCCATTCGCAACAAATGTGGAGTCTCTGGTACTGAAACAGAACAGAAA 238
QY      41  ValAla-----HisSerAlaIysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db      239  GGAGCTGTAAAGCTCTGGCAAGTTAAAGTGTGGCTTG--TCTGAAACAGCACT 295

RESULT 8
US-11-331-019-40055
; Sequence 40055, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 40055
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-048-Q1-K1-C1
US-11-331-019-40055

Alignment Scores:
Pred. No.:      4.36e-15      Length:      401
Score:          174.50      Matches:      38
Percent Similarity: 76.7%      Conservative: 8
Best Local Similarity: 63.3%      Mismatches: 11
Query Match:    58.8%      Indels:      3
DB:             8          Gaps:      2

US-10-628-525A-35 (1-58) x US-11-331-019-40055 (1-401)
QY      1  MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20
Db      122  ATGGCACAGCTTTTAGCACCTCAACTCAATGGCAATGACACTACCAAGACCTCAACC 181
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Qy 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 182 TATGGAAGTCCCTTACACAAAATGTGGAGTTCTCTGGTACTGAAACACAAAGAAA 241
Qy 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAlaSerGluAenGlyThr 58
Db 242 GGAGCTGCTAAAGCTCTGGCAAGTTTAAAGTGGTTGCCTTG---TCTGAAACAGCACT 298

RESULT 9
US-11-331-019-36769
; Sequence 36769, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR FILING DATE: 2000-08-11
; PRIOR FILING DATE: 2000-08-11
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 36769
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-006-P1-K4-A9
US-11-331-019-36769

Alignment Scores:
Pred. No.: 9.9e-15 Length: 723
Score: 174.50 Matches: 38
Percent Similarity: 76.7% Conservatives: 8
Best Local Similarity: 63.3% Mismatches: 11
Query Match: 58.8% Indels: 3
DB: 2 Gaps: 2

US-10-628-525A-35 (1-58) x US-11-331-019-36769 (1-723)

Qy 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 116 ATGGCACAGCTTTTAGCACCTCACTCAATGGCAATGACACTACCAAGACCTCAACC 175
Qy 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 176 TATGGAAGTCCCTTACACAAAATGTGGAGTTCTCTGGTACTGAAACACAAAGAAA 235
Qy 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAlaSerGluAenGlyThr 58
Db 236 GGAGCTGCTAAAGCTCTGGCAAGTTTAAAGTGGTTGCCTTG---TCTGAAACAGCACT 292

RESULT 10
US-11-331-019-40579
; Sequence 40579, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR FILING DATE: 2000-08-11
; PRIOR FILING DATE: 2000-08-11
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 40579
; LENGTH: 340
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-056-P1-K1-D10
US-11-331-019-40579

Alignment Scores:
Pred. No.: 9.29e-15 Length: 340
Score: 171.50 Matches: 37
Percent Similarity: 76.7% Conservatives: 9
Best Local Similarity: 61.7% Mismatches: 11
Query Match: 57.7% Indels: 3
DB: 2 Gaps: 2

US-10-628-525A-35 (1-58) x US-11-331-019-40579 (1-340)

Qy 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 135 ATGGCACAGCTTTTATCACCTCACTCAATGGCAATGACACTACCAAGACCTCAACC 194
Qy 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 195 TATGGAAGTCCCTTACACAAAATGTGGAGTTCTCTGGTACTGAAACACAAAGAAA 254
Qy 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAlaSerGluAenGlyThr 58
Db 255 GGAGCTGCTAAAGCTCTGGCAAGTTTAAAGTGGTTGCCTTG---TCTGAAACAGCACT 311

RESULT 11
US-11-331-019-7837
; Sequence 7837, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR FILING DATE: 2000-08-11
; PRIOR FILING DATE: 2000-08-11
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 7837
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3120-024-Q1-K1-F11
US-11-331-019-7837

Alignment Scores:
Pred. No.: 4.96e-14 Length: 441
Score: 167.50 Matches: 37
Percent Similarity: 75.0% Conservatives: 8
Best Local Similarity: 61.7% Mismatches: 12
Query Match: 56.4% Indels: 3
DB: 2 Gaps: 2

US-10-628-525A-35 (1-58) x US-11-331-019-7837 (1-441)

Qy 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 82 ATGGCACAGCTTTTAGCACCTCACTCAATGGCAATGACACTACCAAGACCTCAACC 141
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QY 21 CysAlaThrProIleThrSerIysMetTrpSerSerLeuValMetIysGlnThrIysLys 40
Db 142 TATGGAAGTCCCATTCGCAACAAAATGTGGAGTTCTCTGGTACTGAAACAGACAGAAA 201
QY 41 ValAla-----HisSerAlaIysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 202 GGAGCTGCTAAAGAGCTCTGCAAGGTTAAAGTGTTCCTTG---TCTGAAACAGCACT 258

RESULT 12
US-11-331-019-6654
; Sequence 6654, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 6654
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3120-010-Q1-K1-B1
US-11-331-019-6654

Alignment Scores:
Pred. No.: 6,07e-14 Length: 167.00 Matches: 453
Score: 167.00 Matches: 34
Percent Similarity: 73.3% Conservatives: 10
Best Local Similarity: 56.7% Mismatches: 14
Query Match: 56.2% Indels: 2
DB: 8 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-331-019-6654 (1-453)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20
Db 110 ATGGCAGATATCTTGGACCTTCAACTCAATGGCCGATGAGAGTACCAAGAGCTGGACC 169
QY 21 CysAlaThrProIleThrSerIysMetTrpSerSerLeuValMetIysGlnThrIysLys 40
Db 170 TTTGGAGGCCCATTCGCAACAAAATGTGGAGTCTCTGATCTTGAACAGACCATGAAA 229
QY 41 ValAla-----HisSerAlaIysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 230 GGAGCAGCCAAAAGTCTGCGCAAAATTCAGAGTGTTCCTTGCACTCTGAGAACAGCACT 289

RESULT 13
US-11-331-019-36617
; Sequence 36617, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
```

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; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 36617
; LENGTH: 376
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3165-006-P1-K2-A9
US-11-331-019-36617

Alignment Scores:
Pred. No.: 2,06e-13 Length: 162.50 Matches: 376
Score: 162.50 Matches: 36
Percent Similarity: 71.7% Conservatives: 7
Best Local Similarity: 60.0% Mismatches: 14
Query Match: 54.7% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-35 (1-58) x US-11-331-019-36617 (1-376)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20
Db 116 ATGGCAGAGCTTTTAACACCCCTCAACTCAATGCGCAAAATGACACTACCAAGACCTCAACC 175
QY 21 CysAlaThrProIleThrSerIysMetTrpSerSerLeuValMetIysGlnThrIysLys 40
Db 176 TATGGAAAGTCCCATTCGCAACAAAATGTGGAGTCTCTGGTACTGAAACAGACAGAAA 235
QY 41 ValAla-----HisSerAlaIysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 236 GGAGCTGCTAAAGAGCTCTGCGCAAGATTAAGTGGCTGCTTG---TCTGAAACAGCACT 292

RESULT 14
US-11-331-019-8967
; Sequence 8967, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 8967
; LENGTH: 203
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3120-046-P1-K1-C10
US-11-331-019-8967

Alignment Scores:
Pred. No.: 1,4e-06 Length: 112.00 Matches: 203
Score: 112.00 Matches: 21
Percent Similarity: 73.0% Conservatives: 6
Best Local Similarity: 56.8% Mismatches: 10
Query Match: 37.7% Indels: 0
DB: 8 Gaps: 0

US-10-628-525A-35 (1-58) x US-11-331-019-8967 (1-203)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20
Db 7 CTGGCAGAGCTTTTAGCACCCCTCAACTCAATGCGCAAAATGACACTACCAAGACCTTGTC 66
```

QY 21 CysAlaThrProLeuThrSerLysMetTrpSerSerLeuValMetLysGln 37  
Db 67 TGTGAAGTCCATTGCGCAATAATGTGGAGTCTCTGCTACTGATACAG 117

## RESULT 15

US-11-331-019-8122  
; Sequence 8122, Application US/11331019  
; GENERAL INFORMATION:  
; APPLICANT: Fincher, Karen L.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: McCarter, David W.  
; APPLICANT: Pear, Julie R.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US  
; CURRENT APPLICATION NUMBER: US/11/331,019  
; PRIOR FILING DATE: 2006-01-13  
; PRIOR APPLICATION NUMBER: US 09/637,086  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: US 60/149,881  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 52949  
; SEQ ID NO 8122  
; LENGTH: 314  
; TYPE: DNA  
; ORGANISM: Gossypium hirsutum  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3120-028-Q1-K1-B3  
US-11-331-019-8122

Alignment Scores:  
Pred. No.: 3,56e-05 Length: 314  
Score: 104.00 Matches: 20  
Percent Similarity: 75.0% Conservative: 7  
Best Local Similarity: 55.6% Mismatches: 9  
Query Match: 35.0% Indels: 0  
DB: 8 Gaps: 0

US-10-628-525A-35 (1-58) x US-11-331-019-8122 (1-314)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db 115 ATGGCAAACTTTTAAACCGTCACTAAGCGCAATGACACTACCAAGGACCTCATCC 174

QY 21 CysAlaThrProLeuThrSerLysMetTrpSerSerLeuValMetLys 36  
Db 175 TATGAAGTCCATTGCGCAAAAATGTGGCGTCTCTTGGTACTGAA 222

## RESULT 16

US-11-329-388-15715  
; Sequence 15715, Application US/11329388  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Fisher, Dana K.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 16517.357 - 38-21(15503)C/US  
; CURRENT APPLICATION NUMBER: US/11/329,388  
; CURRENT FILING DATE: 2006-01-11  
; PRIOR APPLICATION NUMBER: 09/553,094  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 18831  
; SEQ ID NO 15715  
; LENGTH: 401  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB83-002-Q1-E1-B8  
US-11-329-388-15715

Alignment Scores:  
Pred. No.: 0.956 Length: 401  
Score: 74.00 Matches: 16

Percent Similarity: 43.6% Conservative: 1  
Best Local Similarity: 41.0% Mismatches: 22  
Query Match: 24.9% Indels: 0  
DB: 8 Gaps: 0

US-10-628-525A-35 (1-58) x US-11-329-388-15715 (1-401)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25  
Db 93 GCACCCCATCAGCGTGGCTCTTCGGCGAGCGCGCATCACCATGGCGCAAGCCGTGG 152  
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSer 44  
Db 153 GCAAGCCCAATGTGGCGGTGTCTGCGAGCGCGTGTACGCGCCCGCCGCGTCAAGT 209

## RESULT 17

US-11-056-355B-82922  
; Sequence 82922, Application US/11056355B  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nickolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; PRIOR FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 82922  
; LENGTH: 1830  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1830)  
; OTHER INFORMATION: Ceres Seq. ID no. 12667901  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1830)  
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 12613725  
; OTHER INFORMATION: as cited in SEQ ID NO 68196  
US-11-056-355B-82922

Alignment Scores:  
Pred. No.: 12.9 Length: 1830  
Score: 72.50 Matches: 21  
Percent Similarity: 38.2% Conservative: 13  
Best Local Similarity: 23.6% Mismatches: 20  
Query Match: 24.4% Indels: 35  
DB: 8 Gaps: 4

US-10-628-525A-35 (1-58) x US-11-056-355B-82922 (1-1830)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db 775 TTGGTGGCTTTTGTGGCCCAACAGCAATATCGTTAT-----GTCAAGCCG 822  
QY 21 CysAlaThrProIle-----ThrSerLysMetTrpSer 31  
Db 823 TGTGTTAACCCGTGTGCTGCTGCGGCAAGTATTGTTGGCCACTGCTCGTAAGTGAGT 882  
QY 32 SerLeu-----ValMet 35  
Db 883 GTTGTTCGACGAGAGATCCGATGAGTGTAGCAACTTGAAGGCTCTGAATCCGCATT 942  
QY 36 LysGlnThrLysValAlaHisSerAlaLysPhe-----ArgVal 49  
Db 943 AAAGGAAGTCGAAAGATATTTCATAGTACCAAAATTTCTTCTTGTGATAGACGACGAGT 1002  
QY 50 MetAlaValAsnSerGluAsnGlyThr 58  
Db 1003 ATTACAGGAATGATAGGAATGGACA 1029

```
RESULT 18
US-11-266-748A-189520/c
; Sequence 189520, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 189520
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-189520

Alignment Scores:
Pred. No.: 20.6 Length: 1594
Score: 70.50 Matches: 15
Percent Similarity: 57.1% Conservative: 5
Best Local Similarity: 42.9% Mismatches: 14
Query Match: 23.7% Indels: 1
DB: 10 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-266-748A-189520 (1-1594)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 852 TCACCATCCCAAGCTGGAGACCCCAACCCAGACATCGACCTGTATACCAACCATGT 793
QY 26 ThrSerLysMetTrp---SerSerLeuValMetLysGlnThrLys 39
Db 792 ACATGGAGGCCCTGGTGAAGCTCTTCGACAAGCAACAAAGACCAAG 748

RESULT 19
US-11-266-748A-243182
; Sequence 243182, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
```

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; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 243182
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-243182

Alignment Scores:
Pred. No.: 20.6 Length: 1594
Score: 70.50 Matches: 15
Percent Similarity: 57.1% Conservative: 5
Best Local Similarity: 42.9% Mismatches: 14
Query Match: 23.7% Indels: 1
DB: 10 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-266-748A-243182 (1-1594)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 743 TCACCATCCCAAGCTGGAGACCCCAACCCAGACATCGACCTGTATACCAACCATGT 802
QY 26 ThrSerLysMetTrp---SerSerLeuValMetLysGlnThrLys 39
Db 803 ACATGGAGGCCCTGGTGAAGCTCTTCGACAAGCAACAAAGACCAAG 847

RESULT 20
US-11-360-355-45019/c
; Sequence 45019, Application US/11360355
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijong
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/11/360,355
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 45019
; LENGTH: 958
; TYPE: DNA
; ORGANISM: Heterodera glycines
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (941)..(941)
; OTHER INFORMATION: n is a, c, g, or t
US-11-360-355-45019

Alignment Scores:
Pred. No.: 14.1 Length: 958
Score: 69.50 Matches: 16
Percent Similarity: 56.1% Conservative: 16
Best Local Similarity: 28.1% Mismatches: 10
Query Match: 23.4% Indels: 15
DB: 8 Gaps: 3
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US-10-628-525A-35 (1-58) x US-11-360-355-45019 (1-958)
Qy 3 GlnLeuAlaProSerThrGlnMetArgIleThrLysThrSerProCysAla 22
Db 446 AAGTGATGGCAGCAGCGATTTGGCGATGGCGTCACTTGGACAGCAATTTGTCTC 387
Qy 23 -----ThrProIleThrSerLysMet---TriSer 31
Db 386 GACCAGCGCAACATCATCGGTACGAGCTGCGGATGGTCTCCAAATTCCTGGACA 327
Qy 32 SerLeuValMetLys-----GlnThrLysLysValAlaHisSer 44
Db 326 AACATTTGGTGAAGCGCTCAATAGCAGACCAACAGCGGAGCAAAATCG 276
RESULT 21
US-10-533-232A-345/c
; Sequence 345, Application US/10533232A
; GENERAL INFORMATION:
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: CELL PROLIFERATION-RELATED POLYPEPTIDES AND USES THEREFOR
; FILE REFERENCE: 1392-10-19-2
; CURRENT APPLICATION NUMBER: US/10/533,232A
; CURRENT FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/436,565
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 345
; LENGTH: 1950
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1950)
US-10-533-232A-345
Alignment Scores:
Pred. No.: 44.6 Length: 1950
Score: 69.00 Matches: 18
Percent Similarity: 63.6% Conservative: 10
Best Local Similarity: 40.9% Mismatches: 10
Query Match: 23.2% Indels: 6
DB: 7 Gaps: 2
US-10-628-525A-35 (1-58) x US-10-533-232A-345 (1-1950)
Qy 4 IleLeuAlaProSerThrGlnTrp---GlnMetArgIleThrLysThrSerPro----- 20
Db 758 CTCTTGAATTTTGCAAAAGTGGTGGACCATCGGTGTGCAAAATCTTCACCAACCAAGA 699
Qy 21 -----CysAlaThrProIleThrSerLysMetTriSerSerLeuValMetLysGln 37
Db 698 TGGGTGTCCACCACTGTGGCTTGACTCAAGATACCTCTCTCAATGTGAAGAGGGA 639
Qy 38 ThrLysLysVal 41
Db 638 ACATCAAGGTA 627
RESULT 22
US-11-266-748A-162817
; Sequence 162817, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
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; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 162817
; LENGTH: 1053
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-162817
Alignment Scores:
Pred. No.: 22.3 Length: 1053
Score: 68.50 Matches: 18
Percent Similarity: 52.3% Conservative: 5
Best Local Similarity: 40.9% Mismatches: 16
Query Match: 23.1% Indels: 5
DB: 10 Gaps: 2
US-10-628-525A-35 (1-58) x US-11-266-748A-162817 (1-1053)
Qy 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26
Db 483 CCACTACCAGGTGGGTGAGACGCTGACTCGCAGATCAAGTTGT-----CCA 530
Qy 27 SerLysMetTriSer---SerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 531 TCAAGCGCTGTGTCCACCAAGCGGTGCTCTCAAGCAGACCAAGGGGTGGGGCTCGGG 590
Qy 46 LysPheArgVal 49
Db 591 TCCTTCGGGCTA 602
RESULT 23
US-11-239-610A-11005
; Sequence 11005, Application US/11239610A
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 16517.341 - 38-21(15793)C/US
; CURRENT APPLICATION NUMBER: US/11/239,610A
; PRIOR FILING DATE: 2005-09-30
; CURRENT APPLICATION NUMBER: US 09/565,240
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 54005
; SEQ ID NO 11005
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3092-013-Q1-K1-E1
US-11-239-610A-11005
Alignment Scores:
Pred. No.: 7.13 Length: 412
Score: 68.00 Matches: 22
Percent Similarity: 55.9% Conservative: 11
Best Local Similarity: 37.3% Mismatches: 23
Query Match: 22.9% Indels: 3
DB: 8 Gaps: 1
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US-10-628-525A-35 (1-58) x US-11-239-610A-11005 (1-412)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 10 ATGGATCAAAATTCGGCTCGCTTTACGCAACGGCTTTATTAGATGTGCAAGGTGCTATTCA 69
QY 21 CysAlaThrProIleThrSerLysMet-TrpSerSerLeuValMetLysGlnThrLysLys 40
Db 70 TATGGCATGCTATTACATCAACATTTTGCATTCCTTATTGTGGAAACAAATAAGAA 129
QY 40 sVal-----AlaHisSerAlaLysPheArgValMetAlaValAlaSerGluAsn 56
Db 130 CGCTTAACCTACCAGTATGCTAAATTTACAGTGCTGCTGATTAATTCAGCAAT 184

RESULT 24
US-10-540-898-254/c
; Sequence 254, Application US/10540898
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: CHIR0056-101 (PP023367.0003)
; CURRENT APPLICATION NUMBER: US/10/540,898
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 10/330,773
; PRIOR FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; TYPE: DNA
; LENGTH: 86149
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(86149)
; OTHER INFORMATION: n = A,T,C or G
US-10-540-898-254

Alignment Scores:
Pred. No.: 1.21e+04 Length: 86149
Score: 68.00 Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9% Indels: 0
DB: 7 Gaps: 0

US-10-628-525A-35 (1-58) x US-10-540-898-254 (1-86149)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 46678 GCCCGCGCACTCACCATGGTAGATGATATCTGGAGACCCCTGTTCAGCCCTCAGAGATT 46619
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 46618 TGCAGAGCCCATGGGCGAGATGGAGATGGTGGGACAACTGGATGGTCCCTCAGGG 46559
QY 46 LysPheArgValMetAlaValAlaSerGluAsnGlyThr 58
Db 46558 AGATTTCAGCAGCTCAACAGGAACTGGGAGAAAGGCACT 46520

RESULT 25
US-10-917-503B-11416
; Sequence 11416, Application US/10917503B
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HAYASHI, KOJI
; APPLICANT: SAITO, KAORU
; APPLICANT: YAMAMOTO, JUNICHI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: SUGIYAMA, TOMOYASU

```

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; APPLICANT: WAKAMATSU, AI
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: OTSUKI, TETSUJI
; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE
; FILE REFERENCE: 084335/0123
; CURRENT APPLICATION NUMBER: US/10/917,503B
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US/09/629,469
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: JP 1999-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 1999-300253
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,322
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 19025
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11416
; LENGTH: 2103
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (102)..(2021)
US-10-917-503B-11416

Alignment Scores:
Pred. No.: 81.2 Length: 2103
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservative: 11
Best Local Similarity: 28.3% Mismatches: 18
Query Match: 22.7% Indels: 9
DB: 7 Gaps: 1

US-10-628-525A-35 (1-58) x US-10-917-503B-11416 (1-2103)
QY 1 MetAlaGlnIleLeuAla-----ProSerThrGlnTrp 11
Db 949 ATGGGAGAGATCTTTCCCACTCTTAATGAACCGCAGCGTGTGCCCAAAGTTTGGTGG 1008
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSer 31
Db 1009 AAAATGCAAGAACTTCCCTCAGTGTGTCTAGATAATCTCTGACCAAGAGTGTGGAT 1068
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
Db 1069 GGTATACCTGCTAAAGACTTCATTGTTGGAGAGTCACTCA 1107

RESULT 26
US-60-751-455-3689
; Sequence 3689, Application US/60751455
; GENERAL INFORMATION:
; APPLICANT: Radich, Jerald P.
; APPLICANT: Dai, Hongyue
; APPLICANT: Mao, Mao
; APPLICANT: Schelter, Janell
; APPLICANT: Linsley, Peter S.
; TITLE OF INVENTION: GENES ASSOCIATED WITH PROGRESSION AND RESPONSE IN
; TITLE OF INVENTION: CHRONIC MYELOID LEUKEMIA AND USES THEREOF
; FILE REFERENCE: 9301-253-888
; CURRENT APPLICATION NUMBER: US/60/751,455
; CURRENT FILING DATE: 2005-12-15
; NUMBER OF SEQ ID NOS: 7936
; SOFTWARE: FastSeq 4.01
; SEQ ID NO 3689

```

```
; LENGTH: 2103
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-751-455-3689

Alignment Scores:
Pred. No.:      81.2      Length:      2103
Score:          67.50     Matches:      15
Percent Similarity: 49.1% Conservative: 11
Best Local Similarity: 28.3% Mismatches: 18
Query Match:    22.7%   Indels:      9
DB:             12      Gaps:       1

US-10-628-525A-35 (1-58) x US-60-751-455-3689 (1-2103)
QY 1 MetAlaGlnIleLeuLa-----ProSerThrGlnTrp 11
   ||| :|||:|||||:|
Db 949 ATGGGAGAGATCTTTCCCACTCTAATGAACGCCAGCGTGCGCCAAAGTTTGGTGG 1008
   ||| :|||:|||||:|

QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSer 31
   ||| :|||:|||||:|
Db 1009 AAAATGCAAGAAGACTTCCCTCAGTGTGTGCTAGAAATCTCTGACCAAGAAGTGTGGAAAT 1068
   ||| :|||:|||||:|

QY 32 SerLeuValMetLysGlnThrLysLysValAlaAlaHisSer 44
   ||| :|||:|||||:|
Db 1069 GGTATACTGCTAAGAAGACTTCATTTGTTGGGAAGTCACTCA 1107
   ||| :|||:|||||:|

RESULT 27
US-10-515-325-1611/c
; Sequence 1611, Application US/10515325
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Higgs, Brandon
; APPLICANT: Elaeheoff, Michael
; TITLE OF INVENTION: Molecular Nephrotoxicology Modeling
; FILE REFERENCE: 044921-5089-02-US
; CURRENT APPLICATION NUMBER: US/10/515,325
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 10/301,856
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: PCT/US2003/037556
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1611
; LENGTH: 1366
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-515-325-1611

Alignment Scores:
Pred. No.:      52.5      Length:      1366
Score:          67.00     Matches:      19
Percent Similarity: 59.1% Conservative: 7
Best Local Similarity: 43.2% Mismatches: 12
Query Match:    22.6%   Indels:      6
DB:             7      Gaps:       3

US-10-628-525A-35 (1-58) x US-10-515-325-1611 (1-1366)
QY 4 IleLeuAlaProSerThrGlnTrp---GlnMetArgIleThrLysThrSerPro----- 20
   ||| :|||:|||||:|
Db 645 CTCCTTGAAGTCTCTCCAGAGAGTGGCTCACCAGCGGTGTGCAAGTCTCTCCCGCCAGG 586
   ||| :|||:|||||:|

QY 21 CysAlaThrPro-----IleThrSerLysMetTrpSerSerLeuValMetLysGln 37
   ||| :|||:|||||:|
Db 585 TCGGTGTCCCGCGCGTGGCCTTCACTCGAAGATGCCGCTCGTGTGATCGTCAGGATGGAC 526
   ||| :|||:|||||:|

QY 38 ThrLysLysVal 41
   ||| :|||:|||||:|
```

```
Db 525 ACGTCGAACGTG 514
RESULT 28
US-11-266-748A-249122
; Sequence 249122, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 249122
; LENGTH: 1412
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (271)..(288)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (601)..(609)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-249122

Alignment Scores:
Pred. No.:      54.9      Length:      1412
Score:          67.00     Matches:      12
Percent Similarity: 55.0% Conservative: 10
Best Local Similarity: 30.0% Mismatches: 18
Query Match:    22.6%   Indels:      0
DB:            10      Gaps:       0

US-10-628-525A-35 (1-58) x US-11-266-748A-249122 (1-1412)
QY 5 LeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrPro 24
   ||| :|||:|||||:|
Db 908 GTGTGCCCCAAAGTGTGGTGGAAATGCAAGAACTTCCTCAGTGTGTGCTAGAAATCT 967
   ||| :|||:|||||:|

QY 25 IleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSer 44
   ||| :|||:|||||:|
Db 968 CTGAACAAGAGTGTGGAAATGGTATCTGCTAAAGACTTCATTGTTGGGAAGTCACTCA 1027
   ||| :|||:|||||:|

RESULT 29
US-10-018-470B-1/c
; Sequence 1, Application US/10018470B
; GENERAL INFORMATION:
; APPLICANT: FRASER, Claire Marie
; APPLICANT: HICKEY, Erin Kathleen
; APPLICANT: PETERSON, Jeremy D.
; APPLICANT: TETTELIN, Herve
; APPLICANT: VENTER, J. Craig
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; APPLICANT: MASIGNANI, Vega
; APPLICANT: GALEOTTI, Cesira
; APPLICANT: MORA, Marirosa
; APPLICANT: RATTI, Giulio
; APPLICANT: SCARSELLI, Maria
; APPLICANT: SCARLATO, Vincenzo
; APPLICANT: RAPPUOLI, Rino
; APPLICANT: PIZZA, Mariagrazia
; APPLICANT: GRANDI, Guido
; TITLE OF INVENTION: NEISSERIA GENOMIC SEQUENCES AND METHODS OF THEIR USE
; FILE REFERENCE: 223002100400
; CURRENT APPLICATION NUMBER: US/10/018,470B
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: PCT/US00/05928
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: US 60/132,068
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: GB 0004695.3
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PCT/US99/23573
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Seqwin99, version 1.0.4
; SEQ ID NO 1
; LENGTH: 2242716
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-018-470B-1

Alignment Scores:
Pred. No.: 1.72e+06 Length: 2242716
Score: 66.50 Matches: 18
Percent Similarity: 47.7% Conservative: 3
Best Local Similarity: 40.9% Mismatches: 18
Query Match: 22.4% Indels: 5
DB: 7 Gaps: 1

US-10-628-525A-35 (1-58) x US-10-018-470B-1 (1-2242716)
QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAla----- 22
Db 660554 CGGTCAACCTCTTGGACACGCGCGGACACCAAGACTTCTCCGAGACACCTACCGCGTTT 660495
QY 23 ---ThrProIleThrSerLysMetTrpSerLeuValMetLysGlnThrLysLysVal 41
Db 660494 TAACCGCGGTGGACAGCGCATTAATGGTCAUCGACGCGGCAAGGCGTGGAGCGCAA 660435
QY 42 AlaHisSerAla 45
Db 660434 CCATCAAGCTCT 660423

RESULT 30
US-10-187-187-434
; Sequence 434, Application US/10501187
; GENERAL INFORMATION:
; APPLICANT: Hansen, Rhonda
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; FILE REFERENCE: 2300-17767
; CURRENT APPLICATION NUMBER: US/10/501,187
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/345,637
; PRIOR FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 516
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 434
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-501-187-434

Alignment Scores:
Pred. No.: 18.1 Length: 503
```

```
Score: 66.00 Matches: 19
Percent Similarity: 45.3% Conservative: 5
Best Local Similarity: 35.8% Mismatches: 18
Query Match: 22.2% Indels: 12
DB: 7 Gaps: 2

US-10-628-525A-35 (1-58) x US-10-501-187-434 (1-503)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 277 TCACCATCCCAAGCTGGGACACCCACCAAGCAAGACATCGACCTGTACCACCATGT 336
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 337 ACATGGAGGCCCTGGT-AAGCTCTTTCGACAG-----CACAGACC 377
QY 46 LysPhe-----ArgValMetAlaValAsn 53
Db 378 AAGTTCGGGCTCCCGGAGAGACTGAGGTCTCTGGAGGTGAAC 416

Search completed: April 2, 2006, 04:09:35
Job time : 276.468 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search using ~~us-10-628-525a-36.p2n~~ model

Run on: April 1, 2006, 04:29:01 ; Search time 1473.89 Seconds  
(without alignments)  
2853.949 Million cell updates/sec

Title: US-10-628-525A-36

Perfect score: 368

Sequence: 1 MAALATSQLVATAGHGVDP.....RHQQQARRGRPFPSLIVC 74

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-Q=/abes/ABSSWEB spool/US10628525/runat\_31032006\_095113\_16622/app\_query.fasta\_1  
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -IOOPCL=0 -IOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abes06h  
-USER=US10628525 @CGN 1.1 4375 @runat\_31032006\_095113\_16622 -NCPU=6 -ICPU=3  
-NO\_WMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.in.\*

3: gb.env.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pr.\*

9: gb.ro.\*

10: gb.ste.\*

11: gb.sy.\*

12: gb.un.\*

13: gb.vi.\*

14: gb.htg.\*

15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
| 1          | 333   | 90.5        | 1018   | 6  | AR427888 Sequence |
| 2          | 333   | 90.5        | 4274   | 15 | AF544096          |
| 3          | 333   | 90.5        | 4287   | 15 | AF544092          |

|    |       |      |        |    |           |
|----|-------|------|--------|----|-----------|
| 4  | 333   | 90.5 | 4449   | 15 | AF544094  |
| 5  | 333   | 90.5 | 4467   | 15 | AF544071  |
| 6  | 333   | 90.5 | 4470   | 15 | AF544088  |
| 7  | 333   | 90.5 | 4477   | 15 | AF544091  |
| 8  | 333   | 90.5 | 4484   | 15 | AF544074  |
| 9  | 333   | 90.5 | 4800   | 6  | AR106490  |
| 10 | 333   | 90.5 | 4800   | 15 | ZMWAXY    |
| 11 | 337   | 88.9 | 4090   | 15 | AF544079  |
| 12 | 336   | 88.6 | 4427   | 15 | AF544098  |
| 13 | 336   | 88.6 | 4433   | 15 | AF544099  |
| 14 | 336   | 88.6 | 4444   | 15 | AF544083  |
| 15 | 322   | 87.5 | 4395   | 15 | AF544089  |
| 16 | 316.5 | 86.0 | 3533   | 15 | AF544077  |
| 17 | 316.5 | 86.0 | 4210   | 15 | AF544078  |
| 18 | 316.5 | 86.0 | 4230   | 15 | AF544075  |
| 19 | 316.5 | 86.0 | 4436   | 15 | AF544085  |
| 20 | 316.5 | 86.0 | 4436   | 15 | AF544087  |
| 21 | 316.5 | 86.0 | 4436   | 15 | AF544090  |
| 22 | 316.5 | 86.0 | 4438   | 15 | AF544095  |
| 23 | 316.5 | 86.0 | 4463   | 15 | AF544069  |
| 24 | 316.5 | 86.0 | 4463   | 15 | AF544097  |
| 25 | 316.5 | 86.0 | 4475   | 15 | AF544081  |
| 26 | 307   | 83.4 | 4246   | 15 | AF544086  |
| 27 | 298   | 81.0 | 4420   | 15 | AF544072  |
| 28 | 293   | 79.6 | 143300 | 15 | AF488416  |
| 29 | 289   | 78.5 | 2267   | 6  | AR195560  |
| 30 | 286   | 77.7 | 4449   | 15 | AF544093  |
| 31 | 282.5 | 76.8 | 4428   | 15 | AF544080  |
| 32 | 279   | 75.8 | 1915   | 6  | BD071184  |
| 33 | 279   | 75.8 | 4433   | 15 | AF544084  |
| 34 | 237.5 | 64.5 | 2287   | 15 | AF488412  |
| 35 | 237.5 | 64.5 | 130987 | 15 | AF488412  |
| 36 | 219   | 55.8 | 2115   | 15 | AB089141  |
| 37 | 205.5 | 55.8 | 4416   | 15 | AF544076  |
| 38 | 183   | 49.7 | 121    | 6  | AX325915  |
| 39 | 183   | 49.7 | 121    | 6  | AX325916  |
| 40 | 175   | 47.6 | 121    | 6  | AX325911  |
| 41 | 175   | 47.6 | 121    | 6  | AX325912  |
| 42 | 172.5 | 46.9 | 123096 | 15 | AF488414  |
| 43 | 159   | 43.2 | 121    | 6  | AX325919  |
| 44 | 159   | 43.2 | 121    | 6  | AX325920  |
| 45 | 155   | 42.1 | 121    | 6  | AX325923  |
| 46 | 155   | 42.1 | 121    | 6  | AX325924  |
| 47 | 153.5 | 41.7 | 4443   | 15 | AF544082  |
| 48 | 128.5 | 34.9 | 1636   | 15 | AF092444  |
| 49 | 128.5 | 34.9 | 1642   | 15 | AF092443  |
| 50 | 128.5 | 34.9 | 1937   | 6  | BD185620  |
| 51 | 128.5 | 34.9 | 1937   | 6  | BD185621  |
| 52 | 128.5 | 34.9 | 1937   | 15 | AB066093  |
| 53 | 128.5 | 34.9 | 1937   | 15 | AB066094  |
| 54 | 128.5 | 34.9 | 1939   | 15 | AF515480  |
| 55 | 128.5 | 34.9 | 1939   | 15 | AF515481  |
| 56 | 128.5 | 34.9 | 1939   | 15 | AF515482  |
| 57 | 128.5 | 34.9 | 1939   | 15 | AF515483  |
| 58 | 128.5 | 34.9 | 2175   | 15 | AK070431  |
| 59 | 128.5 | 34.9 | 2286   | 6  | E05044    |
| 60 | 128.5 | 34.9 | 2542   | 6  | AR106491  |
| 61 | 128.5 | 34.9 | 2542   | 15 | OSWX      |
| 62 | 128.5 | 34.9 | 2597   | 6  | AX755432  |
| 63 | 128.5 | 34.9 | 4100   | 15 | OSWAXYL   |
| 64 | 128.5 | 34.9 | 4252   | 15 | RICWAXYA  |
| 65 | 128.5 | 34.9 | 5035   | 15 | OSWAX     |
| 66 | 128.5 | 34.9 | 5317   | 15 | OSWAXYG   |
| 67 | 128.5 | 34.9 | 5356   | 15 | AF141954  |
| 68 | 128.5 | 34.9 | 5379   | 15 | AF031162  |
| 69 | 128.5 | 34.9 | 5408   | 15 | AF141955  |
| 70 | 128.5 | 34.9 | 5499   | 15 | OSWAXY    |
| 71 | 128.5 | 34.9 | 110000 | 15 | AP008212  |
| 72 | 128.5 | 34.9 | 136866 | 15 | AF488413  |
| 73 | 128.5 | 34.9 | 151997 | 14 | OSJN01010 |
| 74 | 128.5 | 34.9 | 156266 | 15 | AP002542  |
| 75 | 113   | 30.7 | 121    | 6  | AX325907  |
| 76 | 113   | 30.7 | 121    | 6  | AX325908  |

|                                                                                 |      |                                                               |        |   |             |                    |
|---------------------------------------------------------------------------------|------|---------------------------------------------------------------|--------|---|-------------|--------------------|
| c 150                                                                           | 86.5 | 23.5                                                          | 110000 | 1 | EA000030_45 | Continuation (46 o |
| ALIGNMENTS                                                                      |      |                                                               |        |   |             |                    |
| RESULT 1                                                                        |      |                                                               |        |   |             |                    |
| LOCUS AR427888 1818 bp DNA linear PAT 18-DEC-2003                               |      |                                                               |        |   |             |                    |
| DEFINITION Sequence 3 from patent US 6639126.                                   |      |                                                               |        |   |             |                    |
| ACCESSION AR427888                                                              |      |                                                               |        |   |             |                    |
| VERSION AR427888.1 GI:40186908                                                  |      |                                                               |        |   |             |                    |
| KEYWORDS Unknown.                                                               |      |                                                               |        |   |             |                    |
| SOURCE Unknown.                                                                 |      |                                                               |        |   |             |                    |
| ORGANISM Unclassified.                                                          |      |                                                               |        |   |             |                    |
| REFERENCE 1 (bases 1 to 1818)                                                   |      |                                                               |        |   |             |                    |
| AUTHORS Sewalt,V.J.H. and Singletary,G.W.                                       |      |                                                               |        |   |             |                    |
| TITLE Production of modified polysaccharides                                    |      |                                                               |        |   |             |                    |
| JOURNAL Patent: US 6639126-A 3 28-OCT-2003;                                     |      |                                                               |        |   |             |                    |
| Pioneer Hi-Bred International, Inc.; Des Moines, IA                             |      |                                                               |        |   |             |                    |
| FEATURES                                                                        |      |                                                               |        |   |             |                    |
| source Location/Qualifiers                                                      |      |                                                               |        |   |             |                    |
| 1..1818                                                                         |      |                                                               |        |   |             |                    |
| /organism="unknown"                                                             |      |                                                               |        |   |             |                    |
| /mol_type="genomic DNA"                                                         |      |                                                               |        |   |             |                    |
| ORIGIN                                                                          |      |                                                               |        |   |             |                    |
| Alignment Scores: 7.27e-14 Length: 1818                                         |      |                                                               |        |   |             |                    |
| Pred. No.: 333.00 Matches: 71                                                   |      |                                                               |        |   |             |                    |
| Score: 95.9% Conservative: 0                                                    |      |                                                               |        |   |             |                    |
| Best Local Similarity: 95.9% Mismatches: 1                                      |      |                                                               |        |   |             |                    |
| Query Match: 90.5% Indels: 2                                                    |      |                                                               |        |   |             |                    |
| DB: 6 Gaps: 1                                                                   |      |                                                               |        |   |             |                    |
| US-10-628-525A-36 (1-74) x AR427888 (1-1818)                                    |      |                                                               |        |   |             |                    |
| QY                                                                              | 1    | MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAasp | 20     |   |             |                    |
| Db                                                                              | 1    | ATGGCGGCTCTGGCCACGCTCGACGCTCGACGCGCGCGCGCTGGCGGCTCCGGAC       | 60     |   |             |                    |
| QY                                                                              | 21   | AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla  | 40     |   |             |                    |
| Db                                                                              | 61   | CGGTCCACGTTCCGCGCGCGCGCGCGCTGAGCGCGCGCGCGCGCGCGCGCGG          | 120    |   |             |                    |
| QY                                                                              | 41   | AlaSerThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla     | 60     |   |             |                    |
| Db                                                                              | 121  | CGGACACGCTCAGATCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG          | 180    |   |             |                    |
| QY                                                                              | 61   | ArgArgGlyGlyArgPheProPheProSerLeuValValCys                    | 74     |   |             |                    |
| Db                                                                              | 181  | CGCGCGCGGGGCGAGG-----TTCCCGTCTGCTGCTGTGTC                     | 216    |   |             |                    |
| RESULT 2                                                                        |      |                                                               |        |   |             |                    |
| AF544096 4274 bp DNA linear PLN 27-APR-2004                                     |      |                                                               |        |   |             |                    |
| LOCUS Zea mays subsp. mays cultivar Pa91 granule-bound starch synthase          |      |                                                               |        |   |             |                    |
| DEFINITION (waxy1) gene, partial sequence.                                      |      |                                                               |        |   |             |                    |
| ACCESSION AF544096                                                              |      |                                                               |        |   |             |                    |
| VERSION AF544096.1 GI:23395317                                                  |      |                                                               |        |   |             |                    |
| KEYWORDS Zea mays                                                               |      |                                                               |        |   |             |                    |
| SOURCE Zea mays                                                                 |      |                                                               |        |   |             |                    |
| ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;     |      |                                                               |        |   |             |                    |
| Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD               |      |                                                               |        |   |             |                    |
| clade; Panicoideae; Andropogoneae; Zea.                                         |      |                                                               |        |   |             |                    |
| REFERENCE 1 (bases 1 to 4274)                                                   |      |                                                               |        |   |             |                    |
| AUTHORS Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S. IV. |      |                                                               |        |   |             |                    |
| TITLE Genetic diversity and selection in the maize starch pathway               |      |                                                               |        |   |             |                    |
| JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2002) In press                           |      |                                                               |        |   |             |                    |
| PUBMED 12244216                                                                 |      |                                                               |        |   |             |                    |
| REFERENCE 2 (bases 1 to 4274)                                                   |      |                                                               |        |   |             |                    |
| AUTHORS Whitt,S.R. and Buckler,E.S. IV.                                         |      |                                                               |        |   |             |                    |

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TITLE      Direct Submission
JOURNAL    Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State
           Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
FEATURES   source
           1. .4274
           /organism="Zea mays"
           /mol_type="genomic DNA"
           /cultivar="PA91"
           /db_xref="taxon:4577"
           <1..>4274
gene       /gene="waxy1"
           /note="granule-bound starch synthase; wx1"

ORIGIN
Alignment Scores:
Pred. No.:      1.47e-13      Length:      4274
Score:          333.00      Matches:      71
Percent Similarity: 95.9%      Conservative: 0
Best Local Similarity: 95.9%      Mismatches:  1
Query Match:    90.5%      Indels:      2
DB:             15      Gaps:         1

US-10-628-525A-36 (1-74) x AF544092 (1-4287)

Qy      1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db      826 ATGGCGGCTCTGGCCACGTCGCAGCTCGTGCACACGCGCGCGCGCGCGCGCGCGCG 885
Qy      21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db      886 GCCTCCACGTTCCCG 945
Qy      41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60
Db      946 GCGGACACGCTCAGCATGCGGACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1005
Qy      61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db      1006 CG 1041

RESULT 4
AF544094
LOCUS     AF544094
DEFINITION Zea mays subsp. mays cultivar Oh43 granule-bound starch synthase (waxy1) gene, partial sequence.
ACCESSION AF544094
VERSION   AF544094.1 GI:23395315
KEYWORDS
SOURCE    Zea mays
           Zea mays
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 4449)
AUTHORS   Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.
           IV.
TITLE      Genetic diversity and selection in the maize starch pathway
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. (2002) In press
PUBMED    12244216
REFERENCE 2 (bases 1 to 4449)
AUTHORS   Whitt,S.R. and Buckler,E.S. IV.
TITLE      Direct Submission
JOURNAL   Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State
           Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
FEATURES   source
           1. .4449
           /organism="Zea mays"
           /mol_type="genomic DNA"
           /cultivar="OH43"
           /db_xref="taxon:4577"
           <1..>4449
gene       /gene="waxy1"
           /note="granule-bound starch synthase; wx1"

ORIGIN
Alignment Scores:
Pred. No.:      1.52e-13      Length:      4449
Score:          333.00      Matches:      71
Percent Similarity: 95.9%      Conservative: 0
Best Local Similarity: 95.9%      Mismatches:  1
Query Match:    90.5%      Indels:      2
DB:             15      Gaps:         1

US-10-628-525A-36 (1-74) x AF544094 (1-4449)

```

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProAap 20  
 Db 987 ATGGCGGCTCTGGCCACGTCGACAGCTCGTCGCAACCGCGCGCGCTGGCGCTCCCGGAC 1046

QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 Db 1047 GCGTCCACGTTCCGCGCGCGCGCGCGAGGCGCTCAGGGGGCGCGCGCGTCCGGCG 1106

QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 1107 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1166

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 1167 CGCCCGCGGGGGCAGG-----TTCCCGTCGCTCGTCGTGTGC 1202

RESULT 5  
 AF544071  
 LOCUS  
 DEFINITION Zea mays subsp. mays cultivar B14A granule-bound starch synthase  
 ACCESSION AF544071  
 VERSION AF544071.1 GI:23395292  
 KEYWORDS  
 SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE 1 (bases 1 to 4467)  
 AUTHORS Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.  
 IV.  
 TITLE Genetic diversity and selection in the maize starch pathway  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2002) In press  
 PUBMED 12244216  
 REFERENCE 2 (bases 1 to 4467)  
 AUTHORS Whitt,S.R. and Buckler,E.S. IV.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA

FEATURES  
 source  
 1..4467  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /cultivar="B14A"  
 /db\_xref="taxon:4577"  
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 /gene="waxy1"  
 /note="granule-bound starch synthase; wx1"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.52e-13 Length: 4467  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 15 Gaps: 1

US-10-628-525A-36 (1-74) x AF544071 (1-4467)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProAap 20  
 Db 1004 ATGGCGGCTCTGGCCACGTCGACAGCTCGTCGCAACCGCGCGCGCTGGCGCTCCCGGAC 1063

QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 Db 1064 GCGTCCACGTTCCGCGCGCGCGCGAGGCGCTCAGGGGGCGCGCGCGTCCGGCG 1123

QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 1124 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1183

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 1184 CGCCCGCGGGGGCAGG-----TTCCCGTCGCTCGTCGTGTGC 1219

RESULT 6  
 AF544088  
 LOCUS  
 DEFINITION Zea mays subsp. mays cultivar Ky21 granule-bound starch synthase  
 ACCESSION AF544088  
 VERSION AF544088.1 GI:23395309  
 KEYWORDS  
 SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE 1 (bases 1 to 4470)  
 AUTHORS Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.  
 IV.  
 TITLE Genetic diversity and selection in the maize starch pathway  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2002) In press  
 PUBMED 12244216  
 REFERENCE 2 (bases 1 to 4470)  
 AUTHORS Whitt,S.R. and Buckler,E.S. IV.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA

FEATURES  
 source  
 1..4470  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /cultivar="Ky21"  
 /db\_xref="taxon:4577"  
 <1..>4470  
 /gene="waxy1"  
 /note="granule-bound starch synthase; wx1"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.52e-13 Length: 4470  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 15 Gaps: 1

US-10-628-525A-36 (1-74) x AF544088 (1-4470)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProAap 20  
 Db 1003 ATGGCGGCTCTGGCCACGTCGACAGCTCGTCGCAACCGCGCGCGCTGGCGCTCCCGGAC 1062

QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 Db 1063 GCGTCCACGTTCCGCGCGCGCGCGAGGCGCTCAGGGGGCGCGCGCGTCCGGCG 1122

QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 1123 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1182

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 1183 CGCCCGCGGGGGCAGG-----TTCCCGTCGCTCGTCGTGTGC 1218

RESULT 7  
 AF544091  
 LOCUS  
 DEFINITION Zea mays subsp. mays cultivar N28ht granule-bound starch synthase  
 ACCESSION AF544091  
 VERSION AF544091.1 GI:23395312  
 KEYWORDS







polyA\_site 4625

ORIGIN

Alignment Scores:  
 Pred. No.: 1.62e-13 Length: 4800  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 15 Gaps: 1

US-10-628-525A-36 (1-74) x ZMWAXY (1-4800)

Qy 1 MetAlaLaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
 |||||  
 Db 1233 ATGCGCGCTCTGGCCACGTCGTCAGCTGTCGCAACGGCGCGCGGCTGGGGCTCCCGGAC 1292

Qy 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 |||||  
 Db 1293 GCGTCCACGTTCCCGCGCGCGCGCGCGAGGCTGAGGGGGCGCGCGGCTCGCGCGCG 1352

Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 |||||  
 Db 1353 GCGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGG 1412

Qy 61 ArgArgGlyArgPheProPheProSerLeuValValCys 74  
 |||||  
 Db 1413 CGCGCGCGGCGGCGG-----TTCCCGTCGCTCGTCGTGTGC 1448

RESULT 11

LOCUS AF544079 4090 bp DNA linear PLN 27-APR-2004

DEFINITION Zea mays subsp. mays cultivar D940Y granule-bound starch synthase (waxy1) gene, partial sequence.

ACCESSION AF544079

VERSION AF544079.1 GI:23395300

KEYWORDS

SOURCE Zea mays

ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 4090)  
 Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.  
 IV.

REFERENCE  
 TITLE Genetic diversity and selection in the maize starch pathway  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2002) In press  
 PUBMED 1224216  
 2 (bases 1 to 4090)  
 Whitt,S.R. and Buckler,E.S. IV.  
 DIRECT SUBMISSION  
 TITLE Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State  
 JOURNAL Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA

FEATURES  
 source Location/Qualifiers  
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 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:4577"  
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 /note="granule-bound starch synthase; waxy1"

gene

ORIGIN

Alignment Scores:  
 Pred. No.: 3.59e-13 Length: 4090  
 Score: 327.00 Matches: 70  
 Percent Similarity: 94.6% Conservative: 0  
 Best Local Similarity: 94.6% Mismatches: 2  
 Query Match: 88.9% Indels: 2  
 DB: 15 Gaps: 1

US-10-628-525A-36 (1-74) x AF544079 (1-4090)

[illegible]

```

REFERENCE 2 (bases 1 to 4395)
AUTHORS Whitt,S.R. and Buckler,E.S. IV.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA

FEATURES
source
    1..4395
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        /mol_type="genomic DNA"
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        /db_xref="taxon:4577"
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    /gene="waxy1"
    /note="granule-bound starch synthase; wx1"

ORIGIN
Alignment Scores:
Pred. No.: 8.25e-13 Length: 4395
Score: 322.00 Matches: 69
Percent Similarity: 93.2% Conservative: 0
Best Local Similarity: 93.2% Mismatches: 3
Query Match: 87.5% Indels: 2
DB: 15 Gaps: 1

US-10-628-525A-36 (1-74) x AF544089 (1-4395)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 972 ATGGCGGCTCTGGCCAGTTCGAGCTGCTGCACCGCCCGCGCTGGCGCTCCCGGAC 1031
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 1032 GCGTCCACGTTCCGCGCGCGCGCCGAGCGCTGAGGGGGCGCGCGCGCGCGCG 1091
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 1092 GCGGACACGCTCAGCTAGTCGACGACGCGCGCGCGCGCGCGCGCGCGCGCG 1151
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 1152 CGCGCGGGGGCAGG-----TTCCGCTCGCTCGTGTGTGC 1187

RESULT 16
AF544077
LOCUS
DEFINITION Zea mays subsp. mays cultivar CML258 granule-bound starch synthase
(waxy1) gene, partial sequence.
ACCESSION AF544077
VERSION AF544077.1 GI:23395298
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 3533)
AUTHORS Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.
IV.
TITLE Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. (2002) In press
PUBMED 12244216
REFERENCE 2 (bases 1 to 4210)
AUTHORS Whitt,S.R. and Buckler,E.S. IV.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
FEATURES
source
    1..4210
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        /mol_type="genomic DNA"
        /cultivar="CML333"
        /db_xref="taxon:4577"
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    /gene="waxy1"
    /note="granule-bound starch synthase; wx1"

ORIGIN
Alignment Scores:
Pred. No.: 1.87e-12 Length: 4210
Score: 316.50 Matches: 70
Percent Similarity: 93.3% Conservative: 0
Best Local Similarity: 93.3% Mismatches: 2
Query Match: 86.0% Indels: 3
DB: 15 Gaps: 2

US-10-628-525A-36 (1-74) x AF544077 (1-3533)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 439 ATGGCGGCTCTGGCCAGTTCGAGCTGCTGCACCGCCCGCGCTGGCGCTCCCGGAC 498
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 499 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 558
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln---GlnGln 59
Db 559 GCGGACACGCTCAGCTAGTCGACGACGCGCGCGCGCGCGCGCGCGCGCGCG 618
QY 60 AlaArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 619 GCGCGCGGGGGCAGG-----TTCCGCTCGCTCGTGTGTGC 657

RESULT 17
AF544078
LOCUS
DEFINITION Zea mays subsp. mays cultivar CML333 granule-bound starch synthase
(waxy1) gene, partial sequence.
ACCESSION AF544078
VERSION AF544078.1 GI:23395299
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 4210)
AUTHORS Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.
IV.
TITLE Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. (2002) In press
PUBMED 12244216
REFERENCE 2 (bases 1 to 4210)
AUTHORS Whitt,S.R. and Buckler,E.S. IV.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
FEATURES
source
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        /cultivar="CML333"
        /db_xref="taxon:4577"
        <1..>4210
    /gene="waxy1"
    /note="granule-bound starch synthase; wx1"

ORIGIN
Alignment Scores:
Pred. No.: 1.87e-12 Length: 4210
Score: 316.50 Matches: 70
Percent Similarity: 93.3% Conservative: 0
Best Local Similarity: 93.3% Mismatches: 2
Query Match: 86.0% Indels: 3
DB: 15 Gaps: 2

```

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US-10-628-525A-36 (1-74) x AF544078 (1-4210)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProasp 20
DB 751 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTCGCAACGCGCGCGCTGGCGCTGCCGGAC 810
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
DB 811 GCGTCCACGTCG 870
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGln---GlnGln 59
DB 871 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 930
QY 60 AlaArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB 931 GCG 969

RESULT 18
AF544075
LOCUS AF544075
DEFINITION Zea mays subsp. mays cultivar CI187 granule-bound starch synthase
ACCESSION AF544075
VERSION AF544075.1 GI:23395296
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 4430)
AUTHORS Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.
IV.
Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. (2002) In press
PUBMED 12244216
AUTHORS Whitt,S.R. and Buckler,E.S. IV.
DIRECT SUBMISSION
TITLE Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State
JOURNAL Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
FEATURES
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/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="CI187"
/db_xref="taxon:4577"
<1..>4430
/gene="waxy1"
/note="granule-bound starch synthase; wx1"

ORIGIN
Alignment Scores:
Pred. No.: 1,95e-12 Length: 4430
Score: 316.50 Matches: 70
Percent Similarity: 93.3% Conservative: 0
Best Local Similarity: 93.3% Mismatches: 2
Query Match: 86.0% Indels: 3
DB: 15 Gaps: 2
US-10-628-525A-36 (1-74) x AF544075 (1-4430)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProasp 20
DB 1003 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTCGCAACGCGCGCGCTGGCGCTGCCGGAC 1062
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
DB 1063 GCGTCCACGTCG 1122
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGln---GlnGln 59
DB 1122 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1221

RESULT 19
AF544085
LOCUS AF544085
DEFINITION Zea mays subsp. mays cultivar IL101 granule-bound starch synthase
(waxy1) gene, partial sequence.
ACCESSION AF544085
VERSION AF544085.1 GI:23395306
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 4436)
AUTHORS Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.
IV.
Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. (2002) In press
PUBMED 12244216
AUTHORS Whitt,S.R. and Buckler,E.S. IV.
DIRECT SUBMISSION
TITLE Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State
JOURNAL Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
FEATURES
source
1..4436
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="IL101"
/db_xref="taxon:4577"
<1..>4436
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/note="granule-bound starch synthase; wx1"

ORIGIN
Alignment Scores:
Pred. No.: 1,95e-12 Length: 4436
Score: 316.50 Matches: 70
Percent Similarity: 93.3% Conservative: 0
Best Local Similarity: 93.3% Mismatches: 2
Query Match: 86.0% Indels: 3
DB: 15 Gaps: 2
US-10-628-525A-36 (1-74) x AF544085 (1-4436)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProasp 20
DB 1009 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTCGCAACGCGCGCGCTGGCGCTGCCGGAC 1068
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
DB 1069 GCGTCCACGTCG 1128
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGln---GlnGln 59
DB 1129 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1227

RESULT 20
AF544087
LOCUS AF544087
DEFINITION Zea mays subsp. mays cultivar Ki21 granule-bound starch synthase
(waxy1) gene, partial sequence.
ACCESSION AF544087

```





|                                                                                                                                                                              |      |                                                           |        |    |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------------------------------------------------------|--------|----|
| US-10-628-525A-36 (1-74) x AF544069 (1-4463)                                                                                                                                 |      |                                                           |        |    |
| QY                                                                                                                                                                           | 1    | MetaAlaLeuAlaThrsGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp  | 20     |    |
| Db                                                                                                                                                                           | 1003 | ATGGCGGCTCTGGCCACGTCGCAGCTCGTCGCACGCGCGCGCTGGCGCTCCCGGAC  | 1062   |    |
| QY                                                                                                                                                                           | 21   | AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla | 40     |    |
| Db                                                                                                                                                                           | 1063 | GGGTCCACGTTCCGCGCGCGCGCGCGCTGAGGGGGCCCGGGCGTCCGGCGG       | 1122   |    |
| QY                                                                                                                                                                           | 41   | AlaAspThrLeuSerMetArgThrSerAlaAlaProArgHisGln---          | GlnGln | 59 |
| Db                                                                                                                                                                           | 1123 | GCGGACACGTCAGCATCGGACCGCGCGCGCGCCAGCCAGCACCAGCAGCAG       | 1182   |    |
| QY                                                                                                                                                                           | 60   | AlaArgArgGlyGlyArgPheProPheProSerLeuValValCys             | 74     |    |
| Db                                                                                                                                                                           | 1183 | GCGCGCGCGGGGCCAGG-----TTCCGCTCGCTCGTGTGTGC                | 1221   |    |
| RESULT 24                                                                                                                                                                    |      |                                                           |        |    |
| AF544097                                                                                                                                                                     |      |                                                           |        |    |
| LOCUS                                                                                                                                                                        |      |                                                           |        |    |
| DEFINITION                                                                                                                                                                   |      |                                                           |        |    |
| Zea mays subsp. mays cultivar T232 granule-bound starch synthase (waxy1) gene, partial sequence.                                                                             |      |                                                           |        |    |
| ACCESSION                                                                                                                                                                    |      |                                                           |        |    |
| AF544097                                                                                                                                                                     |      |                                                           |        |    |
| VERSION                                                                                                                                                                      |      |                                                           |        |    |
| AF544097.1 GI:23395318                                                                                                                                                       |      |                                                           |        |    |
| KEYWORDS                                                                                                                                                                     |      |                                                           |        |    |
| Zea mays                                                                                                                                                                     |      |                                                           |        |    |
| SOURCE                                                                                                                                                                       |      |                                                           |        |    |
| Zea mays                                                                                                                                                                     |      |                                                           |        |    |
| ORGANISM                                                                                                                                                                     |      |                                                           |        |    |
| Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. |      |                                                           |        |    |
| REFERENCE                                                                                                                                                                    |      |                                                           |        |    |
| 1 (bases 1 to 4463)                                                                                                                                                          |      |                                                           |        |    |
| AUTHORS                                                                                                                                                                      |      |                                                           |        |    |
| Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S. IV.                                                                                                       |      |                                                           |        |    |
| TITLE                                                                                                                                                                        |      |                                                           |        |    |
| Genetic diversity and selection in the maize starch pathway                                                                                                                  |      |                                                           |        |    |
| JOURNAL                                                                                                                                                                      |      |                                                           |        |    |
| Proc. Natl. Acad. Sci. U.S.A. (2002) In press                                                                                                                                |      |                                                           |        |    |
| PUBMED                                                                                                                                                                       |      |                                                           |        |    |
| 12244216                                                                                                                                                                     |      |                                                           |        |    |
| REFERENCE                                                                                                                                                                    |      |                                                           |        |    |
| 2 (bases 1 to 4463)                                                                                                                                                          |      |                                                           |        |    |
| AUTHORS                                                                                                                                                                      |      |                                                           |        |    |
| Whitt,S.R. and Buckler,E.S. IV.                                                                                                                                              |      |                                                           |        |    |
| TITLE                                                                                                                                                                        |      |                                                           |        |    |
| Direct Submission                                                                                                                                                            |      |                                                           |        |    |
| JOURNAL                                                                                                                                                                      |      |                                                           |        |    |
| Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA                                                       |      |                                                           |        |    |
| FEATURES                                                                                                                                                                     |      |                                                           |        |    |
| Location/Qualifiers                                                                                                                                                          |      |                                                           |        |    |
| source                                                                                                                                                                       |      |                                                           |        |    |
| 1..4463                                                                                                                                                                      |      |                                                           |        |    |
| /organism="Zea mays"                                                                                                                                                         |      |                                                           |        |    |
| /mol_type="genomic DNA"                                                                                                                                                      |      |                                                           |        |    |
| /cultivar="T232"                                                                                                                                                             |      |                                                           |        |    |
| /db_xref="taxon:4577"                                                                                                                                                        |      |                                                           |        |    |
| <1..>4463                                                                                                                                                                    |      |                                                           |        |    |
| /gene="waxy1"                                                                                                                                                                |      |                                                           |        |    |
| /note="granule-bound starch synthase; wxl"                                                                                                                                   |      |                                                           |        |    |
| ORIGIN                                                                                                                                                                       |      |                                                           |        |    |
| Alignment Scores:                                                                                                                                                            |      |                                                           |        |    |
| Pred. No.: 1.96e-12 Length: 4463                                                                                                                                             |      |                                                           |        |    |
| Score: 316.50 Matches: 70                                                                                                                                                    |      |                                                           |        |    |
| Percent Similarity: 93.3% Conservative: 0                                                                                                                                    |      |                                                           |        |    |
| Best Local Similarity: 93.3% Mismatches: 2                                                                                                                                   |      |                                                           |        |    |
| Query Match: 86.0% Indels: 3                                                                                                                                                 |      |                                                           |        |    |
| DB: 15 Gaps: 2                                                                                                                                                               |      |                                                           |        |    |
| US-10-628-525A-36 (1-74) x AF544097 (1-4463)                                                                                                                                 |      |                                                           |        |    |
| QY                                                                                                                                                                           | 1    | MetaAlaLeuAlaThrsGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp  | 20     |    |
| Db                                                                                                                                                                           | 1002 | ATGGCGGCTCTGGCCACGTCGCAGCTCGTCGCACGCGCGCGCTGGCGCTCCCGGAC  | 1061   |    |
| QY                                                                                                                                                                           | 21   | AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla | 40     |    |
| Db                                                                                                                                                                           | 1062 | GGGTCCACGTTCCGCGCGCGCGCGCGCTGAGGGGGCCCGGGCGTCCGGCGG       | 1121   |    |
| QY                                                                                                                                                                           | 41   | AlaAspThrLeuSerMetArgThrSerAlaAlaProArgHisGln---          | GlnGln | 59 |

|                                                                                                                                                                              |      |                                                            |        |    |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|------------------------------------------------------------|--------|----|
| <1..>4438                                                                                                                                                                    |      |                                                            |        |    |
| /gene="waxy1"                                                                                                                                                                |      |                                                            |        |    |
| /note="granule-bound starch synthase; wxl"                                                                                                                                   |      |                                                            |        |    |
| ORIGIN                                                                                                                                                                       |      |                                                            |        |    |
| Alignment Scores:                                                                                                                                                            |      |                                                            |        |    |
| Pred. No.: 1.95e-12 Length: 4438                                                                                                                                             |      |                                                            |        |    |
| Score: 316.50 Matches: 70                                                                                                                                                    |      |                                                            |        |    |
| Percent Similarity: 93.3% Conservative: 0                                                                                                                                    |      |                                                            |        |    |
| Best Local Similarity: 93.3% Mismatches: 2                                                                                                                                   |      |                                                            |        |    |
| Query Match: 86.0% Indels: 3                                                                                                                                                 |      |                                                            |        |    |
| DB: 15 Gaps: 2                                                                                                                                                               |      |                                                            |        |    |
| US-10-628-525A-36 (1-74) x AF544095 (1-4438)                                                                                                                                 |      |                                                            |        |    |
| QY                                                                                                                                                                           | 1    | MetaAlaLeuAlaThrsGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp   | 20     |    |
| Db                                                                                                                                                                           | 1009 | ATGGCGGCTCTGGCCACGTCGCAGCTCGTCGCACACGCGCGCGCTGGCGCTCCCGGAC | 1068   |    |
| QY                                                                                                                                                                           | 21   | AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla  | 40     |    |
| Db                                                                                                                                                                           | 1069 | GGGTCCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGCCCGGGCGTCCGGCGG      | 1128   |    |
| QY                                                                                                                                                                           | 41   | AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln---     | GlnGln | 59 |
| Db                                                                                                                                                                           | 1129 | GCGGACACGCTCAGCATCGGACCGCGCGCGCGCGCCAGCCAGCACCAGCAGCAG     | 1188   |    |
| QY                                                                                                                                                                           | 60   | AlaArgArgGlyGlyArgPheProPheProSerLeuValValCys              | 74     |    |
| Db                                                                                                                                                                           | 1189 | GCGCGCGCGGGGCCAGG-----TTCCGCTCGCTCGTGTGTGC                 | 1227   |    |
| RESULT 23                                                                                                                                                                    |      |                                                            |        |    |
| AF544069                                                                                                                                                                     |      |                                                            |        |    |
| LOCUS                                                                                                                                                                        |      |                                                            |        |    |
| DEFINITION                                                                                                                                                                   |      |                                                            |        |    |
| Zea mays subsp. mays cultivar A6 granule-bound starch synthase (waxy1) gene, partial sequence.                                                                               |      |                                                            |        |    |
| ACCESSION                                                                                                                                                                    |      |                                                            |        |    |
| AF544069                                                                                                                                                                     |      |                                                            |        |    |
| VERSION                                                                                                                                                                      |      |                                                            |        |    |
| AF544069.1 GI:23395290                                                                                                                                                       |      |                                                            |        |    |
| KEYWORDS                                                                                                                                                                     |      |                                                            |        |    |
| Zea mays                                                                                                                                                                     |      |                                                            |        |    |
| SOURCE                                                                                                                                                                       |      |                                                            |        |    |
| Zea mays                                                                                                                                                                     |      |                                                            |        |    |
| ORGANISM                                                                                                                                                                     |      |                                                            |        |    |
| Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. |      |                                                            |        |    |
| REFERENCE                                                                                                                                                                    |      |                                                            |        |    |
| 1 (bases 1 to 4463)                                                                                                                                                          |      |                                                            |        |    |
| AUTHORS                                                                                                                                                                      |      |                                                            |        |    |
| Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S. IV.                                                                                                       |      |                                                            |        |    |
| TITLE                                                                                                                                                                        |      |                                                            |        |    |
| Genetic diversity and selection in the maize starch pathway                                                                                                                  |      |                                                            |        |    |
| JOURNAL                                                                                                                                                                      |      |                                                            |        |    |
| Proc. Natl. Acad. Sci. U.S.A. (2002) In press                                                                                                                                |      |                                                            |        |    |
| PUBMED                                                                                                                                                                       |      |                                                            |        |    |
| 12244216                                                                                                                                                                     |      |                                                            |        |    |
| REFERENCE                                                                                                                                                                    |      |                                                            |        |    |
| 2 (bases 1 to 4463)                                                                                                                                                          |      |                                                            |        |    |
| AUTHORS                                                                                                                                                                      |      |                                                            |        |    |
| Whitt,S.R. and Buckler,E.S. IV.                                                                                                                                              |      |                                                            |        |    |
| TITLE                                                                                                                                                                        |      |                                                            |        |    |
| Direct Submission                                                                                                                                                            |      |                                                            |        |    |
| JOURNAL                                                                                                                                                                      |      |                                                            |        |    |
| Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA                                                       |      |                                                            |        |    |
| FEATURES                                                                                                                                                                     |      |                                                            |        |    |
| Location/Qualifiers                                                                                                                                                          |      |                                                            |        |    |
| source                                                                                                                                                                       |      |                                                            |        |    |
| 1..4463                                                                                                                                                                      |      |                                                            |        |    |
| /organism="Zea mays"                                                                                                                                                         |      |                                                            |        |    |
| /mol_type="genomic DNA"                                                                                                                                                      |      |                                                            |        |    |
| /cultivar="A6"                                                                                                                                                               |      |                                                            |        |    |
| /db_xref="taxon:4577"                                                                                                                                                        |      |                                                            |        |    |
| <1..>4463                                                                                                                                                                    |      |                                                            |        |    |
| /genes="waxy1"                                                                                                                                                               |      |                                                            |        |    |
| /note="granule-bound starch synthase; wxl"                                                                                                                                   |      |                                                            |        |    |
| ORIGIN                                                                                                                                                                       |      |                                                            |        |    |
| Alignment Scores:                                                                                                                                                            |      |                                                            |        |    |
| Pred. No.: 1.96e-12 Length: 4463                                                                                                                                             |      |                                                            |        |    |
| Score: 316.50 Matches: 70                                                                                                                                                    |      |                                                            |        |    |
| Percent Similarity: 93.3% Conservative: 0                                                                                                                                    |      |                                                            |        |    |
| Best Local Similarity: 93.3% Mismatches: 2                                                                                                                                   |      |                                                            |        |    |
| Query Match: 86.0% Indels: 3                                                                                                                                                 |      |                                                            |        |    |
| DB: 15 Gaps: 2                                                                                                                                                               |      |                                                            |        |    |



|                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                                                                                              |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| JOURNAL                                                                                                                                                                                                                                                                                                                                                                                                                               | Proc. Natl. Acad. Sci. U.S.A. (2002) In press                                                                                                                                |
| PUBMED                                                                                                                                                                                                                                                                                                                                                                                                                                | 12244216                                                                                                                                                                     |
| REFERENCE                                                                                                                                                                                                                                                                                                                                                                                                                             | 2 (bases 1 to 4420)                                                                                                                                                          |
| AUTHORS                                                                                                                                                                                                                                                                                                                                                                                                                               | Whitt,S.R. and Buckler,E.S. IV.                                                                                                                                              |
| TITLE                                                                                                                                                                                                                                                                                                                                                                                                                                 | Direct Submission                                                                                                                                                            |
| JOURNAL                                                                                                                                                                                                                                                                                                                                                                                                                               | Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA                                                       |
| FEATURES                                                                                                                                                                                                                                                                                                                                                                                                                              | Location/Qualifiers                                                                                                                                                          |
| source                                                                                                                                                                                                                                                                                                                                                                                                                                | 1..4420                                                                                                                                                                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                       | /organism="Zea mays"                                                                                                                                                         |
|                                                                                                                                                                                                                                                                                                                                                                                                                                       | /mol_type="genomic DNA"                                                                                                                                                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                       | /cultivar="B37"                                                                                                                                                              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                       | /db_xref="taxon:"B37"                                                                                                                                                        |
| gene                                                                                                                                                                                                                                                                                                                                                                                                                                  | <1..>4420                                                                                                                                                                    |
|                                                                                                                                                                                                                                                                                                                                                                                                                                       | /gene="waxy1"                                                                                                                                                                |
|                                                                                                                                                                                                                                                                                                                                                                                                                                       | /note="granule-bound starch synthase; wx1"                                                                                                                                   |
| ORIGIN                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                              |
| Alignment Scores:                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                                                                                                                              |
| Pred. No.:                                                                                                                                                                                                                                                                                                                                                                                                                            | 3,41e-11                                                                                                                                                                     |
| Score:                                                                                                                                                                                                                                                                                                                                                                                                                                | 298.00                                                                                                                                                                       |
| Length:                                                                                                                                                                                                                                                                                                                                                                                                                               | 4420                                                                                                                                                                         |
| Matches:                                                                                                                                                                                                                                                                                                                                                                                                                              | 68                                                                                                                                                                           |
| Conservative:                                                                                                                                                                                                                                                                                                                                                                                                                         | 0                                                                                                                                                                            |
| Percent Similarity:                                                                                                                                                                                                                                                                                                                                                                                                                   | 91.9%                                                                                                                                                                        |
| Best Local Similarity:                                                                                                                                                                                                                                                                                                                                                                                                                | 91.9%                                                                                                                                                                        |
| Mismatches:                                                                                                                                                                                                                                                                                                                                                                                                                           | 4                                                                                                                                                                            |
| Query Match:                                                                                                                                                                                                                                                                                                                                                                                                                          | 81.0%                                                                                                                                                                        |
| Indels:                                                                                                                                                                                                                                                                                                                                                                                                                               | 3                                                                                                                                                                            |
| DB:                                                                                                                                                                                                                                                                                                                                                                                                                                   | 15                                                                                                                                                                           |
| Gaps:                                                                                                                                                                                                                                                                                                                                                                                                                                 | 1                                                                                                                                                                            |
| US-10-628-525A-36 (1-74) x AF544072 (1-4420)                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                                                                                                              |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                    | 1 MetAlaLaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAep 20                                                                                                             |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                    | 956 ATGCGGCTCTGGCCACGTGCGTGGC-ACGCGCGCGCGCTGGCGCTCCCGGAC 1014                                                                                                                |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                    | 21 AlaSerThrPhaArgArgGlyAlaLaGlnGlyLeuArgGlyAlaArgAlaSerAlaLa 40                                                                                                             |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                    | 1015 GCGTCACGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1074                                                                                                              |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                    | 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60                                                                                                              |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                    | 1075 GCGGACACGCTAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1134                                                                                                             |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                    | 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74                                                                                                                             |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                    | 1135 CGCCGCGGGCGGAGG-----TTCCGTCGCTCGTCGTGTCG 1170                                                                                                                           |
| RESULT 28                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                                                                                                                              |
| AF488416                                                                                                                                                                                                                                                                                                                                                                                                                              | AF488416 143300 bp DNA linear PLN 19-DEC-2004                                                                                                                                |
| LOCUS                                                                                                                                                                                                                                                                                                                                                                                                                                 | Zea mays chromosome 9 BAC 9C20 complete sequence.                                                                                                                            |
| DEFINITION                                                                                                                                                                                                                                                                                                                                                                                                                            | AF488416                                                                                                                                                                     |
| ACCESSION                                                                                                                                                                                                                                                                                                                                                                                                                             | AF488416.1 GI:33321038                                                                                                                                                       |
| VERSION                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                                                                                                                              |
| KEYWORDS                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                                                                                                                              |
| SOURCE                                                                                                                                                                                                                                                                                                                                                                                                                                | Zea mays                                                                                                                                                                     |
| ORGANISM                                                                                                                                                                                                                                                                                                                                                                                                                              | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. |
| REFERENCE                                                                                                                                                                                                                                                                                                                                                                                                                             | 1 (bases 1 to 143300)                                                                                                                                                        |
| AUTHORS                                                                                                                                                                                                                                                                                                                                                                                                                               | Ma,J., SanMiguel,P.J., Dubcovsky,J., Shiloff,B.A., Rostoks,N., Jiang,Z., Busso,C.S., Kleinhofs,A., Devos,K.M., Ramakrishna,W. and Bennetzen,J.L.                             |
| TITLE                                                                                                                                                                                                                                                                                                                                                                                                                                 | Comparative sequence analysis of homologous wx1 regions in barley, maize, pearl millet, rice, sorghum and diploid wheat                                                      |
| JOURNAL                                                                                                                                                                                                                                                                                                                                                                                                                               | Unpublished                                                                                                                                                                  |
| REFERENCE                                                                                                                                                                                                                                                                                                                                                                                                                             | 2 (bases 1 to 143300)                                                                                                                                                        |
| AUTHORS                                                                                                                                                                                                                                                                                                                                                                                                                               | Ma,J., SanMiguel,P.J., Dubcovsky,J., Shiloff,B.A., Rostoks,N., Jiang,Z., Busso,C.S., Kleinhofs,A., Devos,K.M., Ramakrishna,W. and Bennetzen,J.L.                             |
| TITLE                                                                                                                                                                                                                                                                                                                                                                                                                                 | Direct Submission                                                                                                                                                            |
| JOURNAL                                                                                                                                                                                                                                                                                                                                                                                                                               | Submitted (27-FEB-2002) Department of Biological Sciences, Purdue University, West Lafayette, IN 47907, USA                                                                  |
| FEATURES                                                                                                                                                                                                                                                                                                                                                                                                                              | Location/Qualifiers                                                                                                                                                          |
| source                                                                                                                                                                                                                                                                                                                                                                                                                                | 1..143300                                                                                                                                                                    |
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| /clone="BAC 9C20"                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                                                                                                                              |
| 409. .540                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                                                                                                                              |
| /transposon="MITE"                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                                                                                                                              |
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| <14796. .>18743                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                                                                                              |
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| 15721. .15736                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                              |
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| 23620. .24987                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                              |
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Alignment Scores:  
Pred. No.: 1,29e-09 Length: 143300  
Score: 293.00 Matches: 65  
Percent Similarity: 85.9% Conservative: 2  
Best Local Similarity: 83.3% Mismatches: 5  
Query Match: 79.6% Indels: 6  
DB: 15 Gaps: 2

US-10-628-525A-36 (1-74) x AP488416 (1-143300)

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Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40  
Db 61468 GCGTCCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGCGCGGACGCGTCCGCG 61527

Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArg-----His 56  
Db 61528 GCGGACACGCTCAGCATGCGGACACGCGCGCGCGCGCGCGCGCGCGCGCGCG 61587

Qy 57 GlnGlnGlnAlaArgGlyGlyArgPhePhePropPheSerLeuValValCys 74  
Db 61588 CAGCAGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 61635

RESULT 29  
AR195560  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

AR195560 2267 bp DNA linear PAT 20-APR-2002  
Sequence 25 from patent US 6350934.  
AR195560  
AR195560.1 GI:20244997  
Unknown.  
Unknown.  
Unclassified.  
1 (bases 1 to 2267)  
Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P. Ann.Owens.,  
Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.  
Nucleic acid encoding delta-9 desaturase  
Patent: US 6350934-A 25 26-FEB-2002;  
Location/Qualifiers  
1. .2267  
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| Pred. No.:                                   | 7.93e-11 | Length:                                                      | 2267 |  |
| Score:                                       | 289.00   | Matches:                                                     | 64   |  |
| Percent Similarity:                          | 85.9%    | Conservative:                                                | 3    |  |
| Best Local Similarity:                       | 82.1%    | Mismatches:                                                  | 5    |  |
| Query Match:                                 | 78.5%    | Indels:                                                      | 6    |  |
| DB:                                          | 6        | Gaps:                                                        | 2    |  |
| US-10-628-525A-36 (1-74) x AR195560 (1-2267) |          |                                                              |      |  |
| QY                                           | 1        | MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp | 20   |  |
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| QY                                           | 21       | AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla | 40   |  |
| Db                                           | 237      | GGGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGACGGCGTCCGGCG   | 296  |  |
| QY                                           | 41       | AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArg-----His        | 56   |  |
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| QY                                           | 57       | GlnGlnAlaAlaArgArgGlyArgPheProPheProSerLeuValValCys          | 74   |  |
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Search completed: April 1, 2006, 15:15:52  
Job time : 1500.89 secs

|                                              |                                                                                                                                                                              |               |        |                 |
|----------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------|--------|-----------------|
| RESULT 30                                    |                                                                                                                                                                              |               |        |                 |
| AF544093                                     | 4449 bp                                                                                                                                                                      | DNA           | linear | PLN 27-APR-2004 |
| LOCUS                                        | Zea mays subsp. mays cultivar NC348 granule-bound starch synthase                                                                                                            |               |        |                 |
| DEFINITION                                   | (waxy1) gene, partial sequence.                                                                                                                                              |               |        |                 |
| ACCESSION                                    | AF544093                                                                                                                                                                     |               |        |                 |
| VERSION                                      | AF544093.1 GI:23395314                                                                                                                                                       |               |        |                 |
| KEYWORDS                                     | Zea mays                                                                                                                                                                     |               |        |                 |
| SOURCE                                       | Zea mays                                                                                                                                                                     |               |        |                 |
| ORGANISM                                     | Zea mays                                                                                                                                                                     |               |        |                 |
| REFERENCE                                    | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. |               |        |                 |
| AUTHORS                                      | Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S. IV.                                                                                                      |               |        |                 |
| TITLE                                        | Genetic diversity and selection in the maize starch pathway                                                                                                                  |               |        |                 |
| JOURNAL                                      | Proc. Natl. Acad. Sci. U.S.A. (2002) In press                                                                                                                                |               |        |                 |
| PUBMED                                       | 12244216                                                                                                                                                                     |               |        |                 |
| REFERENCE                                    | 2 (bases 1 to 4449)                                                                                                                                                          |               |        |                 |
| AUTHORS                                      | Whitt,S.R. and Buckler,E.S. IV.                                                                                                                                              |               |        |                 |
| TITLE                                        | Direct Submission                                                                                                                                                            |               |        |                 |
| JOURNAL                                      | Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA                                                       |               |        |                 |
| FEATURES                                     | Location/Qualifiers                                                                                                                                                          |               |        |                 |
| source                                       | 1..4449                                                                                                                                                                      |               |        |                 |
|                                              | /organism="Zea mays"                                                                                                                                                         |               |        |                 |
|                                              | /mol_type="genomic DNA"                                                                                                                                                      |               |        |                 |
|                                              | /cultivar="NC348"                                                                                                                                                            |               |        |                 |
|                                              | /db_xref="taxon:4577"                                                                                                                                                        |               |        |                 |
| gene                                         | <1..4449                                                                                                                                                                     |               |        |                 |
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|                                              | /note="granule-bound starch synthase; wx1"                                                                                                                                   |               |        |                 |
| ORIGIN                                       |                                                                                                                                                                              |               |        |                 |
| Alignment Scores:                            |                                                                                                                                                                              |               |        |                 |
| Pred. No.:                                   | 2.2e-10                                                                                                                                                                      | Length:       | 4449   |                 |
| Score:                                       | 286.00                                                                                                                                                                       | Matches:      | 60     |                 |
| Percent Similarity:                          | 95.2%                                                                                                                                                                        | Conservative: | 0      |                 |
| Best Local Similarity:                       | 95.2%                                                                                                                                                                        | Mismatches:   | 1      |                 |
| Query Match:                                 | 77.7%                                                                                                                                                                        | Indels:       | 2      |                 |
| DB:                                          | 15                                                                                                                                                                           | Gaps:         | 1      |                 |
| US-10-628-525A-36 (1-74) x AF544093 (1-4449) |                                                                                                                                                                              |               |        |                 |

|    |      |                                                                 |      |
|----|------|-----------------------------------------------------------------|------|
| QY | 12   | ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly    | 31   |
| Db | 1030 | ACGCGCGCGGCTGGGCGTCCCGACGCTCCACGTTCCCGCGCGCGCGCGCGGC            | 1089 |
| QY | 32   | LeuArgGlyAlaAlaArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSerAlaArg | 51   |
| Db | 1090 | CTGAGGGGGCGCGCGCGTCCGGCGGCGGACACGCTCAGCATGCGGACCGCGCGC          | 1149 |
| QY | 52   | AlaAlaProArgHisGlnGlnAlaArgArgGlyArgPheProPheProSerLeu          | 71   |
| Db | 1150 | GCGGGCGCCAGGCACCGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG              | 1203 |
| QY | 72   | ValValCys                                                       | 74   |
| Db | 1204 | GTCGTGTC                                                        | 1212 |

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 00:15:06 ; Search time 174.223 Seconds  
(without alignments)  
2830.777 Million cell updates/sec

Title: US-10-628-525A-36

Perfect score: 368

Sequence: 1 MAALATSQLVATAGHGVPD.....RHQQQARRGRFPFPPSLVVC 74

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/abs/ABSSWEB\_spool/US10628525/runat\_31032006\_095109\_16557/app\_query.fasta\_1  
-DB=N Geneseq -QWIT=fastcap -SUFFIX=p2n.rng -MINMATCH=0 -LOPCLI=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=-1 -WATFIX=blosum62 -TRANS=human40.cdi -LIST=150  
-DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs06h  
-USER=US10628525 @CGN 1 1 1404 @runat\_31032006\_095109\_16557 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 21:\*  
1: Geneseqm1980s:\*  
2: Geneseqm1990s:\*  
3: Geneseqm2000s:\*  
4: Geneseqm2001as:\*  
5: Geneseqm2001bs:\*  
6: Geneseqm2002as:\*  
7: Geneseqm2002bs:\*  
8: Geneseqm2003as:\*  
9: Geneseqm2003bs:\*  
10: Geneseqm2003cs:\*  
11: Geneseqm2003ds:\*  
12: Geneseqm2004as:\*  
13: Geneseqm2004bs:\*  
14: Geneseqm2005as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 333   | 90.5        | 1818   | 10 | Aad63600 Maize UDP |
| 2          | 333   | 90.5        | 1818   | 14 | Adw87816 Maize gra |
| 3          | 333   | 90.5        | 1818   | 14 | Adw87799 Maize gra |
| 4          | 333   | 90.5        | 1915   | 2  | Aax60319 DNA seque |

|    |       |      |        |    |             |
|----|-------|------|--------|----|-------------|
| 5  | 333   | 90.5 | 2263   | 11 | ADM77903    |
| 6  | 333   | 90.5 | 2263   | 11 | ADM77902    |
| 7  | 333   | 90.5 | 4627   | 14 | ADM87817    |
| 8  | 333   | 90.5 | 4800   | 2  | AAV29752    |
| 9  | 333   | 90.5 | 4800   | 8  | ABX09931    |
| 10 | 333   | 90.5 | 4800   | 11 | ADM77906    |
| 11 | 326   | 88.6 | 1406   | 13 | ADX34893    |
| 12 | 326   | 88.6 | 1409   | 13 | ADX33821    |
| 13 | 326   | 88.6 | 1416   | 13 | ADX36735    |
| 14 | 316.5 | 86.0 | 1818   | 8  | ACC44559    |
| 15 | 316.5 | 86.0 | 4207   | 14 | ADM87804    |
| 16 | 306.5 | 83.3 | 1863   | 14 | ADM87808    |
| 17 | 306.5 | 83.3 | 4442   | 14 | ADM87815    |
| 18 | 306.5 | 83.3 | 4470   | 14 | ADM87798    |
| 19 | 289   | 78.5 | 2267   | 2  | AAX63355    |
| 20 | 183   | 49.7 | 121    | 6  | ABK26694    |
| 21 | 183   | 49.7 | 121    | 6  | ABK26693    |
| 22 | 183   | 49.7 | 121    | 12 | ADN45385    |
| 23 | 183   | 49.7 | 121    | 12 | ADN45384    |
| 24 | 175   | 47.6 | 121    | 6  | ABK26690    |
| 25 | 175   | 47.6 | 121    | 6  | ABK26689    |
| 26 | 175   | 47.6 | 121    | 12 | ADN45381    |
| 27 | 175   | 47.6 | 121    | 12 | ADN45380    |
| 28 | 159   | 43.2 | 121    | 6  | ABK26698    |
| 29 | 159   | 43.2 | 121    | 6  | ABK26697    |
| 30 | 159   | 43.2 | 121    | 12 | ADN45388    |
| 31 | 159   | 43.2 | 121    | 12 | ADN45389    |
| 32 | 155   | 42.1 | 121    | 6  | ABK26702    |
| 33 | 155   | 42.1 | 121    | 6  | ABK26701    |
| 34 | 155   | 42.1 | 121    | 12 | ADN45392    |
| 35 | 155   | 42.1 | 121    | 12 | ADN45393    |
| 36 | 128.5 | 34.9 | 1937   | 10 | ADC53776    |
| 37 | 128.5 | 34.9 | 1937   | 10 | ADC53778    |
| 38 | 128.5 | 34.9 | 2286   | 2  | AAQ45913    |
| 39 | 128.5 | 34.9 | 2542   | 2  | AAV29753    |
| 40 | 128.5 | 34.9 | 2597   | 10 | ADC07867    |
| 41 | 113   | 30.7 | 121    | 6  | ABK26685    |
| 42 | 113   | 30.7 | 121    | 6  | ABK26686    |
| 43 | 113   | 30.7 | 121    | 12 | ADN45376    |
| 44 | 113   | 30.7 | 121    | 12 | ADN45377    |
| 45 | 98.5  | 26.8 | 1714   | 10 | ADN45377    |
| 46 | 97.5  | 26.5 | 2028   | 10 | ADF92505    |
| 47 | 97.5  | 26.5 | 2886   | 9  | ADB17811    |
| 48 | 97.5  | 26.5 | 2886   | 10 | ADF92497    |
| 49 | 97.5  | 26.5 | 2886   | 10 | ADF92503    |
| 50 | 97.5  | 26.5 | 2886   | 14 | AEA79538    |
| 51 | 96    | 26.1 | 475    | 9  | ACH45303    |
| 52 | 94    | 25.5 | 2818   | 10 | ADF92501    |
| 53 | 94    | 25.5 | 2818   | 14 | AEA79534    |
| 54 | 90.5  | 24.6 | 1752   | 8  | ACA27181    |
| 55 | 88.5  | 24.0 | 6776   | 14 | ACL64421    |
| 56 | 87    | 23.6 | 1200   | 10 | ADC10049    |
| 57 | 87    | 23.6 | 1548   | 8  | ACA23242    |
| 58 | 87    | 23.6 | 3123   | 10 | ADF81459    |
| 59 | 86    | 23.4 | 201    | 13 | ADQ46462    |
| 60 | 86    | 23.4 | 201    | 13 | ADQ46475    |
| 61 | 86    | 23.4 | 2805   | 10 | ADF92499    |
| 62 | 86    | 23.4 | 2805   | 14 | AEA79536    |
| 63 | 86    | 23.4 | 3785   | 6  | AAK98640    |
| 64 | 85.5  | 23.2 | 2870   | 2  | AAQ91177    |
| 65 | 85    | 23.1 | 1278   | 13 | ADX49818    |
| 66 | 84.5  | 23.0 | 75216  | 6  | ABX09141    |
| 67 | 84.5  | 23.0 | 110000 | 4  | AAI99682_13 |
| 68 | 84.5  | 23.0 | 110000 | 4  | AAI99683_13 |
| 69 | 84    | 22.8 | 109519 | 5  | AAS08693    |
| 70 | 84    | 22.8 | 113193 | 8  | AAS08693    |
| 71 | 83.5  | 22.7 | 1350   | 6  | ABA99445    |
| 72 | 83.5  | 22.7 | 22473  | 11 | ACN43962    |
| 73 | 83.5  | 22.7 | 38064  | 6  | ABA99469    |
| 74 | 83    | 22.6 | 201    | 13 | ADQ46481    |
| 75 | 83    | 22.6 | 201    | 13 | ADQ46481    |
| 76 | 83    | 22.6 | 1161   | 11 | ACL29132    |
| 77 | 82    | 22.3 | 2778   | 5  | AAS76843    |

Adm77903 Maize wax  
Adm77902 Maize wax  
Adw87817 Maize gra  
Aav29752 Zea maye  
Abx09931 DNA encod  
Adm77906 Granule-b  
Adx34893 Plant ful  
Adx33821 Plant ful  
Adx36735 Plant ful  
Acc44559 Maize gra  
Adw87804 Corn inbr  
Adw87808 Corn line  
Adw87815 Corn line  
Adw87798 Corn line  
Aax63355 Granule b  
Aax26694 Waxy star  
Abk26693 Waxy star  
Adn45385 Mutant ce  
Adn45384 Mutant ce  
Abk26690 Waxy star  
Abk26689 Waxy star  
Adn45381 Mutant ce  
Adn45380 Mutant ce  
Abk26698 Waxy star  
Abk26697 Waxy star  
Adn45388 Mutant ce  
Adn45389 Mutant ce  
Abk26702 Waxy star  
Abk26701 Waxy star  
Adn45392 Mutant ce  
Adn45393 Mutant ce  
Ades3776 Low amylo  
Ades3778 Low amylo  
Aac45913 Rice star  
Aav29753 Oryza sat  
Abc07867 Rice DNA  
Abk26685 Waxy star  
Abk26686 Waxy star  
Adn45376 Mutant ce  
Adn45377 Mutant ce  
Adn45377 Mutant ce  
Adn45377 Human cDN  
Adf92505 Bread whe  
Adf92497 Bread whe  
Adf92503 Bread whe  
Aea79538 waxy gene  
Aea79534 waxy gene  
Aea79534 waxy gene  
Aca27181 Prokaryot  
Acl64421 M. xanthu  
Adc10049 Human NOV  
Aca3242 Prokaryot  
Adf81459 Leukaemia  
Adq46462 Myocardia  
Adq46475 Myocardia  
Adf92499 Bread whe  
Aea79536 waxy gene  
Aak98640 Wheat car  
Aaq91177 Lipase an  
Adx49818 Plant ful  
Abx09141 Mycobacte  
Contribution (14 o  
Continuation (14 o  
Aas08693 Micromono  
Aad54645 Streptomy  
Aba99445 Actinopla  
Aca43962 Human gen  
Aba99469 Actinopla  
Adq46481 Myocardia  
Adq46481 Myocardia  
ACL29132 Rice abio  
Aas76843 DNA encod





Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 121 GCGACACGCTCAGCATGCGACACGCGCGCGCGCCAGGACACGACGAGCG 180  
 Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 181 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGTGC 216

RESULT 2  
 ADW87816  
 ID ADW87816 standard; DNA; 1818 BP.  
 AC ADW87816;  
 XX  
 DT 07-APR-2005 (first entry)  
 DE Maize granule bound starch synthase (GBSS) coding region.  
 XX  
 KW Seed oil; feedstuff; food; crop improvement; transgenic plant;  
 KW granule bound starch synthase; plant; gene; ds.  
 XX  
 OS Zea mays.  
 XX  
 PN US2005005327-A1.  
 XX  
 PD 06-JAN-2005.  
 XX  
 PF 25-JUN-2004; 2004US-00877645.  
 XX  
 PR 27-JUN-2003; 2003US-0483491P.  
 XX  
 PA (RAVA/) RAVANELLO M P.  
 PA (FOLE/) FOLEY T J.  
 PA (LEDE/) LEDEAUX J R.  
 PA (WYRI/) WYRICK A E.  
 PA (SAVA/) SAVAGE T J.  
 XX  
 PI Ravanello MP, Foley TJ, Ledeaux JR, Wyrick AE, Savage TJ;  
 DR WPI; 2005-065279/07.  
 XX  
 PT New purified HOI001 granule bound starch synthase nucleic acid, useful  
 PT for increasing oil levels in maize plants or for creating maize plants  
 PT that include the nucleic acids.  
 XX  
 PS Disclosure; Fig 1; 74pp; English.  
 XX  
 CC The invention relates to HOI001 granule bound starch synthase (GBSS)  
 CC nucleic acid and its protein sequence. The invention also relates to a  
 CC method for increasing oil levels in corn kernel tissue by expression of  
 CC an HOI001 GBSS allele. The GBSS nucleic acid is useful for increasing oil  
 CC levels in maize plants and creating maize plants that include the nucleic  
 CC acids. The present sequence is the maize GBSS gene coding region.  
 XX  
 SQ Sequence 1818 BP; 345 A; 591 C; 613 G; 269 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2,16e-22 Length: 1818  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 14 Gaps: 1

US-10-628-525A-36 (1-74) x ADW87816 (1-1818)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
 Db 1 ATGGCGGCTCTGGCCACGTCGCGACGTCGTCGCAACGCGCGCGCTGCGGCTCCCGGAC 60  
 Qy 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 61 GCGTCCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGCCCCGGGCGTCCGCGCGCG 120  
 Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 121 GCGACACGCTCAGCATGCGACACGCGCGCGCGCCAGGACACGACGAGCG 180  
 Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 181 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGTGC 216

RESULT 3  
 ADW87799  
 ID ADW87799 standard; DNA; 1818 BP.  
 AC ADW87799;  
 XX  
 DT 07-APR-2005 (first entry)  
 DE Maize granule bound starch synthase (GBSS) gene.  
 XX  
 KW Seed oil; feedstuff; food; crop improvement; transgenic plant;  
 KW granule bound starch synthase; plant; gene; ds.  
 XX  
 OS Zea mays.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..1818  
 FT /tag= a  
 FT /product= "Maize granule bound starch synthase (GBSS)"  
 XX  
 PN US2005005327-A1.  
 XX  
 PD 06-JAN-2005.  
 XX  
 PF 25-JUN-2004; 2004US-00877645.  
 XX  
 PR 27-JUN-2003; 2003US-0483491P.  
 XX  
 PA (RAVA/) RAVANELLO M P.  
 PA (FOLE/) FOLEY T J.  
 PA (LEDE/) LEDEAUX J R.  
 PA (WYRI/) WYRICK A E.  
 PA (SAVA/) SAVAGE T J.  
 XX  
 PI Ravanello MP, Foley TJ, Ledeaux JR, Wyrick AE, Savage TJ;  
 DR WPI; 2005-065279/07.  
 DR P-PSDB; ADW87801.  
 DR EMBL; X03935.  
 XX  
 PT New purified HOI001 granule bound starch synthase nucleic acid, useful  
 PT for increasing oil levels in maize plants or for creating maize plants  
 PT that include the nucleic acids.  
 XX  
 PS Example 1; SEQ ID NO 2; 74pp; English.  
 XX  
 CC The invention relates to HOI001 granule bound starch synthase (GBSS)  
 CC nucleic acid and its protein sequence. The invention also relates to a  
 CC method for increasing oil levels in corn kernel tissue by expression of  
 CC an HOI001 GBSS allele. The GBSS nucleic acid is useful for increasing oil  
 CC levels in maize plants and creating maize plants that include the nucleic  
 CC acids. The present sequence is the maize GBSS gene. Note: This sequence  
 CC is stated to be similar to the sequence shown in figure 1, but these  
 CC sequences differ.  
 XX  
 SQ Sequence 1818 BP; 346 A; 592 C; 612 G; 268 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2,16e-22 Length: 1818  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2

```

DB: 14 Gaps: 1
US-10-628-525A-36 (1-74) x ADM87799 (1-1818)
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProApp 20
DB 1 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTGCACACGCGCGCGCTGGCGCTGCCGGAC 60
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
DB 61 GGTCTCACGTTCCGCGCGCGCGCGCGAGGCGCTGAGGGGGGCGCGCGCGCTGCCGGAC 120
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60
DB 121 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB 181 CGCCGCGGGGCGAGG-----TTCCGCTCGCTCGTGTGC 216

RESULT 4
AAX60319
ID AAX60319 standard; DNA; 1915 BP.
XX
AC AAX60319;
XX
DT 23-AUG-1999 (first entry)
XX
DE DNA sequence of the maize waxy gene.
XX
KW Non-glycogen-like polysaccharide production; fermentation; waxy gene;
KW starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis;
KW non-starch branching gene; amylopectin; amylose; plant-like starch; ss.
XX
OS Zea mays.
XX
PN WO9844780-A1.
XX
PD 15-OCT-1998.
XX
PF 03-APR-1998; 98WO-US006660.
XX
PR 04-APR-1997; 97US-0042939P.
XX
PA (EXSE-) EXSEED GENETICS LLC.
XX
PI Guan H, Keeling PL;
XX
DR WPI; 1998-568285/48.
DR P-PSDB; AAY16604.
XX
PT Producing non-glycogen-like polysaccharides in bacteria, fungi or plants
PT - transformed with genes for enzymes involved in starch or glycogen
PT synthesis allows fermentative production of starches with engineered
PT properties.
XX
PS Disclosure; Fig 49; 150pp; English.
XX
CC The specification describes a method for the production of non-glycogen-
CC like polysaccharides in a host. The method comprises transforming a host,
CC suitable for fermentation, with genes encoding starch- or glycogen-
CC synthetase enzymes, and fermenting the transformants. The specification
CC also describes hosts transformed with a gene active in glycogen synthesis
CC and at least one non-starch branching gene, involved in production of
CC amylopectin or amylose in its original host. The method is used to
CC produce plant-like starches by fermentation and new starches in plants.
CC These starches are useful for all food and non-food applications of
CC starch. The present sequence is used in the course of the invention
XX
SQ Sequence 1915 BP; 365 A; 610 C; 641 G; 299 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 2.28e-22 Length: 1915

```

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Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 2 Gaps: 1
US-10-628-525A-36 (1-74) x AAX60319 (1-1915)
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProApp 20
DB 1 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTGCACACGCGCGCGCTGGCGCTGCCGGAC 60
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
DB 61 GGTCTCACGTTCCGCGCGCGCGCGAGGCGCTGAGGGGGGCGCGCGCGCTGCCGGAC 120
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60
DB 121 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB 181 CGCCGCGGGGCGAGG-----TTCCGCTCGCTCGTGTGC 216

RESULT 5
ADM77903
ID ADM77903 standard; DNA; 2263 BP.
XX
AC ADM77903;
XX
DT 03-JUN-2004 (first entry)
XX
DE Maize waxy-E starch EX385wx-E1 DNA G1643A SeqID 2.
XX
KW maize; EX385wx-E1; ds; plant; starch; waxy-E starch; gel; paste;
KW starch storage organ; food stuff; coating; granule-bound starch synthase;
KW GBSS; mutant; gene.
XX
OS Zea mays.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 194..2011
FT /tag= a
FT /product= "EX385wx-E1 protein"
FT mutation replace(1643,G)
FT /tag= b
XX
PN WO2003033540-A2.
XX
PD 24-APR-2003.
XX
PF 17-OCT-2002; 2002WO-US033122.
XX
PR 17-OCT-2001; 2001US-0329525P.
XX
PA (BADI ) BASF PLANT SCI GMBH.
XX
PI Klucinec JD, Keeling PL, Commuri P, Chang M;
XX
DR WPI; 2003-481973/45.
DR P-PSDB; ADM77905.
XX
PT Production of plant starch involves inducing mutation in starch affecting
PT locus of starch storage organ bearing plants, selecting propagative
PT structures, growing plants, and selecting and/or screening starch storing
PT organs.
XX
PS Claim 23; SEQ ID NO 2; 181pp; English.
XX
CC This invention relates to a novel method for producing a plant starch
CC through mutagenesis. Specifically, it refers to the granule-bound starch
CC synthase (GBSS) enzyme of waxy-E starch that exhibits elastic properties

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CC with high viscosity useful for gels and pastes. The present invention  
CC describes inducing a mutation in a starch affecting locus of starch  
CC storage organ bearing plants and selecting propagative structures from  
CC the mutant plants in order to grow such plants and select and/or screen  
CC the starch storing organs. Accordingly, this method is useful for the  
CC production of plant starch used in food stuffs such as pies, puddings,  
CC soups, yogurts or sauces or for coatings and films in foodstuffs  
CC including batter. Furthermore, it provides a plant starch with unique  
CC cooking, thickening, and/or gelling properties that can be stained blue  
CC with iodine stain and exhibits a reduced amylose content compared to wild  
CC type. This polynucleotide sequence is the maize waxy-E starch EX385w-E1  
CC mutant DNA of the invention.

XX Sequence 2263 BP; 451 A; 699 C; 739 G; 374 T; 0 U; 0 Other;

Alignment Scores: 2.72e-22 Length: 2263  
Pred. No.: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 11 Gaps: 1

US-10-628-525A-36 (1-74) x ADM77903 (1-2263)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 194 ATGGCGGCTCTGGCCACGTCGCAGCTCGTGCACACGCGCGCGCTGGCGCTGCCGGAC 253  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 254 GCGTCCACGCTTCGCCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCTCGCGGCG 313  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaAlaProArgHisGlnGlnAla 60  
DB 314 GCGGACACGCTCAGCATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 373  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 374 CGCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTC 409

RESULT 6

ID ADM77902 standard; DNA; 2263 BP.

XX AC ADM77902;

XX DT 03-JUN-2004 (first entry)

XX DE Maize waxy-E starch EX385 DNA SeqID 1.

XX KW maize; EX385w-E1; ds; plant; starch; waxy-E starch; gel; paste;  
KW starch storage organ; food stuff; coating; granule-bound starch synthase;  
KW GBSS; gene.

XX OS Zea mays.

XX FH Key Location/Qualifiers

FT CDS 194..2011

FT FT /\*tag= a

FT FT /product= "EX385 protein"

XX FN W02003033540-A2.

XX PD 24-APR-2003.

XX PP 17-OCT-2002; 2002WO-US033122.

XX PR 17-OCT-2001; 2001US-0329525P.

XX PA (BADI ) BASP PLANT SCI GMBH.

XX PI Klucinec JD, Keeling PL, Commuri P, Chang M;

XX WPI; 2003-481973/45.  
DR P-PSDB; ADM77904.

XX PT Production of plant starch involves inducing mutation in starch affecting  
PT locus of starch storage organ bearing plants, selecting propagative  
PT structures, growing plants, and selecting and/or screening starch storing  
PT organs.

XX PS Example 13; SEQ ID NO 1; 181pp; English.

XX CC This invention relates to a novel method for producing a plant starch  
CC through mutagenesis. Specifically, it refers to the granule-bound starch  
CC synthase (GBSS) enzyme of waxy-E starch that exhibits elastic properties  
CC with high viscosity useful for gels and pastes. The present invention  
CC describes inducing a mutation in a starch affecting locus of starch  
CC storage organ bearing plants and selecting propagative structures from  
CC the mutant plants in order to grow such plants and select and/or screen  
CC the starch storing organs. Accordingly, this method is useful for the  
CC production of plant starch used in food stuffs such as pies, puddings,  
CC soups, yogurts or sauces or for coatings and films in foodstuffs  
CC including batter. Furthermore, it provides a plant starch with unique  
CC cooking thickening, and/or gelling properties that can be stained blue  
CC with iodine stain and exhibits a reduced amylose content compared to wild  
CC type. This polynucleotide sequence is the wild type maize waxy-E starch  
CC EX385 DNA of the invention.

XX SQ Sequence 2263 BP; 450 A; 699 C; 740 G; 374 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.72e-22 Length: 2263  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 11 Gaps: 1

US-10-628-525A-36 (1-74) x ADM77902 (1-2263)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 194 ATGGCGGCTCTGGCCACGTCGCAGCTCGTGCACACGCGCGCGCTGGCGCTGCCGGAC 253  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 254 GCGTCCACGCTTCGCCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCTCGCGGCG 313  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaAlaProArgHisGlnGlnAla 60  
DB 314 GCGGACACGCTCAGCATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 373  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 374 CGCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTC 409

RESULT 7

ADM7817

ID ADM7817 standard; DNA; 4627 BP.

XX AC ADM7817;

XX DT 07-APR-2005 (first entry)

XX DE Maize granule bound starch synthase (GBSS) gene, alternative form.

XX KW Seed oil; feedstuff; food; crop improvement; transgenic plant;  
KW granule bound starch synthase; plant; gene; ds.

XX OS Zea mays.

XX PN US2005005327-A1.

XX PD 06-JAN-2005.

XX 25-JUN-2004; 2004US-00877645.  
XX 27-JUN-2003; 2003US-0483491P.  
XX (RAVA/) RAVANELLO M P.  
XX (FOLE/) FOLEY T J.  
XX (LEDE/) LEDEAUX J R.  
XX (WYRI/) WYRICK A E.  
XX (SAVA/) SAVAGE T J.  
XX Ravanello MP, Foley TJ, Ledeaux JR, Wyrick AE, Savage TJ;  
XX WPI; 2005-065279/07.  
XX EMBL; X03935.  
XX New purified HOI001 granule bound starch synthase nucleic acid, useful  
XX for increasing oil levels in maize plants or for creating maize plants  
XX that include the nucleic acids.  
XX Disclosure; Fig 1; 74pp; English.  
XX The invention relates to HOI001 granule bound starch synthase (GBSS)  
XX nucleic acid and its protein sequence. The invention also relates to a  
XX method for increasing oil levels in corn kernel tissue by expression of  
XX an HOI001 GBSS allele. The GBSS nucleic acid is useful for increasing oil  
XX levels in maize plants and creating maize plants that include the nucleic  
XX acids. The present sequence is the maize GBSS gene, alternative form.  
XX Note: This sequence is stated to be similar to the sequence shown as  
XX seqid:2 in the sequence listing, but these sequences differ.  
XX  
XX Sequence 4627 BP; 895 A; 1373 C; 1417 G; 942 T; 0 U; 0 Other;  
XX  
XX Alignment Scores:  
XX Pred. No.: 5,8e-22 Length: 4627  
XX Score: 333.00 Matches: 71  
XX Percent Similarity: 95.9% Conservative: 0  
XX Best Local Similarity: 95.9% Mismatches: 1  
XX Query Match: 90.5% Indels: 2  
XX DB: 14 Gaps: 1  
XX  
XX US-10-628-525A-36 (1-74) x ADM87817 (1-4627)  
XX  
XX 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProAap 20  
XX  
XX 1233 ATGGGGGCTCTGGCCACGTCGCGAGTCTGCGACAGCGCGCGCTGGGCGTCCGGAC 1292  
XX  
XX 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
XX  
XX 1293 GCGTCCAGCTTCGCGCGCGCGCGCGAGGCGCTGAGGGGGCCCGGCGCTCGCGCGG 1352  
XX  
XX 41 AlaAapThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
XX  
XX 1353 GCGGACAGCTCAGCATCGGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 1412  
XX  
XX 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
XX  
XX 1413 CCCTCCGGGGGGGAGG-----TTCCTGCTGCTGCTGCTGCTG 1448  
XX  
XX RESULT 8  
XX AAV29752  
XX ID AAV29752 standard; DNA; 4800 BP.  
XX XX  
XX AC AAV29752;  
XX XX  
XX DT 11-SEP-1998 (first entry)  
XX XX  
XX DE Zea mays waxy gene.  
XX XX  
XX KW SER; starch-encapsulating region; fusion vector; glucosyl transferase;  
XX 88.  
XX XX Zea mays.  
XX OS

XX Key Location/Qualifiers  
FH repeat\_region 283..287  
FT /tag= a  
FT /note= "direct repeat 1"  
FT 288..292  
FT /tag= b  
FT /note= "direct repeat 1"  
FT 293..297  
FT /tag= c  
FT /note= "direct repeat 1"  
FT 298..302  
FT /tag= d  
FT /note= "direct repeat 1"  
FT 372..385  
FT /tag= e  
FT /note= "GC stretch, potential regulatory factor binding"  
FT 442..468  
FT /tag= f  
FT /note= "GC stretch, potential regulatory factor binding"  
FT 768..782  
FT /tag= g  
FT /note= "GC stretch, potential regulatory factor binding"  
FT 810..822  
FT /tag= h  
FT /note= "GC stretch, potential regulatory factor binding"  
FT 821..828  
FT /tag= i  
FT /note= "target duplication site (Ac7)"  
FT 821..828  
FT /tag= j  
FT 867..873  
FT /tag= k  
FT 887..900  
FT /tag= l  
FT /note= "GC stretch, potential regulatory factor"  
FT 901..1080  
FT /tag= o  
FT /number= 1  
FT 901  
FT /tag= m  
FT /note= "transcriptional start site"  
FT 1081..1219  
FT /tag= p  
FT /number= 1  
FT 1220..1553  
FT /tag= q  
FT /number= 2  
FT 1449..4343  
FT /tag= n  
FT /product= "glucosyl transferase"  
FT /note= "contains introns"  
FT 1554..1684  
FT /tag= r  
FT /number= 2  
FT 1685..1765  
FT /tag= s  
FT /number= 3  
FT 1766..1859  
FT /tag= t  
FT /number= 3  
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FT 1959..2054  
FT /tag= v  
FT /number= 4  
FT 2055..2144  
FT /tag= w  
FT /number= 5  
FT 2145..2225  
FT /tag= x  
FT /number= 5

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FT exon 2226. .2289
FT /*tag= y
FT /number= 6
FT intron 2290. .2412
FT /*tag= z
FT exon 2413. .2513
FT /*tag= aa
FT intron 2514. .2650
FT /*tag= bb
FT exon 2651. .2760
FT /*tag= cc
FT intron 2761. .2857
FT /*tag= dd
FT exon 2858. .3101
FT /*tag= ee
FT intron 3102. .3211
FT /*tag= ff
FT exon 3212. .3394
FT /*tag= gg
FT misc_feature 3358. .3489
FT /*tag= hh
FT intron 3395. .3489
FT /*tag= ii
FT exon 3490. .3681
FT /*tag= jj
FT misc_feature 3570. .3572
FT /*tag= kk
FT intron /note= "target duplication site (Spm 18)"
FT 3682. .3792
FT /*tag= ll
FT exon 3793. .3879
FT /*tag= mm
FT intron /number= 12
FT 3880. .3976
FT /*tag= nn
FT exon /number= 12
FT 3977. .4105
FT /*tag= oo
FT intron /number= 13
FT 4106. .4226
FT /*tag= pp
FT exon /number= 13
FT 4227. .4595
FT /*tag= qq
FT polyA_signal /number= 14
FT 4570. .4575
FT polyA_signal /*tag= rr
FT 4593. .4598
FT polyA_signal /*tag= ss
FT 4597. .4602
FT /*tag= tt
FT XX WO9814601-A1.
FT XX
FT XX 09-APR-1998.
FT XX 30-SEP-1997; 97WO-US017555.
FT XX 30-SEP-1996; 96US-0026855P.
FT XX (EXSE-) EXSEED GENETICS LLC.
```

```
XX Keeling P, Guan H;
XX PI 1998-240100/21.
XX DR P-PSDB; AAW56484.
XX PT Hybrid polypeptide comprising starch-encapsulating region and protein -
XX PT useful for, e.g. producing protein(s) resistant to degradation by stomach
XX PT acids.
XX PS Example 2; Page 29-31; 156pp; English.
XX CC The sequence is that of the waxy gene which codes for glucosyl
XX CC transferase. It can be used in the production of a hybrid polypeptide
XX CC comprising a starch-encapsulating region (SER) fused to a payload
XX CC protein. The hybrid polypeptide can be used to make modified starches
XX CC comprising the payload protein, selected from, e.g. hormones, growth
XX CC factors, antibodies, enzymes, dyes, immunoglobulins, etc. The modified
XX CC starch can also be used to provide grain feeds enriched in amino acids.
XX CC By encapsulating the payload protein in starch, it is more resistant to
XX CC degradation by stomach acids
XX SQ Sequence 4800 BP; 935 A; 1414 C; 1446 G; 1005 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.03e-22 Length: 4800
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 2 Gaps: 1

US-10-628-525A-36 (1-74) x AAV29752 (1-4800)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 1233 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTGGCAACGCGCGCGCTGGCGCTCCCGGAC 1292

QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40
DB 1293 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCTGAGGGGGGCCCGGGGCTCGGGCGG 1352

QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGlnGlnAla 60
DB 1353 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCCAGGACCCAGCAGGCGG 1412

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB 1413 CGCCGCGGGGGCAGG-----TTCCGCTCGCTCGTGTGC 1448

RESULT 9
ABX09931
ID ABX09931 standard; DNA; 4800 BP.
XX
AC ABX09931;
XX
DT 17-FEB-2003 (first entry)
XX
DE DNA encoding maize granule bound starch synthase (GBSS).
XX
KW Starch; starch synthase; glucan association domain; GLASS; linker domain;
KW LINKR; glucosyl transferase domain; GLYTR; C-terminal end; CTEND;
KW granule bound starch synthase; GBSS; morphology; retrogradation;
KW waterbinding; swelling potential; gene; ds.
XX
OS Zea mays.
XX
PN WO200279410-A2.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-US009574.
XX
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FT      /number= 11
FT      3977. .4105
FT      /*tag= x
FT      /number= 12
FT      4106. .4226
FT      /*tag= y
FT      /number= 12
FT      4227. .4343
FT      /*tag= z
FT      /number= 13
XX      WO2003033540-A2.
XX      24-APR-2003.
XX      17-OCT-2002; 2002WO-US033122.
XX      17-OCT-2001; 2001US-0329525P.
XX      (BADI ) BASP PLANT SCI GMBH.
XX      Klucinec JD, Keeling PL, Commuri P, Chang M;
XX      WPI; 2003-481973/45.
XX      P-PSDB; ADM77907.
XX      Production of plant starch involves inducing mutation in starch affecting
XX      PT locus of starch storage organ bearing plants, selecting propagative
XX      PT structures, growing plants, and selecting and/or screening starch storing
XX      PT organs.
XX      Example 13; SEQ ID NO 5; 181pp; English.
XX      This invention relates to a novel method for producing a plant starch
XX      CC through mutagenesis. Specifically, it refers to the granule-bound starch
XX      CC synthase (GBSS) enzyme of waxy-E starch that exhibits elastic properties
XX      CC with high viscosity useful for gels and pastes. The present invention
XX      CC describes inducing a mutation in a starch affecting locus of starch
XX      CC storage organ bearing plants and selecting propagative structures from
XX      CC the mutant plants in order to grow such plants and select and/or screen
XX      CC the starch storing organs. Accordingly, this method is useful for the
XX      CC production of plant starch used in food stuffs such as pies, puddings,
XX      CC soups, yogurts or sauces or for coatings and films in foodstuffs
XX      CC including batter. Furthermore, it provides a plant starch with unique
XX      CC cooking, thickening, and/or gelling properties that can be stained blue
XX      CC with iodine stain and exhibits a reduced amylose content compared to wild
XX      CC type. This polynucleotide sequence is the maize GBSS DNA of the
XX      CC invention.
XX      SQ Sequence 4800 BP; 935 A; 1413 C; 1447 G; 1005 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      6.03e-22      Length:      4800
Score:      333.00      Matches:      71
Percent Similarity:      95.9%      Conservative:      0
Best Local Similarity:      95.9%      Mismatches:      1
Query Match:      90.5%      Indels:      2
DB:      11      Gaps:      1

US-10-628-525A-36 (1-74) x ADM77906 (1-4800)

QY      1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB      1233 ATGGCGGCTCTGGCCACGTCGAGCTCGTCGCAACGCGCGCGCTGGCGGTCCGGAC 1292

QY      21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
DB      1293 GGGTCACAGTTCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCGGGG 1352

QY      41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
DB      1353 GCGGACACGCTCAGCATGCGGACCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1412
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QY      61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB      1413 CGCGCGGCGGCGCAGG-----TTCCCGTCGCTCGTCGTGTC 1448

RESULT 11
ADX34893
ID      ADX34893 standard; cDNA; 1406 BP.
XX      AC      ADX34893;
XX      DT      21-APR-2005 (first entry)
XX      DE      Plant full length insert polynucleotide seqid 17713.
XX      KW      plant protectant; plant growth regulant; gene therapy; plant;
XX      KW      recombinant DNA construct; physical array; plant breeding marker;
XX      KW      cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX      KW      extreme osmotic condition; pathogen tolerance; pest tolerance;
XX      KW      growth rate; cell cycle pathway; disease resistance;
XX      KW      galactomannan production; lignin production; plant growth regulator;
XX      KW      yield; plant growth; plant development; seed oil; protein yield;
XX      KW      protein content; gene; ss.
XX      OS      Unidentified.
XX      PN      US2004034888-A1.
XX      PD      19-FEB-2004.
XX      PF      28-APR-2003; 2003US-00425114.
XX      PR      06-MAY-1999; 99US-00304517.
XX      PR      05-NOV-2001; 2001US-00985678.
XX      PA      (LIU/) LIU J.
XX      PA      (ZHOU/) ZHOU Y.
XX      PA      (KOVA/) KOVALIC D K.
XX      PA      (SCRE/) SCREEN S E.
XX      PA      (TABA/) TABASKA J E.
XX      PA      (CAOV/) CAO Y.
XX      PI      Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX      WPI; 2004-180133/17.
XX      PT      New recombinant DNA construct, useful for improving plant tolerance to
XX      PT      cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX      PT      pests, for conferring increased resistance to plant disease, or for
XX      PT      improving yield.
XX      PS      Claim 1; SEQ ID NO 17713; 15pp; English.
XX      CC      The invention describes a recombinant DNA construct comprising a
XX      CC      polynucleotide consisting of a sequence encoding an amino acid sequence
XX      CC      available in electronic form from the US patent office at
XX      CC      ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX      CC      of the invention are also useful in physical arrays of molecules and as
XX      CC      plant breeding markers. The recombinant DNA construct is useful for
XX      CC      improving plant tolerance to cold, heat, drought, herbicides, extreme
XX      CC      osmotic conditions, pathogens or pests, for manipulating growth rate in
XX      CC      plant cells by modification of the cell cycle pathway, for conferring
XX      CC      increased resistance to plant disease, for producing galactomannan,
XX      CC      lignin or plant growth regulators, for increasing the rate of homologous
XX      CC      recombination in plants, for improving yield by modification of
XX      CC      photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX      CC      or by providing improved plant growth and development under at least one
XX      CC      stress condition or for modifying seed oil or protein yield and/or
XX      CC      content. This sequence represents a plant full length insert
XX      CC      polynucleotide that can be used in the recombinant DNA construct of the
XX      CC      invention.
XX      SQ      Sequence 1406 BP; 275 A; 468 C; 457 G; 206 T; 0 U; 0 Other;
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```
PF 28-APR-2003; 2003US-004251114.
XX
XX 06-MAY-1999; 99US-00304517.
PR
PR 05-NOV-2001; 2001US-00985678.
XX
XX (LIUJ/) LIU J.
XX (ZHOU/) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TABA/) TABASKA J E.
XX (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX
XX Claim 1; SEQ ID NO 19555; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.secdat.uspto.gov/sequence.html?docID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This sequence represents a plant full length insert
XX polynucleotide that can be used in the recombinant DNA construct of the
XX invention.
XX
XX Sequence 1416 BP; 275 A; 471 C; 463 G; 207 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 7.69e-22 Length: 1416
Score: 326.00 Matches: 70
Percent Similarity: 94.6% Conservative: 0
Best Local Similarity: 94.6% Mismatches: 2
Query Match: 88.6% Indels: 2
DB: 13 Gaps: 1
US-10-628-525A-36 (1-74) x ADX36735 (1-1416)
QY 1 MetalAlaLeuAlaThrSerGlnLeuValAlaThrArgNlaGlyHisGlyValProAap 20
Db 173 ATGGCGGCTGTGGCCACGTCGCGAGCTGTCGCAACGCCGCCGCTGGCGGTCGCGGAC 232
QY 21 AlaSerThrPheArgArgGlyAlaGlnGlyLeuArgGlyValaArgAlaSerAlaA 40
Db 233 GCGTCCACGTTCCG 292
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 293 GCGGACACGCTACGATGCGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 352
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 353 CGCCGCGCGCGCGCAGG-----TTCCCGTCGCTCGCTGTCGTCG 388
RESULT 14
ACC44559
ID ACC44559 standard; cDNA; 1818 BP.
```

```
XX ACC44559;
XX
XX 02-JUN-2003 (first entry)
XX
XX Maize granule-bound starch synthase encoding cDNA SEQ ID NO:7.
XX
XX Self-processing plant; plant; processing enzyme; alpha-amylase; grain;
XX pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase;
XX mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch;
XX maltodextrin; ethanol; fermentation; beverage; enzyme; gene; ss.
XX
XX Zea mays.
XX
XX Key Location/Qualifiers
XX CDS 1..1818
XX FT /*tag= a
XX FT /partial
XX FT /product= "granule-bound starch synthase (waxy)"
XX FT /note= "no stop codon given"
XX
XX WO2003018766-A2.
XX
XX 06-MAR-2003.
XX
XX 27-AUG-2002; 2002WO-US027129.
XX
XX 27-AUG-2001; 2001US-0315281P.
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Lanahan MB, Basu SS, Batie CJ, Chen W, Craig J, Kinkema M;
XX WPI; 2003-268420/26.
XX P-PSDB; ABP96605.
XX
XX Novel polynucleotide encoding hyperthermophilic processing enzymes e.g.
XX alpha-amylase, useful for producing plant to produce food products having
XX improved taste or fermentable substrates for ethanol.
XX
XX Example 2; Page 90-91; 158pp; English.
XX
XX The present invention describes polynucleotides which encode processing
XX enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose
XX isomerase, or glucoamylase) that are optimised for expression in plants.
XX The polynucleotides encode mesophilic thermophilic or hyperthermophilic
XX processing enzymes, which are activated under suitable conditions to act
XX upon the desired substrate. Also described are self-processing transgenic
XX plants and plant parts, e.g. grain, which express one or more of these
XX enzymes and have an altered composition that facilitates plant and grain
XX processing. Also described is a method (M) for converting starch to
XX starch-derived products in a transformed plant part (TPP), by activating
XX the starch processing enzyme contained in it. Transgenic grain is useful
XX for preparing maltodextrin. A transformed plant (TP) can be used to
XX produce food products having improved taste and to produce fermentable
XX substrates for ethanol and fermented beverages. (M) eliminates the need
XX to mill or physically disrupt the integrity of plant parts prior to
XX recovery of starch-derived products. The present sequence encodes maize
XX granule-bound starch synthase (waxy), which is given in the
XX exemplification of the present invention
XX
XX Sequence 1818 BP; 346 A; 596 C; 609 G; 267 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 8.02e-21 Length: 1818
Score: 316.50 Matches: 70
Percent Similarity: 93.3% Conservative: 0
Best Local Similarity: 93.3% Mismatches: 2
Query Match: 86.0% Indels: 3
DB: 8 Gaps: 2
US-10-628-525A-36 (1-74) x ACC44559 (1-1818)
```

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 1 ATGGCGGCTCTGGCCACGTCGAGCTCGTCGCAACGCGCGCCGCTGGCGCTCCCGAC 60  
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40  
DB 61 GCGTCCACGTTCCGCGCGCGCGCGAGGCTCGAGGGGCGCGCGGCTGGCGGCG 120  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGln---GlnGln 59  
DB 121 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCCAGGACCGACCGACGAG 180  
QY 60 AlaArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 181 GCGGCGCGCGGGGCCAGG-----TTCCCGTCGCTCGTGTGTGC 219  
RESULT 15  
ADW87804  
ID ADW87804 standard; DNA; 4207 BP.  
XX  
AC ADW87804;  
XX  
DT 07-APR-2005 (first entry)  
XX  
DE Corn inbred line LH59 granule bound starch synthase (GBSS) DNA.  
XX  
KW Seed oil; feedstuff; food; crop improvement; transgenic plant;  
KW granule bound starch synthase; plant; ds.  
XX  
OS Zea mays.  
XX  
PN US2005005327-A1.  
XX  
PD 06-JAN-2005.  
XX  
PF 25-JUN-2004; 2004US-00877645.  
XX  
PR 27-JUN-2003; 2003US-0483491P.  
XX  
PA (RAVA/) RAVANELLO M P.  
PA (FOLE/) FOLEY T J.  
PA (LEDE/) LEDEAUX J R.  
PA (WYRI/) WYRICK A E.  
PA (SAVA/) SAVAGE T J.  
XX  
PI Ravanello MP, Foley TJ, Ledeaux JR, Wyrick AE, Savage TJ;  
XX WPI; 2005-065279/07.  
XX  
PT New purified HOI001 granule bound starch synthase nucleic acid, useful  
PT for increasing oil levels in maize plants or for creating maize plants  
PT that include the nucleic acids.  
XX  
PS Example 1; SEQ ID NO 7; 74pp; English.  
XX  
CC The invention relates to HOI001 granule bound starch synthase (GBSS)  
CC nucleic acid and its protein sequence. The invention also relates to a  
CC method for increasing oil levels in corn kernel tissue by expression of  
CC an HOI001 GBSS allele. The GBSS nucleic acid is useful for increasing oil  
CC levels in maize plants and creating maize plants that include the nucleic  
CC acids. The present sequence is the corn inbred line LH59 GBSS DNA. Note:  
CC This sequence is said to encode seqid:8, however this does not appear to  
CC be the case.  
XX  
SQ Sequence 4207 BP; 805 A; 1282 C; 1299 G; 821 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: Length: 4207  
Score: 316.50 Matches: 70  
Percent Similarity: 93.3% Conservatives: 0  
Best Local Similarity: 93.3% Mismatches: 2  
Query Match: 86.0% Indels: 3  
DB: 14 Gaps: 2

US-10-628-525A-36 (1-74) x ADW87804 (1-4207)  
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 1130 ATGGCGGCTCTGGCCACGTCGAGCTCGTCGCAACGCGCGCGCTGGCGCTCCCGAC 1189  
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40  
DB 1190 GCGTCCACGTTCCGCGCGCGCGCGAGGCTCGAGGGGCGCGCGGCTGGCGGCG 1249  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGln---GlnGln 59  
DB 1250 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCCAGGACCGACCGACGAG 1309  
QY 60 AlaArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 1310 GCGGCGCGCGGGGCCAGG-----TTCCCGTCGCTCGTGTGTGC 1348  
RESULT 16  
ADW87808  
ID ADW87808 standard; DNA; 1863 BP.  
XX  
AC ADW87808;  
XX  
DT 07-APR-2005 (first entry)  
XX  
DE Corn line HOI001 GBSS cDNA coding region.  
XX  
KW Seed oil; feedstuff; food; crop improvement; transgenic plant;  
KW granule bound starch synthase; plant; gene; ss.  
XX  
OS Zea mays.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1863  
FT /tag= a  
FT /product= "Corn line HOI001 granule bound starch synthase  
FT (GBSS)"  
XX  
US2005005327-A1.  
XX  
PN 06-JAN-2005.  
XX  
PD 25-JUN-2004; 2004US-00877645.  
XX  
PF 27-JUN-2003; 2003US-0483491P.  
XX  
PA (RAVA/) RAVANELLO M P.  
PA (FOLE/) FOLEY T J.  
PA (LEDE/) LEDEAUX J R.  
PA (WYRI/) WYRICK A E.  
PA (SAVA/) SAVAGE T J.  
XX  
PI Ravanello MP, Foley TJ, Ledeaux JR, Wyrick AE, Savage TJ;  
XX WPI; 2005-065279/07.  
XX  
DR P-PSDB; ADW87800.  
XX  
PT New purified HOI001 granule bound starch synthase nucleic acid, useful  
PT for increasing oil levels in maize plants or for creating maize plants  
PT that include the nucleic acids.  
XX  
PS Claim 1; SEQ ID NO 11; 74pp; English.  
XX  
CC The invention relates to HOI001 granule bound starch synthase (GBSS)  
CC nucleic acid and its protein sequence. The invention also relates to a  
CC method for increasing oil levels in corn kernel tissue by expression of  
CC an HOI001 GBSS allele. The GBSS nucleic acid is useful for increasing oil  
CC levels in maize plants and creating maize plants that include the nucleic  
CC acids. The present sequence is the corn line HOI001 GBSS cDNA coding  
XX region.

```
SQ Sequence 1863 BP; 355 A; 596 C; 614 G; 298 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 7.36e-20 Length: 1863
Score: 306.50 Matches: 69
Percent Similarity: 87.3% Conservative: 0
Best Local Similarity: 87.3% Mismatches: 3
Query Match: 83.3% Indels: 7
DB: 14 Gaps: 2

US-10-628-525A-36 (1-74) x ADW87808 (1-1863)
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 1 ATGGCGGCTCTGGCCACGTCGCAGCTCGTCGAACGCGCGCCGCTGGGGCGTCCCGGAC 60
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
DB 61 GCGTCCACGTTCCG 120
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArg----- 55
DB 121 GCGGACACGCTCAGCATGCGGACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 56 HisGlnGlnGlnAlaArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB 181 CAGCAGCAGCAGCG 231

RESULT 17
ADW87815
ID ADW87815 standard; DNA; 4442 BP.
XX
AC ADW87815;
XX
DT 07-APR-2005 (first entry)
XX
DE Corn line HO1001 granule bound starch synthase gene, alternative form.
XX
KW Seed oil; feedstuff; food; crop improvement; transgenic plant;
KW granule bound starch synthase; plant; gene; ds.
XX
OS Zea mays.
XX
PN US2005005327-A1.
XX
PD 06-JAN-2005.
XX
PF 25-JUN-2004; 2004US-00877645.
XX
PR 27-JUN-2003; 2003US-0483491P.
XX
PA (RAVA/) RAVANELLO M P.
PA (FOLE/) FOLEY T J.
PA (LEDE/) LEDEAUX J R.
PA (WYRI/) WYRICK A E.
PA (SAVA/) SAVAGE T J.
XX
PI Ravanello MP, Foley TJ, Ledeaux JR, Wyrick AE, Savage TJ;
XX WPI; 2005-065279/07.
XX
PT New purified HO1001 granule bound starch synthase nucleic acid, useful
PT for increasing oil levels in maize plants or for creating maize plants
PT that include the nucleic acids.
XX
PS Claim 1; Fig 1; 74pp; English.
XX
CC The invention relates to HO1001 granule bound starch synthase (GBSS)
CC nucleic acid and its protein sequence. The invention also relates to a
CC method for increasing oil levels in corn kernel tissue by expression of
CC an HO1001 GBSS allele. The GBSS nucleic acid is useful for increasing oil
CC levels in maize plants and creating maize plants that include the nucleic
CC acids. The present sequence is the corn line HO1001 GBSS gene,

CC alternative form. Note: This sequence is stated to be similar to the
CC sequence shown as seqid:1 in the sequence listing, but these sequences
CC differ.
XX
SQ Sequence 4442 BP; 877 A; 1300 C; 1350 G; 915 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.84e-19 Length: 4442
Score: 306.50 Matches: 69
Percent Similarity: 87.3% Conservative: 0
Best Local Similarity: 87.3% Mismatches: 3
Query Match: 83.3% Indels: 7
DB: 14 Gaps: 2

US-10-628-525A-36 (1-74) x ADW87815 (1-4442)
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 1127 ATGGCGGCTCTGGCCACGTCGCAGCTCGTCGAACGCGCGCCGCTGGGGCGTCCCGGAC 1186
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
DB 1187 GCGTCCACGTTCCG 1246
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArg----- 55
DB 1247 GCGGACACGCTCAGCATGCGGACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1306
QY 56 HisGlnGlnGlnAlaArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB 1307 CAGCAGCAGCAGCG 1357

RESULT 18
ADW87798
ID ADW87798 standard; DNA; 4470 BP.
XX
AC ADW87798;
XX
DT 07-APR-2005 (first entry)
XX
DE Corn line HO1001 granule bound starch synthase (GBSS) gene.
XX
KW Seed oil; feedstuff; food; crop improvement; transgenic plant;
KW granule bound starch synthase; single nucleotide polymorphism; SNP;
KW SNP detection; plant; gene; ds.
XX
OS Zea mays.
XX
FH Key
FH variation Location/Qualifiers
FT replace(158,T)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism"
FT replace(343,A)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism"
FT replace(349,A)
FT /*tag= c
FT /standard_name= "Single nucleotide polymorphism"
FT replace(441,A)
FT /*tag= d
FT /standard_name= "Single nucleotide polymorphism"
FT replace(1450,A)
FT /*tag= e
FT /standard_name= "Single nucleotide polymorphism"
FT replace(1709,C)
FT /*tag= f
FT /standard_name= "Single nucleotide polymorphism"
FT replace(1761,T)
FT /*tag= g
FT /standard_name= "Single nucleotide polymorphism"
FT replace(1836,A)
FT /*tag= h
FT /standard_name= "Single nucleotide polymorphism"
FT
```

| Qy                | 1           | MetaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp                | 20   |
|-------------------|-------------|---------------------------------------------------------------------------|------|
| Db                | 1143        | ATGGCGGCTCTGGCCACGTCGTCGACGCGCGCGCGCTGGCGGCTCCCGGAC                       | 1202 |
| Qy                | 21          | AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla                 | 40   |
| Db                | 1203        | GGCTCCACGTTCCCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCGCGCG                      | 1262 |
| Qy                | 41          | AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArg                             | 55   |
| Db                | 1263        | GGGACACGCTCAGATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG                      | 1322 |
| Qy                | 56          | HisGlnGlnAlaArgGlyGlyArgPheProPheProSerLeuValValCys                       | 74   |
| Db                | 1323        | CAGCAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG                      | 1373 |
| RESULT            | 19          |                                                                           |      |
| ID                | AAK63355    |                                                                           |      |
| XX                | AAK63355    | standard; cDNA; 2267 BP.                                                  |      |
| AC                | AAK63355;   |                                                                           |      |
| XX                | 16-JUL-1999 | (first entry)                                                             |      |
| XX                |             | Granule bound starch synthase encoding cDNA.                              |      |
| XX                |             | Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate;       |      |
| XX                |             | granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;     |      |
| XX                |             | modulation; gene expression; transgenic plant; cleavage; canola plant;    |      |
| XX                |             | caffeine synthesis; coffee plant; nicotine production; tobacco;           |      |
| XX                |             | fruit ripening; flower pigmentation; lignin production; ss.               |      |
| XX                |             | Zea mays.                                                                 |      |
| XX                |             | WO9710328-A2.                                                             |      |
| XX                |             | 20-MAR-1997.                                                              |      |
| XX                |             | 12-JUL-1996; 96WO-US011689.                                               |      |
| XX                |             | 13-JUL-1995; 95US-0001135P.                                               |      |
| XX                |             | (RIBO-) RIBOZYME PHARM INC.                                               |      |
| XX                |             | (DOWC) DOWELANCO.                                                         |      |
| XX                |             | Zwick MG, Edington BE, Mcswiggen JA, Merlo PAO, Guo L, Skokut TA;         |      |
| XX                |             | Young SA, Folkerts O, Merlo DJ;                                           |      |
| XX                |             | WPI; 1997-202224/18.                                                      |      |
| XX                |             | Ribozyme which modulates plant gene expression - preferably modulates     |      |
| XX                |             | expression of DELTA-9 desaturase or granule bound starch synthase in      |      |
| XX                |             | maize or canola.                                                          |      |
| XX                |             | Example 9; Page 31-33; 155pp; English.                                    |      |
| XX                |             | The present invention describes an enzymatic nucleic acid molecule (I)    |      |
| XX                |             | with RNA cleaving activity, which modulates the expression of a plant     |      |
| XX                |             | gene. Also described is a gene comprising a cDNA sequence encoding maize  |      |
| XX                |             | Delta-9 desaturase. (I) can be used to modulate expression of a gene,     |      |
| XX                |             | preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)   |      |
| XX                |             | gene, in a plant (preferably a maize or canola plant). (I) can be used to |      |
| XX                |             | modulate caffeine synthesis in a coffee plant, nicotine production in a   |      |
| XX                |             | tobacco plant, fruit ripening processes in an apple, tomato, pear, plum   |      |
| XX                |             | or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or  |      |
| XX                |             | marigold plant or lignin production in a tobacco, aspen, poplar or pine   |      |
| XX                |             | plant                                                                     |      |
| XX                |             | Sequence 2267 BP; 465 A; 699 C; 733 G; 370 T; 0 U; 0 Other;               |      |
| XX                |             | SQ                                                                        |      |
| Alignment Scores: |             |                                                                           |      |
| Pred. No.:        |             | 4.19e-18                                                                  | 2267 |



PF 01-JUN-2001; 2001WO-US017672.  
XX  
PR 01-JUN-2000; 2000US-0208538P.  
PR 30-OCT-2000; 2000US-0244989P.  
PR 27-MAR-2001; 2001US-00818875.  
XX  
PA (UYDE ) UNIV DELAWARE.  
XX  
PI Kmiec EB, Gamper HB, Rice MC, Kim J;  
XX WPI; 2002-106307/14.  
DR  
XX  
XX New oligonucleotides with modified nuclease-resistant termini, useful for  
PT creating plants with desired phenotypes, e.g. stress tolerance, improved  
PT nutritional value, herbicide or disease resistance, or modified oil  
PT production.  
XX  
PS Claim 7; Page 165; 220pp; English.  
XX  
CC The invention relates to an oligonucleotide for targeted alteration of a  
CC genetic sequence, which comprises a single-stranded oligonucleotide  
CC having a DNA domain. The DNA domain has at least one mismatch with  
CC respect to the genetic sequence to be altered and further comprises  
CC chemical modifications of the oligonucleotide. The chemical modifications  
CC consist of O-methyl modification, an RNA modification, two or more  
CC phosphorothioate linkages on a terminus, or a combination of any two or  
CC more of these modifications. The oligonucleotides are useful for  
CC directing repair or alteration of plant genetic information. The  
CC oligonucleotides are particularly useful for creating plants with desired  
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
CC nutritional value (e.g. altering amino acid content of plants or  
CC conferring amino acid over production), herbicide resistance (e.g.  
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
CC resistance, porphyrin herbicide resistance or triazine resistance),  
CC disease resistance, modified oil production, modified starch production  
CC (e.g. increased starch or production of waxy starch), altered floral  
CC morphology (e.g. male-sterile plants) or modified fatty acid content  
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
CC The oligonucleotides are also useful for producing albino mutants for the  
CC analysis of photosynthetic processes. This sequence represents a genome  
CC altering oligonucleotide of the invention  
XX  
SQ Sequence 121 BP; 15 A; 48 C; 50 G; 8 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 2.3e-09 Length: 121  
Score: 183.00 Matches: 38  
Percent Similarity: 97.4% Conservative: 0  
Best Local Similarity: 97.4% Mismatches: 1  
Query Match: 49.7% Indels: 0  
DB: 6 Gaps: 0  
  
US-10-628-525A-36 (1-74) x ABK26693 (1-121)  
  
QY 19 ProAspAlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSer 38  
Db 3 CGGACGCGTCCACGTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTAG 62  
  
QY 39 AlaAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln 57  
Db 63 GCGGCGCGCGGACACGCTCAGCATGCGGACACGCGCGCGCGCGCGCGCGCGCGCGCAG 119  
  
RESULT 22  
ADN45385/c  
ID ADN45385 standard; DNA; 121 BP.  
XX  
AC ADN45385;  
XX  
XX 15-JUL-2004 (first entry)  
XX  
DE Mutant cell identification-related mutagenic oligonucleotide SeqID2054.  
XX  
XX cell identification; oligonucleotide-directed sequence alteration;  
KW

KW selectable phenotype; transgenic plant; herbicide resistance;  
KW sterile plant; abiotic stress tolerance; albino plant;  
KW amino acid production; ss.  
XX  
OS Zea mays.  
OS Synthetic.  
XX  
PN WO2004033708-A2.  
XX  
PD 22-APR-2004.  
XX  
XX 07-OCT-2003; 2003WO-US031862.  
PF  
XX 07-OCT-2002; 2002US-0416983P.  
PR  
PR 07-MAR-2003; 2003US-0453360P.  
XX  
XX (UYDE ) UNIV DELAWARE.  
PA  
PA (NAPR-) NAPRO BIO THERAPEUTICS INC.  
XX  
XX Kmiec EB, Van Brabant A;  
PI  
XX WPI; 2004-340941/31.  
DR  
XX  
XX Identifying a cell with a desired oligonucleotide-directed sequence  
PT alteration at a nucleic acid target site within the cell by identifying  
PT the desired sequence alteration in cells selected for the presence of a  
PT selectable phenotype.  
XX  
PS Example 28; SEQ ID NO 2054; 303pp; English.  
XX  
CC This invention relates to a novel method of identifying a cell having a  
CC desired oligonucleotide-directed sequence alteration at a first nucleic  
CC acid target site within the cell. The method comprises identifying the  
CC desired sequence alteration in cells that have been selected for the  
CC presence of a selectable phenotype conferred by a concurrent  
CC oligonucleotide-directed sequence alteration at a second nucleic acid  
CC target site within the cells. The method is useful in identifying a cell  
CC having a desired oligonucleotide-directed sequence alteration at a first  
CC nucleic acid target site within the cell. The method may be useful for  
CC the production of plants with herbicide resistance, male or female  
CC sterile plants, abiotic stress tolerance, albino plants or plants with  
CC altered amino acid production as well as for use in mammalian cell lines.  
CC The present sequence is that of a mutagenic oligonucleotide which was  
CC used in the exemplification of the invention.  
XX  
SQ Sequence 121 BP; 8 A; 50 C; 48 G; 15 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 2.3e-09 Length: 121  
Score: 183.00 Matches: 38  
Percent Similarity: 97.4% Conservative: 0  
Best Local Similarity: 97.4% Mismatches: 1  
Query Match: 49.7% Indels: 0  
DB: 12 Gaps: 0  
  
US-10-628-525A-36 (1-74) x ADN45385 (1-121)  
  
QY 19 ProAspAlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSer 38  
Db 119 CGGACGCGTCCACGTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTAG 60  
  
QY 39 AlaAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln 57  
Db 59 GCGGCGCGGACACGCTCAGCATGCGGACACGCGCGCGCGCGCGCGCGCGCGCGCAG 3  
  
RESULT 23  
ADN45384  
ID ADN45384 standard; DNA; 121 BP.  
XX  
AC ADN45384;  
XX  
XX 15-JUL-2004 (first entry)  
XX  
XX





Best Local Similarity: 95.0% Mismatches: 2  
Query Match: 47.6% Indels: 0  
DB: 6 Gaps: 0

US-10-628-525A-36 (1-74) x ABK26690 (1-121)

QY 10 ValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAla 29  
DB 121 GTCGCAACGCGCGCGCTGGCGGTCCGCGACGGTCCACGTTCGCGCGCGCGCGG 62  
QY 30 GlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSer 49  
DB 61 TAGGGCCTGAGGGGGCGCGCGTGGCGGGCGGCGGACACGCTCAGCATGGGACCAGC 2

RESULT 25

ABK26689

ID ABK26689 standard; DNA; 121 BP.

AC ABK26689;

DT 09-APR-2002 (first entry)

DE Waxy starch production genome altering oligonucleotide #345.

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
KW o-methyl modification; LNA modification; phosphorothioate linkage;  
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;  
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;  
KW amino acid over production; herbicide resistance; glyphosate resistance;  
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
KW porphyrin herbicide resistance; triazine resistance; disease resistance;  
KW modified oil production; modified starch production; waxy starch;  
KW altered floral morphology; male-sterile plant; albino mutant;  
KW modified fatty acid content; reduced palmitate production; albino plant;  
KW increased stearate production; reduced linolenic acid production;  
KW photosynthetic process.

XX Zea mays.

OS Synthetic.

XX WO200192512-A2.

PD 06-DEC-2001.

XX 01-JUN-2001; 2001WO-US017672.

XX 01-JUN-2000; 2000US-0208538P.

PR 30-OCT-2000; 2000US-0244989P.

PR 27-MAR-2001; 2001US-00818875.

XX (UYDE ) UNIV DELAWARE.

XX Kmiec EB, Gamper HB, Rice MC, Kim J;

XX WPI; 2002-106307/14.

XX New oligonucleotides with modified nuclease-resistant termini, useful for  
PT creating plants with desired phenotypes, e.g. stress tolerance, improved  
PT nutritional value, herbicide or disease resistance, or modified oil  
PT production.

PS Claim 7; Page 165; 220pp; English.

XX The invention relates to an oligonucleotide for targeted alteration of a  
CC genetic sequence, which comprises a single-stranded oligonucleotide  
CC having a DNA domain. The DNA domain has at least one mismatch with  
CC respect to the genetic sequence to be altered and further comprises  
CC chemical modifications of the oligonucleotide. The chemical modifications  
CC consist of o-methyl modification, an RNA modification, two or more  
CC phosphorothioate linkages on a terminus, or a combination of any two or  
CC more of these modifications. The oligonucleotides are useful for  
CC directing repair or alteration of plant genetic information. The  
CC oligonucleotides are particularly useful for creating plants with desired

CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
CC nutritional value (e.g. altering amino acid content of plants or  
CC conferring amino acid over production), herbicide resistance (e.g.  
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
CC resistance, porphyrin herbicide resistance or triazine resistance),  
CC disease resistance, modified oil production, modified starch production  
CC (e.g. increased starch or production of waxy starch), altered floral  
CC morphology (e.g. male-sterile plants) or modified fatty acid content  
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
CC The oligonucleotides are also useful for producing albino mutants for the  
CC analysis of photosynthetic processes. This sequence represents a genome  
CC altering oligonucleotide of the invention

SQ Sequence 121 BP; 12 A; 46 C; 52 G; 11 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.33e-08 Length: 121  
Score: 175.00 Matches: 38  
Percent Similarity: 95.0% Conservative: 0  
Best Local Similarity: 95.0% Mismatches: 2  
Query Match: 47.6% Indels: 0  
DB: 6 Gaps: 0

US-10-628-525A-36 (1-74) x ABK26689 (1-121)

QY 10 ValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAla 29  
DB 1 GTCGCAACGCGCGCGCTGGCGGTCCGCGACGGTCCACGTTCGCGCGCGCGCGG 60  
QY 30 GlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSer 49  
DB 61 TAGGGCCTGAGGGGGCGCGCGTGGCGGGCGGCGGACACGCTCAGCATGGGACCAGC 120

RESULT 26

ADN45381/c

ID ADN45381 standard; DNA; 121 BP.

XX ADN45381;

XX 15-JUL-2004 (first entry)

DE Mutant cell identification-related mutagenic oligonucleotide SeqID2050.

XX cell identification; oligonucleotide-directed sequence alteration;

XX selectable phenotype; transgenic plant; herbicide resistance;

XX sterile plant; abiotic stress tolerance; albino plant;

XX amino acid production; ss.

OS Zea mays.

OS Synthetic.

XX WO2004033708-A2.

XX 22-APR-2004.

XX 07-OCT-2003; 2003WO-US031862.

XX 07-OCT-2002; 2002US-0416983P.

PR 07-MAR-2003; 2003US-0453360P.

XX (UYDE ) UNIV DELAWARE.

XX (NAPR-) NAPRO BIO THERAPEUTICS INC.

XX Kmiec EB, Van Brabant A;

XX WPI; 2004-340941/31.

XX Identifying a cell with a desired oligonucleotide-directed sequence  
PT alteration at a nucleic acid target site within the cell by identifying  
PT the desired sequence alteration in cells selected for the presence of a  
PT selectable phenotype.

PS Example 28; SEQ ID NO 2050; 303pp; English.

XX This invention relates to a novel method of identifying a cell having a  
 CC desired oligonucleotide-directed sequence alteration at a first nucleic  
 CC acid target site within the cell. The method comprises identifying the  
 CC desired sequence alteration in cells that have been selected for the  
 CC presence of a selectable phenotype conferred by a concurrent  
 CC oligonucleotide-directed sequence alteration at a second nucleic acid  
 CC target site within the cells. The method is useful in identifying a cell  
 CC having a desired oligonucleotide-directed sequence alteration at a first  
 CC nucleic acid target site within the cell. The method may be useful for  
 CC the production of plants with herbicide resistance, male or female  
 CC sterile plants, abiotic stress tolerance, albino plants or plants with  
 CC altered amino acid production as well as for use in mammalian cell lines.  
 CC The present sequence is that of a mutagenic oligonucleotide which was  
 CC used in the exemplification of the invention.

XX SQ Sequence 121 BP; 11 A; 52 C; 46 G; 12 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1.33e-08 Length: 121  
 Score: 175.00 Matches: 38  
 Percent Similarity: 95.0% Conservative: 0  
 Best Local Similarity: 95.0% Mismatches: 2  
 Query Match: 47.6% Indels: 0  
 DB: 12 Gaps: 0

US-10-628-525A-36 (1-74) x ADM45381 (1-121)

QY 10 ValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAala 29  
 DB 121 GTGCAACGGCGCGCGGCTGGGGCGTCCGGAGCGGTCCACGTTCCGCCGCGCGCG 62  
 QY 30 GlnGlyLeuArgGlyAlaArgAlaSerAlaAalaAspThrLeuSerMetArgThrSer 49  
 DB 61 TAGGGCTGTAGGGGGGCGCGCGGTGCGGGCGGCGGACACGCTCAGCATGCGGACCAGC 2

#### RESULT 27

ADM45380  
 ID ADM45380 standard; DNA; 121 BP.

XX AC ADM45380;

XX DT 15-JUL-2004 (first entry)

XX DE Mutant cell identification-related mutagenic oligonucleotide SeqID2049.

XX KW cell identification; oligonucleotide-directed sequence alteration;  
 KW selectable phenotype; transgenic plant; herbicide resistance;  
 KW sterile plant; abiotic stress tolerance; albino plant;  
 KW amino acid production; ss.

XX OS Zea mays.  
 OS Synthetic.

XX PN WO2004033708-A2.

XX PD 22-APR-2004.

XX PF 07-OCT-2003; 2003WO-US031862.

XX PR 07-OCT-2002; 2002US-0416983P.

XX PR 07-MAR-2003; 2003US-0453360P.

XX PR (UYDE ) UNIV DELAWARE.

PA (NAPR-) NAPRO BIO THERAPEUTICS INC.

XX PI Kmiec EB, Van Brabant A;

XX DR WPI; 2004-340941/31.

XX Identifying a cell with a desired oligonucleotide-directed sequence  
 PT alteration at a nucleic acid target site within the cell by identifying  
 PT the desired sequence alteration in cells selected for the presence of a

#### selectable phenotype.

XX Example 28; SEQ ID NO 2049; 303pp; English.

XX This invention relates to a novel method of identifying a cell having a  
 CC desired oligonucleotide-directed sequence alteration at a first nucleic  
 CC acid target site within the cell. The method comprises identifying the  
 CC desired sequence alteration in cells that have been selected for the  
 CC presence of a selectable phenotype conferred by a concurrent  
 CC oligonucleotide-directed sequence alteration at a second nucleic acid  
 CC target site within the cells. The method is useful in identifying a cell  
 CC having a desired oligonucleotide-directed sequence alteration at a first  
 CC nucleic acid target site within the cell. The method may be useful for  
 CC the production of plants with herbicide resistance, male or female  
 CC sterile plants, abiotic stress tolerance, albino plants or plants with  
 CC altered amino acid production as well as for use in mammalian cell lines.  
 CC The present sequence is that of a mutagenic oligonucleotide which was  
 CC used in the exemplification of the invention.

XX SQ Sequence 121 BP; 12 A; 46 C; 52 G; 11 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1.33e-08 Length: 121  
 Score: 175.00 Matches: 38  
 Percent Similarity: 95.0% Conservative: 0  
 Best Local Similarity: 95.0% Mismatches: 2  
 Query Match: 47.6% Indels: 0  
 DB: 12 Gaps: 0

US-10-628-525A-36 (1-74) x ADM45380 (1-121)

QY 10 ValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAala 29

DB 1 GTGCAACGGCGCGCGGCTGGGGCGTCCGGAGCGGTCCACGTTCCGCCGCGCGCG 60

QY 30 GlnGlyLeuArgGlyAlaArgAlaSerAlaAalaAspThrLeuSerMetArgThrSer 49

DB 61 TAGGGCTGTAGGGGGGCGCGCGGTGCGGGCGGCGGACACGCTCAGCATGCGGACCAGC 120

#### RESULT 28

ABK26698/C

ID ABK26698 standard; DNA; 121 BP.

XX AC ABK26698;

XX DT 09-APR-2002 (first entry)

XX DE Waxy starch production genome altering oligonucleotide #354.

XX KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
 KW o-methyl modification; LNA modification; phosphorothioate linkage;  
 KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;  
 KW abiotic stress tolerance; improved nutritional value; hygromycin-B;  
 KW amino acid over production; herbicide resistance; glyphosate resistance;  
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;  
 KW modified oil production; modified starch production; waxy starch;  
 KW altered floral morphology; male-sterile plant; albino mutant;  
 KW modified fatty acid content; reduced palmitate production; albino plant;  
 KW increased stearate production; reduced linolenic acid production;  
 KW photosynthetic process.

XX OS Zea mays.

OS Synthetic.

XX PN WO200192512-A2.

XX PD 06-DEC-2001.

XX PF 01-JUN-2001; 2001WO-US017672.

XX PR 01-JUN-2000; 2000US-0208538P.

XX PR 30-OCT-2000; 2000US-0244989P.



QY 57 GlnGlnGlnAlaArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 61 TAGCAGCAGGCGCGCGCGGCGAGG-----TTCCCGTGGCTCGTGTGC 108

RESULT 30  
 ADN45388  
 ID ADN45388 standard; DNA; 121 BP.  
 XX  
 AC ADN45388;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Mutant cell identification-related mutagenic oligonucleotide SeqID2057.  
 XX  
 KW cell identification; oligonucleotide-directed sequence alteration;  
 KW selectable phenotype; transgenic plant; herbicide resistance;  
 KW sterile plant; abiotic stress tolerance; albino plant;  
 KW amino acid production; ss.  
 XX  
 OS Zea mays.  
 OS Synthetic.  
 XX  
 PN WO2004033708-A2.  
 XX  
 PD 22-APR-2004.  
 XX  
 PF 07-OCT-2003; 2003WO-US031862.  
 XX  
 PR 07-OCT-2002; 2002US-0416983P.  
 PR 07-MAR-2003; 2003US-0453360P.  
 XX  
 PA (UYDE ) UNIV DELAWARE.  
 PA (NAPR-) NAPRO BIO THERAPEUTICS INC.  
 XX  
 PI Kmiec EB, Van Brabant A;  
 XX  
 DR WPI; 2004-340941/31.  
 XX  
 PT Identifying a cell with a desired oligonucleotide-directed sequence  
 PT alteration at a nucleic acid target site within the cell by identifying  
 PT the desired sequence alteration in cells selected for the presence of a  
 PT selectable phenotype.  
 XX  
 PS Example 28; SEQ ID NO 2057; 303pp; English.  
 XX  
 CC This invention relates to a novel method of identifying a cell having a  
 CC desired oligonucleotide-directed sequence alteration at a first nucleic  
 CC acid target site within the cell. The method comprises identifying the  
 CC desired sequence alteration in cells that have been selected for the  
 CC presence of a selectable phenotype conferred by a concurrent  
 CC oligonucleotide-directed sequence alteration at a second nucleic acid  
 CC target site within the cells. The method is useful in identifying a cell  
 CC having a desired oligonucleotide-directed sequence alteration at a first  
 CC nucleic acid target site within the cell. The method may be useful for  
 CC the production of plants with herbicide resistance, male or female  
 CC sterile plants, abiotic stress tolerance, albino plants or plants with  
 CC altered amino acid production as well as for use in mammalian cell lines.  
 CC The present sequence is that of a mutagenic oligonucleotide which was  
 CC used in the exemplification of the invention.  
 XX  
 SQ Sequence 121 BP; 14 A; 46 C; 50 G; 11 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 4.42e-07 Length: 121  
 Score: 159.00 Matches: 35  
 Percent Similarity: 92.1% Conservative: 0  
 Best Local Similarity: 92.1% Mismatches: 1  
 Query Match: 43.2% Indels: 2  
 DB: 12 Gaps: 1

US-10-628-525A-36 (1-74) x ADN45388 (1-121)

QY 37 AlaSerAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHis 56

Db 1 GCCTCGCGCGCGCGGACACGCTCAGCATGCGGACACAGCGCGCGCGCGGCGCAC 60  
 QY 57 GlnGlnGlnAlaArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 61 TAGCAGCAGGCGCGCGCGGCGAGG-----TTCCCGTGGCTCGTGTGC 108

Search completed: April 1, 2006, 04:26:16  
 Job time : 183.223 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 15:18:57 ; Search time 1193.34 Seconds  
(without alignments)  
2901.306 Million cell updates/sec

Title: US-10-628-525a-36

Perfect score: 368

Sequence: 1 MAALATSQLVATAGHVPD.....RHQQQARRGRPPFPLVVC 74

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150  
-DOALIGN=200 -THR\_SCORE=pcp -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=pcp -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abse06h  
-USER=US10628525 @CGN\_1\_11098 @runat\_31032006\_095118\_16742 -NCPU=6 -ICPU=3  
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hc1:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gse1:\*  
10: gb\_gse2:\*  
11: gb\_gse3:\*

c

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description        |
|------------|-------|---------------|--------|----|--------------------|
| 1          | 333   | 90.5          | 735    | 7  | CO455159           |
| 2          | 333   | 90.5          | 771    | 6  | CD440347           |
| 3          | 333   | 90.5          | 803    | 7  | CO460657           |
| 4          | 333   | 90.5          | 805    | 7  | CO456300           |
| 5          | 333   | 90.5          | 811    | 7  | CO469376           |
| 6          | 333   | 90.5          | 812    | 7  | CO461143           |
| 7          | 333   | 90.5          | 813    | 7  | CO464185           |
|            |       |               |        |    | CO464185 MZCCL1504 |

|    |       |      |     |   |          |
|----|-------|------|-----|---|----------|
| 8  | 333   | 90.5 | 816 | 7 | CO462292 |
| 9  | 333   | 90.5 | 828 | 7 | CO460606 |
| 10 | 333   | 90.5 | 830 | 7 | CO456895 |
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| 12 | 333   | 90.5 | 844 | 7 | CO455063 |
| 13 | 333   | 90.5 | 849 | 7 | CO455764 |
| 14 | 333   | 90.5 | 850 | 7 | CO456306 |
| 15 | 333   | 90.5 | 853 | 7 | CO460568 |
| 16 | 333   | 90.5 | 854 | 7 | CO464201 |
| 17 | 333   | 90.5 | 858 | 7 | CO468515 |
| 18 | 333   | 90.5 | 860 | 7 | CO458241 |
| 19 | 333   | 90.5 | 863 | 7 | CO457215 |
| 20 | 333   | 90.5 | 873 | 7 | CO463484 |
| 21 | 333   | 90.5 | 876 | 7 | CO461256 |
| 22 | 333   | 90.5 | 880 | 7 | CO462929 |
| 23 | 333   | 90.5 | 883 | 7 | CO463816 |
| 24 | 333   | 90.5 | 893 | 7 | CO462071 |
| 25 | 333   | 90.5 | 895 | 7 | CO459176 |
| 26 | 333   | 90.5 | 895 | 7 | CO463621 |
| 27 | 333   | 90.5 | 903 | 7 | CO456060 |
| 28 | 333   | 90.5 | 911 | 7 | CO460347 |
| 29 | 333   | 90.5 | 927 | 7 | CO464483 |
| 30 | 329   | 89.4 | 785 | 7 | CO457630 |
| 31 | 329   | 89.4 | 869 | 7 | CO463624 |
| 32 | 327   | 88.9 | 857 | 7 | CO460324 |
| 33 | 326   | 88.6 | 825 | 6 | CD433331 |
| 34 | 324   | 88.0 | 781 | 7 | CO466939 |
| 35 | 319   | 86.7 | 883 | 7 | CO463466 |
| 36 | 316.5 | 86.0 | 709 | 7 | CO467050 |
| 37 | 316.5 | 86.0 | 904 | 7 | CO459604 |
| 38 | 316.5 | 86.0 | 910 | 7 | CO456170 |
| 39 | 316   | 85.9 | 822 | 7 | CO459171 |
| 40 | 314   | 85.3 | 883 | 7 | CO456807 |
| 41 | 307   | 83.4 | 594 | 6 | CD440356 |
| 42 | 304   | 82.6 | 797 | 7 | CO463719 |
| 43 | 304   | 82.6 | 882 | 7 | CO467445 |
| 44 | 304   | 82.6 | 938 | 7 | CO454267 |
| 45 | 303.5 | 82.5 | 905 | 7 | CO456470 |
| 46 | 295   | 80.2 | 832 | 7 | CO465006 |
| 47 | 294   | 79.9 | 621 | 7 | CO460486 |
| 48 | 293   | 79.6 | 436 | 8 | DR824971 |
| 49 | 293   | 79.6 | 495 | 8 | DR789179 |
| 50 | 293   | 79.6 | 536 | 6 | CF647689 |
| 51 | 293   | 79.6 | 546 | 7 | CO525196 |
| 52 | 293   | 79.6 | 598 | 8 | DR795136 |
| 53 | 293   | 79.6 | 606 | 8 | DR795417 |
| 54 | 293   | 79.6 | 615 | 9 | BZ525328 |
| 55 | 293   | 79.6 | 620 | 7 | CO533103 |
| 56 | 293   | 79.6 | 620 | 8 | DR795335 |
| 57 | 293   | 79.6 | 648 | 8 | CO530133 |
| 58 | 293   | 79.6 | 648 | 8 | DR800471 |
| 59 | 293   | 79.6 | 652 | 8 | DR795561 |
| 60 | 293   | 79.6 | 656 | 8 | DR564842 |
| 61 | 293   | 79.6 | 658 | 7 | CO525078 |
| 62 | 293   | 79.6 | 685 | 7 | CO518712 |
| 63 | 293   | 79.6 | 692 | 8 | DR969773 |
| 64 | 293   | 79.6 | 695 | 8 | DR817915 |
| 65 | 293   | 79.6 | 696 | 8 | DR822256 |
| 66 | 293   | 79.6 | 698 | 8 | DR797257 |
| 67 | 293   | 79.6 | 706 | 8 | DR826952 |
| 68 | 293   | 79.6 | 724 | 8 | DR803147 |
| 69 | 293   | 79.6 | 724 | 8 | DR824972 |
| 70 | 293   | 79.6 | 726 | 8 | DR814212 |
| 71 | 293   | 79.6 | 727 | 8 | DR964919 |
| 72 | 293   | 79.6 | 728 | 8 | DR830479 |
| 73 | 293   | 79.6 | 728 | 8 | DR968616 |
| 74 | 293   | 79.6 | 730 | 8 | DR968586 |
| 75 | 293   | 79.6 | 732 | 8 | DR966935 |
| 76 | 293   | 79.6 | 734 | 8 | DR792755 |
| 77 | 293   | 79.6 | 742 | 8 | DR965242 |
| 78 | 293   | 79.6 | 743 | 8 | DR820739 |
| 79 | 293   | 79.6 | 745 | 7 | CO527273 |
| 80 | 293   | 79.6 | 754 | 8 | DR797255 |

|          |           |
|----------|-----------|
| CO462292 | MZCCS1502 |
| CO460606 | MZCCL2002 |
| CO456895 | MZCCL2001 |
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| CO460568 | MZCCL1502 |
| CO464201 | MZCCL1504 |
| CO468515 | MZCCS1504 |
| CO458241 | MZCCS1501 |
| CO457215 | MZCCL2001 |
| CO463484 | MZCCL2003 |
| CO461256 | MZCCL1503 |
| CO462929 | MZCCL2003 |
| CO463816 | MZCCL1503 |
| CO462071 | MZCCS2002 |
| CO459176 | MZCCS1501 |
| CO463621 | MZCCL2003 |
| CO456060 | MZCCL2001 |
| CO460347 | MZCCL1502 |
| CO464483 | MZCCS1503 |
| CO457630 | MZCCS1501 |
| CO463624 | MZCCL2003 |
| CO460324 | MZCCL1502 |
| CD433331 | EL01N0307 |
| CO466939 | MZCCL2004 |
| CO463466 | MZCCL1503 |
| CO467050 | MZCCL2004 |
| CO459604 | MZCCL2002 |
| CO456170 | MZCCS2000 |
| CO459171 | MZCCS1501 |
| CO456807 | MZCCS1500 |
| CD440356 | EL01N0553 |
| CO463719 | MZCCL1503 |
| CO467445 | MZCCL2000 |
| CO454267 | MZCCL1020 |
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| CO465006 | MZCCL1504 |
| CO460486 | MZCCL1502 |
| DR824971 | MZ_BFB006 |
| DR789179 | MZ_BFB000 |
| CF647689 | 3530_1_46 |
| CO525196 | 3530_1_16 |
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| BZ525328 | OGAGQ38TC |
| CO533103 | 3530_1_21 |
| DR795335 | MZ_BFB001 |
| CO530133 | 3530_1_19 |
| DR800471 | MZ_BFB002 |
| DR795561 | MZ_BFB001 |
| DR964842 | MZ_BFB008 |
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| CO518712 | 3530_1_12 |
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| DR822256 | MZ_BFB006 |
| DR797257 | MZ_BFB001 |
| DR826952 | MZ_BFB006 |
| DR803147 | MZ_BFB002 |
| DR824972 | MZ_BFB006 |
| DR814212 | MZ_BFB004 |
| DR964919 | MZ_BFB008 |
| DR830479 | MZ_BFB007 |
| DR968616 | MZ_BFB009 |
| DR968586 | MZ_BFB008 |
| DR966935 | MZ_BFB008 |
| DR792755 | MZ_BFB001 |
| DR965242 | MZ_BFB008 |
| DR820739 | MZ_BFB005 |
| CO527273 | 3530_1_18 |
| DR797255 | MZ_BFB001 |



|       |       |      |      |    |                   |                      |                                                                    |
|-------|-------|------|------|----|-------------------|----------------------|--------------------------------------------------------------------|
| 81    | 293   | 79.6 | 776  | 8  | DR821516          | DR821516 ZM BFB006   | RESULT 1                                                           |
| 82    | 293   | 79.6 | 780  | 7  | CO518868          | CO518868 3530_1_12   | CO455159                                                           |
| 83    | 293   | 79.6 | 782  | 8  | DR804832          | DR804832 ZM BFB003   | LOCUS                                                              |
| 84    | 293   | 79.6 | 786  | 8  | DR814441          | DR814441 ZM BFB004   | DEFINITION                                                         |
| 85    | 293   | 79.6 | 789  | 8  | DR968570          | DR968570 ZM BFB008   | sequence.                                                          |
| 86    | 293   | 79.6 | 790  | 8  | DR823764          | DR823764 ZM BFB006   | CO455159                                                           |
| 87    | 293   | 79.6 | 790  | 8  | DR830404          | DR830404 ZM BFB007   | CO455159.1                                                         |
| 88    | 293   | 79.6 | 806  | 8  | DR797875          | DR797875 ZM BFB002   | GI:67026410                                                        |
| 89    | 293   | 79.6 | 809  | 8  | DR814663          | DR814663 ZM BFB004   | EST.                                                               |
| 90    | 293   | 79.6 | 812  | 10 | CG261938          | CG261938 OGYAE73TH   | Ze mays                                                            |
| 91    | 293   | 79.6 | 826  | 8  | DR794686          | DR794686 ZM BFB001   | Ze mays                                                            |
| 92    | 293   | 79.6 | 837  | 8  | DR825687          | DR825687 ZM BFB006   | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; |
| 93    | 293   | 79.6 | 864  | 8  | DR808766          | DR808766 ZM BFB003   | Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  |
| 94    | 290   | 78.0 | 877  | 7  | CO467381          | CO467381 MZCCL2000   | clade; Panicoideae; Andropogoneae; Zea.                            |
| 95    | 287   | 78.0 | 834  | 9  | CC726093          | CC726093 OGWEL189TV  | 1 (bases 1 to 735)                                                 |
| 96    | 285   | 77.4 | 694  | 10 | CU983517          | CU983517 ZMWBDH000   | REFERENCE                                                          |
| 97    | 284   | 77.2 | 401  | 6  | CF649007          | CF649007 3530_1_62   | AUTHORS                                                            |
| 98    | 284   | 77.2 | 427  | 6  | CF650004          | CF650004 3530_1_80   | Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H., |
| 99    | 277   | 75.3 | 809  | 7  | CO462949          | CO462949 MZCCL2003   | De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and    |
| 100   | 273   | 74.2 | 445  | 6  | CF647636          | CF647636 3530_1_45   | Arruda,P.                                                          |
| 101   | 262   | 71.2 | 925  | 7  | CO459474          | CO459474 MZCCL1502   | Endospore-preferred expression of maize genes as revealed by       |
| 102   | 261   | 70.9 | 296  | 6  | CF648232          | CF648232 3530_1_53   | transcriptome-wide analysis of expressed sequence tags             |
| 103   | 261   | 70.9 | 379  | 3  | BM500492          | BM500492 PACO00000   | Plant Mol. Biol. (2005) In press                                   |
| 104   | 259   | 70.4 | 381  | 8  | DR800828          | DR800828 ZM BFB002   | Contact: Arruda P                                                  |
| 105   | 251   | 68.2 | 428  | 6  | CD433222          | CD433222 ELJN0306    | Centro de Biologia Molecular e Engenharia Genetica                 |
| 106   | 250   | 67.9 | 334  | 8  | DR793659          | DR793659 ZM BFB001   | Universidade Estadual de Campinas                                  |
| c 107 | 249.5 | 67.8 | 626  | 6  | CA269213          | CA269213 SCBGR1307   | Caixa Postal 6010, 13083-970, Campinas SP, Brazil                  |
| 108   | 247   | 67.1 | 952  | 7  | CO460528          | CO460528 MZCCL1502   | Tel: 55 19 3788 1137                                               |
| c 109 | 237.5 | 64.5 | 593  | 10 | CW036057          | CW036057 104_267_1   | Fax: 55 19 3788 1089                                               |
| 110   | 237.5 | 64.5 | 636  | 6  | CF489136          | CF489136 POL1_54_G   | Email: parruda@unicamp.br.                                         |
| 111   | 237.5 | 64.5 | 669  | 10 | CW191886          | CW191886 104_614_1   | Location/Qualifiers                                                |
| 112   | 233   | 63.3 | 337  | 6  | CF648691          | CF648691 3530_1_58   | 1..735                                                             |
| 113   | 226   | 61.4 | 321  | 8  | DR787732          | DR787732 ZM BFB000   | /organism="Zea mays"                                               |
| 114   | 224.5 | 61.0 | 637  | 6  | CF486436          | CF486436 POL1_37_E   | /mol_type="mRNA"                                                   |
| 115   | 197   | 53.5 | 271  | 6  | CF244032          | CF244032 3530_1_26   | /cultivar="F-352 near isogenic line"                               |
| 116   | 185   | 50.3 | 430  | 8  | DN150586          | DN150586 5215_B02    | /db_xref="taxon:4577"                                              |
| 117   | 179   | 48.6 | 967  | 7  | CO464206          | CO464206 MZCCL1504   | /sex="hermaphrodite"                                               |
| 118   | 171   | 46.5 | 577  | 7  | CO455868          | CO455868 MZCCL2000   | /tissue type="endospERM"                                           |
| 119   | 161   | 43.8 | 283  | 6  | CF649487          | CF649487 3530_1_70   | /dev stage="multiple stages (10 to 25 days after                   |
| 120   | 145   | 39.4 | 726  | 7  | CO467589          | CO467589 MZCCL2004   | pollination, see publication for more information)"                |
| 121   | 130   | 35.3 | 263  | 3  | CF647907          | CF647907 3530_1_49   | /clone_lib="Maize EndospERM cDNA Library"                          |
| 122   | 128.5 | 34.9 | 2543 | 10 | CU957023          | CU957023 OsJURA000   | /note="Organ: seed; Vector: pSPORT1; Site 1: SalI; Site 2:         |
| 123   | 127   | 34.5 | 822  | 7  | CO467310          | CO467310 MZCCL2004   | Not; Plant Material and RNA Isolation: Field grown maize           |
| 124   | 116   | 31.5 | 757  | 6  | CF488108          | CF488108 POL1_47_G   | plants from inbred line F352 were used. Ears were                  |
| 125   | 116   | 31.5 | 829  | 7  | CO464830          | CO464830 MZCCL1504   | harvested at 10, 15, 20 and 25 days after pollination              |
| 126   | 113.5 | 30.8 | 470  | 5  | C73133            | C73133 C73133 Rice   | (DAP), seeds were cut from the ear and the upper third of          |
| 127   | 109.5 | 29.8 | 558  | 2  | BE602243          | BE602243 HVSMEH009   | the endosperms, containing only endospERM, aleurone and            |
| 128   | 109.5 | 29.8 | 586  | 3  | BM368238          | BM368238 EBed01_SQ   | pericarpal tissues, was removed, frozen in liquid nitrogen         |
| 129   | 109.5 | 29.8 | 638  | 1  | AL508959          | AL508959 AL508959    | and stored at -80o C. Frozen endosperms were pulverized in         |
| 130   | 109.5 | 29.8 | 700  | 1  | AL508163          | AL508163 AL508163    | liquid nitrogen and total RNA was isolated according the           |
| 131   | 107   | 29.1 | 631  | 7  | CV059967          | CV059967 BNEJ52h9    | method of Manning (9). Poly(A)+RNA was isolated using              |
| 132   | 105.5 | 28.7 | 513  | 1  | AL508933          | AL508933 AL508933    | Oligotex-dT. cDNA libraries were constructed using                 |
| 133   | 98.5  | 26.8 | 1619 | 4  | CR612874          | CR612874 full-length | Superscript Plasmid System for cDNA Synthesis and Plasmid          |
| 134   | 97.5  | 26.5 | 451  | 3  | BQ240789          | BQ240789 TaE05012H   | Cloning Kit as described in Vettore, et al., (2001) The            |
| 135   | 97.5  | 26.5 | 502  | 3  | BQ246003          | BQ246003 TaE15017D   | libraries that made SUCREST. Genet Mol Biol 24: 1-7. cDNAs         |
| 136   | 97.5  | 26.5 | 583  | 1  | AL812068          | AL812068 AL812068    | ranging from 500 to 800 bp in size were assigned as short          |
| 137   | 97.5  | 26.5 | 650  | 5  | BQ608470          | BQ608470 BRY_4375    | libraries (S10, S15, S20), and cDNAs >800 were assigned as         |
| c 138 | 95.5  | 25.0 | 1061 | 10 | CW932270          | CW932270 EDCC45TF    | long libraries (L10, L15, L20, L25). Unamplified                   |
| 139   | 94.5  | 25.7 | 529  | 6  | CA741461          | CA741461 wiaic.pk0   | libraries were plated and individual colonies picked and           |
| 140   | 94.5  | 25.7 | 649  | 6  | CD907459          | CD907459 G468_106P   | transferred to 96 well plates containing liquid Circle             |
| 141   | 94    | 25.5 | 460  | 3  | BQ239647          | BQ239647 TaE05028D   | Grow (CG) medium supplemented with 100 mg/L of ampicillin          |
| 142   | 94    | 25.5 | 473  | 8  | BQ245208          | BQ245208 TaE15029C   | and 8% glycerol. Three copies of each cDNA clone were              |
| c 143 | 94    | 25.5 | 474  | 8  | CX009230          | CX009230 i039d03.b   | stored at -80o C. Additional information can be found in :         |
| 144   | 94    | 25.5 | 503  | 5  | BQ606794          | BQ606794 BRY_2666    | Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,         |
| c 145 | 94    | 25.5 | 539  | 7  | CK504019          | CK504019 rswcc0_00   | Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,            |
| 146   | 94    | 25.5 | 541  | 1  | AL814469          | AL814469 AL814469    | A.L., da Silva, F.R. and Arruda, P. (2005)                         |
| 147   | 94    | 25.5 | 556  | 5  | BQ607263          | BQ607263 BRY_3155    | EndospERM-preferred expression of maize genes as revealed          |
| 148   | 94    | 25.5 | 579  | 6  | CA717812          | CA717812 wdkc.pk0    | by transcriptome-wide analysis of expressed sequence tags.         |
| 149   | 94    | 25.5 | 598  | 6  | CD890114          | CD890114 G118.1130   | Plant Molecular Biology (/in press/)"                              |
| 150   | 94    | 25.5 | 639  | 2  | BE414303          | BE414303 SCU008.C0   |                                                                    |
|       |       |      |      |    | ORIGIN            |                      |                                                                    |
|       |       |      |      |    | Alignment Scores: | 7,22e-24             | Length:                                                            |
|       |       |      |      |    | Pred. No.:        | 333.00               | Matches:                                                           |
|       |       |      |      |    | Score:            |                      | 71                                                                 |

Percent Similarity: 95.9%      Conservative: 0  
 Best Local Similarity: 95.9%      Mismatches: 1  
 Query Match: 90.5%      Indels: 2  
 DB: 7      Gaps: 1

US-10-628-525A-36 (1-74) x C0455159 (1-735)

QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
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 Db 211 ATGCGCGCTCTGCGCACATCGTCGACAGCTCGTCACACGCGCGCCGCGCTGCGCGC 270  
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 QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 |||||  
 Db 271 GCGTCCAGCTTCGCGCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCG 330  
 |||||  
 QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 |||||  
 Db 331 GCGGACACGCTCAGCATGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 390  
 |||||  
 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 |||||  
 Db 391 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGC 426  
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## RESULT 2

CD440347      771 bp      mRNA      linear      EST 03-JUN-2003  
 LOCUS  
 DEFINITION EL01N053F08.b Endosperm\_5 Zea mays cDNA, mRNA sequence.  
 ACCESSION CD440347  
 VERSION CD440347.1 GI:31355990  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 771)  
 AUTHORS Lai J., Dev N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,  
 Larkins, B., Becraft, P. and Messing, J.

TITLE Characterization of the maize endosperm transcriptome and its  
 comparison to the rice genome  
 JOURNAL Genome Res. 14 (10), 1932-1937 (2004)  
 PUBMED 15466291

COMMENT Contact: Lai, Jinheng  
 Dr. Joachim Messing's lab  
 Waksman Institute, Rutgers University  
 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA  
 Tel: 732-445-3801  
 Fax: 732-445-5735  
 Email: jlai@waksman.rutgers.edu  
 Seq primer: T3.

## FEATURES

source  
 1. .771  
 /location/Qualifiers  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="w22"  
 /db\_xref="taxon:4577"  
 /tissue\_type="Endosperm of 7-23DAP"  
 /clone\_lib="Endosperm 5"  
 /notes="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
 XhoI"

## ORIGIN

Alignment Scores:  
 Pred. No.: 7,61e-24      Length: 771  
 Score: 333.00      Matches: 71  
 Percent Similarity: 95.9%      Conservative: 0  
 Best Local Similarity: 95.9%      Mismatches: 1  
 Query Match: 90.5%      Indels: 2  
 DB: 6      Gaps: 1

US-10-628-525A-36 (1-74) x CD440347 (1-771)

QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20

Db 185 ATGCGCGCTCTGCGCACATCGTCGACAGCTCGTCACACGCGCGCCGCGCTGCGCGC 244  
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 QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 |||||  
 Db 245 GCGTCCAGCTTCGCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCG 304  
 |||||  
 QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 |||||  
 Db 305 GCGGACACGCTCAGCATGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 364  
 |||||  
 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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 Db 365 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGC 400  
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## RESULT 3

CO460657      803 bp      mRNA      linear      EST 08-JUN-2005  
 LOCUS  
 DEFINITION MZCL20024G08.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA  
 sequence.  
 ACCESSION CO460657  
 VERSION CO460657.1 GI:67031908  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 803)  
 AUTHORS Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H.,  
 De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and  
 Arruda, P.

TITLE Endosperm-preferred expression of maize genes as revealed by  
 transcriptome-wide analysis of expressed sequence tags  
 JOURNAL Plant Mol. Biol. (2005) In press  
 COMMENT Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.

## FEATURES

source  
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 /location/Qualifiers  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="P-352 near isogenic line"  
 /db\_xref="taxon:4577"  
 /sex="hermaphrodite"  
 /tissue\_type="endosperm"  
 /dev\_stage="multiple stages (10 to 25 days after  
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 /lab\_host="E. coli DH10B"  
 /clone\_lib="Maize Endosperm cDNA Library"  
 /note="Organ: seed; Vector: pSPORT1; Site\_1: SalI; Site\_2:  
 NotI; Plant Material and RNA Isolation: Field grown maize  
 plants from inbred line F352 were used. Ears were  
 harvested at 10, 15, 20 and 25 days after pollination  
 (DAP), seeds were cut from the ear and the upper third of  
 the endosperms, containing only endosperm, aleurone and  
 pericarpal tissues, was removed, frozen in liquid nitrogen  
 and stored at -80o C. Frozen endosperms were pulverized in  
 liquid nitrogen and total RNA was isolated according the  
 method of Manning (9). Poly(A)+RNA was isolated using  
 Oligotex-dT. cDNA libraries were constructed using  
 Superscript Plasmid System for cDNA Synthesis and Plasmid  
 Cloning Kit as described in Vettore, et al., (2001). The  
 libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs  
 ranging from 500 to 800 bp in size were assigned as short  
 libraries (S10, S15, S20), and cDNAs >800 were assigned as  
 long libraries (L10, L15, L20, L25). Unamplified  
 libraries were plated and individual colonies picked and  
 transferred to 96 well plates containing liquid Circle

Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -80°C. Additional information can be found in: Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) EndospERM-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (in press//)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 7,97e-24 Length: 803  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO460657 (1-803)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProasp 20  
 |||||  
 Db 171 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTCCAAACGCGCGCGCTGGCGCTCCCGGAC 230  
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QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyValaArgAlaSerAlaAla 40  
 |||||  
 Db 231 GGGTCCAGCTTCGGCGCGCGCGCGCGAGGCTGTAGGGGGCGCGCGCTCGCGGGCG 290  
 |||||

QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 |||||  
 Db 291 GCGGACACGCTCAGCATCGGACCGAGCGCGCGCGCGCGCGCCAGGACCAGCAGCAGCGG 350  
 |||||

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 |||||  
 Db 351 CGCCGGGGGGGAGG-----TTCCCGTCGCTCGTGTGTCG 386  
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RESULT 4  
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 LOCUS MZCCL15012D08.g Maize EndospERM cDNA Library Zea mays cDNA, mRNA  
 DEFINITION  
 CO456300  
 CO456300.1 GI:67027551  
 EST.  
 KEYWORDS  
 Zea mays  
 ORGANISM  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 805)  
 Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P.

## TITLE

EndospERM-preferred expression of maize genes as revealed by

## JOURNAL

transcriptome-wide analysis of expressed sequence tags

## COMMENT

Plant Mol. Biol. (2005) In press

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br.

Location/Qualifiers

1..805

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="P-352 near isogenic line"

/db\_xref="taxon:4577"

/sex="hermaphrodite"

/tissue\_type="endospERM"

/dev\_stage="multiple stages (10 to 25 days after

pollination, see publication for more information)"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="Maize EndospERM cDNA Library"  
 /note="Organ: seed; Vector: pSPORT1; Site\_1: SalI; Site\_2: NotI; Plant Material and RNA isolation: Field grown maize plants from inbred line F352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP), seeds were cut from the ear and the upper third of the endosperms, containing only endospERM, aleurone and pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -80°C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according the method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dT. cDNA libraries were constructed using SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001) The libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, M15, N15, L20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid Circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -80°C. Additional information can be found in: Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) EndospERM-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (in press//)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 7,99e-24 Length: 805  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO456300 (1-805)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProasp 20  
 |||||  
 Db 201 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTCCAAACGCGCGCGCTGGCGCTCCCGGAC 260  
 |||||

QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyValaArgAlaSerAlaAla 40  
 |||||  
 Db 261 GGGTCCAGCTTCGGCGCGCGCGCGCGAGGCTGTAGGGGGCGCGCGCTCGCGGGCG 320  
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QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 |||||  
 Db 321 GCGGACACGCTCAGCATCGGACCGAGCGCGCGCGCGCGCCAGGACCAGCAGCAGCGG 380  
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QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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 Db 381 CGCCGGGGGGGAGG-----TTCCCGTCGCTCGTGTGTCG 416  
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RESULT 5  
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 LOCUS MZCCS15042H10.g Maize EndospERM cDNA Library Zea mays cDNA, mRNA  
 DEFINITION  
 CO469376  
 CO469376.1 GI:67043121  
 EST.  
 KEYWORDS  
 Zea mays  
 ORGANISM  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 811)

**AUTHORS**  
Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H.,  
De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and  
Arruda,P.

**TITLE**  
Endosperm-preferred expression of maize genes as revealed by  
transcriptome-wide analysis of expressed sequence tags

**JOURNAL**  
Plant Mol. Biol. (2005) In press

**COMMENT**  
Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br.

**FEATURES**  
source  
Location/Qualifiers  
1..811  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="F-352 near isogenic line"  
/db\_xref="taxon:4577"  
/sex="hermaphrodite"  
/tissue\_type="endosperm"  
/dev\_stage="multiple stages (10 to 25 days after  
pollination, see publication for more information)"  
/lab\_host="E. coli DH10B"  
/clone\_lib="Maize Endosperm cDNA Library"  
/note="Organ: seed; Vector: pSPORT1; Site: 1: Sali; Site: 2:  
NotI; Plant Material and RNA Isolation: Field grown maize  
plants from inbred line F352 were used. Bars were  
harvested at 10, 15, 20 and 25 days after pollination  
(DAP). seeds were cut from the ear and the upper third of  
the endosperms, containing only endosperm, aleurone and  
pericarpal tissues, was removed, frozen in liquid nitrogen  
and stored at -800 C. Frozen endosperms were pulverized in  
liquid nitrogen and total RNA was isolated according the  
method of Manning (9). Poly(A)+RNA was isolated using  
Oligotex-dT. cDNA libraries were constructed using  
SuperScript plasmid system for cDNA Synthesis and Plasmid  
Cloning Kit as described in Vettore, et al., (2001). The  
libraries ranging from 500 to 800 bp in size were assigned as short  
libraries (S10, S15, S20), and cDNAs >800 were assigned as  
long libraries (L10, L15, M15, L20, L25). Unamplified  
libraries were plated and individual colonies picked and  
transferred to 96 well plates containing liquid circle  
Grow (CG) medium supplemented with 100 mg/L of ampicillin  
and 8% glycerol. Three copies of each cDNA clone were  
stored at -800 C. Additional information can be found in :  
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,  
Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,  
A.L., da Silva, F.R. and Arruda, P. (2005)  
Endosperm-preferred expression of maize genes as revealed  
by transcriptome-wide analysis of expressed sequence tags.  
Plant Molecular Biology (/in press//)"

**ORIGIN**

Alignment Scores:  
Pred. No.: 8,05e-24 Length: 811  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO469376 (1-811)

**QY**  
1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
|||||

**Db**  
184 ATGGCGGCTCTGGCCACGTCGCGAGCTGTCGCAACGCGCGCCGCGCTGGCGGCGAC 243  
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**QY**  
21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40  
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**Db**  
244 GCGTCCACGTTCCGCGCGCGCGCGCGAGGCGCTGAGGGGGGCCCGCGGCTCGCGGCG 303  
|||||

**QY**  
41 AlaAspThrLeuSerMetArgThrSerAlaAlaProArgHisGlnGlnAla 60  
|||||

**Db**  
304 GCGGACACGCTCAGCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 363  
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**QY**  
61 ArgArgGlyGlyValArgPheProPheProSerLeuValValCys 74  
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**Db**  
364 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 399  
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**RESULT 6**  
CO461143 812 bp mRNA linear EST 08-JUN-2005  
LOCUS MZCCS20023B02.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA  
DEFINITION  
sequence.  
CO461143  
CO461143.1 GI:67032394  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 812)  
Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H.,  
De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and  
Arruda,P.  
Endosperm-preferred expression of maize genes as revealed by  
transcriptome-wide analysis of expressed sequence tags  
Plant Mol. Biol. (2005) In press  
Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br.

**FEATURES**  
source  
Location/Qualifiers  
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/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="F-352 near isogenic line"  
/db\_xref="taxon:4577"  
/sex="hermaphrodite"  
/tissue\_type="endosperm"  
/dev\_stage="multiple stages (10 to 25 days after  
pollination, see publication for more information)"  
/lab\_host="E. coli DH10B"  
/clone\_lib="Maize Endosperm cDNA Library"  
/note="Organ: seed; Vector: pSPORT1; Site: 1: Sali; Site: 2:  
NotI; Plant Material and RNA Isolation: Field grown maize  
plants from inbred line F352 were used. Bars were  
harvested at 10, 15, 20 and 25 days after pollination  
(DAP). seeds were cut from the ear and the upper third of  
the endosperms, containing only endosperm, aleurone and  
pericarpal tissues, was removed, frozen in liquid nitrogen  
and stored at -800 C. Frozen endosperms were pulverized in  
liquid nitrogen and total RNA was isolated according the  
method of Manning (9). Poly(A)+RNA was isolated using  
Oligotex-dT. cDNA libraries were constructed using  
SuperScript Plasmid System for cDNA Synthesis and Plasmid  
Cloning Kit as described in Vettore, et al., (2001). The  
libraries ranging from 500 to 800 bp in size were assigned as short  
libraries (S10, S15, S20), and cDNAs >800 were assigned as  
long libraries (L10, L15, M15, L20, L25). Unamplified  
libraries were plated and individual colonies picked and  
transferred to 96 well plates containing liquid circle  
Grow (CG) medium supplemented with 100 mg/L of ampicillin  
and 8% glycerol. Three copies of each cDNA clone were  
stored at -800 C. Additional information can be found in :  
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,  
Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,  
A.L., da Silva, F.R. and Arruda, P. (2005)  
Endosperm-preferred expression of maize genes as revealed  
by transcriptome-wide analysis of expressed sequence tags.  
Plant Molecular Biology (/in press//)"

by transcriptome-wide analysis of expressed sequence tags.  
Plant Molecular Biology (/in press/)"

|                                                                                                                                                                                                                               |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------|-----|----------|--|-------------|--|-----|--|--|--|--|--|--|--|--|--|--|--|
| ORIGIN                                                                                                                                                                                                                        |     | Alignment Scores:                                            |     | 8.06e-24 |  | Length:     |  | 812 |  |  |  |  |  |  |  |  |  |  |  |
| Pred. No.:                                                                                                                                                                                                                    |     | Score:                                                       |     | 333.00   |  | Matches:    |  | 71  |  |  |  |  |  |  |  |  |  |  |  |
| Percent Similarity:                                                                                                                                                                                                           |     | Conservative:                                                |     | 95.9%    |  | Mismatches: |  | 1   |  |  |  |  |  |  |  |  |  |  |  |
| Best Local Similarity:                                                                                                                                                                                                        |     | Indels:                                                      |     | 95.9%    |  | Gaps:       |  | 2   |  |  |  |  |  |  |  |  |  |  |  |
| Query Match:                                                                                                                                                                                                                  |     | DB:                                                          |     | 90.5%    |  |             |  | 1   |  |  |  |  |  |  |  |  |  |  |  |
| US-10-628-525A-36 (1-74) x CO461143 (1-812)                                                                                                                                                                                   |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| QY                                                                                                                                                                                                                            | 1   | MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAap | 20  |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Db                                                                                                                                                                                                                            | 202 | ATGGCGGCTCTGGCCACGTCGCAGCTCTGCAACGCGCGCGCTGGCGCTCCGGAC       | 261 |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| QY                                                                                                                                                                                                                            | 21  | AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyValaAlaSerAlaAla   | 40  |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Db                                                                                                                                                                                                                            | 262 | GGGTCCACGTTCCGCGCGCGCGCGGCGAGGCGCTGAGGGGGCGCGTCCGGCGG        | 321 |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| QY                                                                                                                                                                                                                            | 41  | AlaAapThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla    | 60  |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Db                                                                                                                                                                                                                            | 322 | GGGGACACGCTCAGCATGGGACACGAGCGCGCGCGCGCCAGGACCAGCAGCAGGCG     | 381 |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| QY                                                                                                                                                                                                                            | 61  | ArgArgGlyGlyArgPheProPheProSerLeuValValCys                   | 74  |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Db                                                                                                                                                                                                                            | 382 | CGCCCGGGGGGCGAGG-----TTCCCGTCGCTCGTGTGTC                     | 417 |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| RESULT 7                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| CO464185                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| LOCUS                                                                                                                                                                                                                         |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| DEFINITION                                                                                                                                                                                                                    |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| MZCC115045G11.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA                                                                                                                                                              |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| CO464185                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| ACCESSION                                                                                                                                                                                                                     |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| VERSION                                                                                                                                                                                                                       |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| CO464185.1 GI:67037339                                                                                                                                                                                                        |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| KEYWORDS                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| EST.                                                                                                                                                                                                                          |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| SOURCE                                                                                                                                                                                                                        |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Zea mays                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| ORGANISM                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.                                                  |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| 1 (bases 1 to 813)                                                                                                                                                                                                            |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,P.T.S., Fisch,P.H., De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and Arruda,P.                                                                                  |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags                                                                                                           |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Plant Mol. Biol. (2005) In press                                                                                                                                                                                              |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Contact: Arruda P                                                                                                                                                                                                             |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| CENTRO DE BIOLOGIA MOLECULAR E ENGENHARIA GENETICA                                                                                                                                                                            |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Universidade Estadual de Campinas                                                                                                                                                                                             |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
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| Tel: 55 19 3788 1137                                                                                                                                                                                                          |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Fax: 55 19 3788 1089                                                                                                                                                                                                          |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Email: parruda@unicamp.br.                                                                                                                                                                                                    |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Location/Qualifiers                                                                                                                                                                                                           |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| 1..813                                                                                                                                                                                                                        |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /organism="Zea mays"                                                                                                                                                                                                          |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /mol_type="mRNA"                                                                                                                                                                                                              |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /cultivar="P-352 near isogenic line"                                                                                                                                                                                          |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /db_xref="taxon:4577"                                                                                                                                                                                                         |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /sex="hermaphrodite"                                                                                                                                                                                                          |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /tissue_type="endosperm"                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /dev_stage="multiple stages (10 to 25 days after pollination, see publication for more information)"                                                                                                                          |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /lab_host="E. coli DH10B"                                                                                                                                                                                                     |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /clone_lib="Maize Endosperm cDNA Library"                                                                                                                                                                                     |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /note="Organ: seed; Vector: pSPORII; Site: 1: SalI; Site 2: NotI; Plant Material and RNA Isolation: Field grown maize plants from inbred line P352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| FEATURES                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| source                                                                                                                                                                                                                        |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| CO462292                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| LOCUS                                                                                                                                                                                                                         |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| DEFINITION                                                                                                                                                                                                                    |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| MZCCS15026D01.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA                                                                                                                                                              |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| CO462292                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| ACCESSION                                                                                                                                                                                                                     |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| VERSION                                                                                                                                                                                                                       |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| CO462292.1 GI:67033543                                                                                                                                                                                                        |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| KEYWORDS                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| EST.                                                                                                                                                                                                                          |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| SOURCE                                                                                                                                                                                                                        |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Zea mays                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| ORGANISM                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.                                                  |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| 1 (bases 1 to 816)                                                                                                                                                                                                            |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,P.T.S., Fisch,P.H., De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and Arruda,P.                                                                                  |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags                                                                                                           |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Plant Mol. Biol. (2005) In press                                                                                                                                                                                              |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Contact: Arruda P                                                                                                                                                                                                             |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| RESULT 8                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| CO462292                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| LOCUS                                                                                                                                                                                                                         |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| DEFINITION                                                                                                                                                                                                                    |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| MZCCS15026D01.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA                                                                                                                                                              |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| CO462292                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| ACCESSION                                                                                                                                                                                                                     |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| VERSION                                                                                                                                                                                                                       |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| CO462292.1 GI:67033543                                                                                                                                                                                                        |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| KEYWORDS                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| EST.                                                                                                                                                                                                                          |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| SOURCE                                                                                                                                                                                                                        |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Zea mays                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| ORGANISM                                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.                                                  |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| 1 (bases 1 to 816)                                                                                                                                                                                                            |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,P.T.S., Fisch,P.H., De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and Arruda,P.                                                                                  |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags                                                                                                           |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Plant Mol. Biol. (2005) In press                                                                                                                                                                                              |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Contact: Arruda P                                                                                                                                                                                                             |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| TITLE                                                                                                                                                                                                                         |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags                                                                                                           |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Plant Mol. Biol. (2005) In press                                                                                                                                                                                              |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Contact: Arruda P                                                                                                                                                                                                             |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| JOURNAL                                                                                                                                                                                                                       |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| COMMENT                                                                                                                                                                                                                       |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| CENTRO DE BIOLOGIA MOLECULAR E ENGENHARIA GENETICA                                                                                                                                                                            |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
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| Fax: 55 19 3788 1089                                                                                                                                                                                                          |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Email: parruda@unicamp.br.                                                                                                                                                                                                    |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| Location/Qualifiers                                                                                                                                                                                                           |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| 1..813                                                                                                                                                                                                                        |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /organism="Zea mays"                                                                                                                                                                                                          |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /mol_type="mRNA"                                                                                                                                                                                                              |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /cultivar="P-352 near isogenic line"                                                                                                                                                                                          |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /db_xref="taxon:4577"                                                                                                                                                                                                         |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /sex="hermaphrodite"                                                                                                                                                                                                          |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /tissue_type="endosperm"                                                                                                                                                                                                      |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /dev_stage="multiple stages (10 to 25 days after pollination, see publication for more information)"                                                                                                                          |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |
| /lab_host="E. coli DH10B"                                                                                                                                                                                                     |     |                                                              |     |          |  |             |  |     |  |  |  |  |  |  |  |  |  |  |  |

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Fax: 55 19 3788 1089  
Email: parruda@unicamp.br.

## FEATURES

## Source

1. .816  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="P-352 near isogenic line"  
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/tissue\_type="endosperm"

/dev\_stage="multiple stages (10 to 25 days after pollination, see publication for more information)"  
/lab\_host="E. coli DH10B"  
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Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)"

## ORIGIN

## Alignment Scores:

Pred. No.: 8.11e-24 Length: 816  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO462292 (1-816)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 196 ATGGCGGCTCTGGCCACGTCGCGAGCTCTGTCGACCGCGCGCGCTGGCGGCGGAC 255  
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyValaArgAlaSerAlaAla 40  
DB 256 GCGTCCACGTTCCGCGCGCGCGCGCGAGGGCTGTAGGGGGGGCCCGGGCGTGGCGGCG 315  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
DB 316 GGGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCCAGGCGCCAGGCGACGAGCGGCG 375  
QY 61 ArgArgGlyGlyValArgPheProPheProSerLeuValValCys 74  
DB 376 CGCCCGCGGGGGCAGG-----TTCCCGTCGCTGCTGTGTC 411

## RESULT 9

CO460606

## LOCUS

## DEFINITION

CO460606

## ACCESSION

CO460606

## VERSION

CO460606

## KEYWORDS

EST.

## SOURCE

CO460606

## ORGANISM

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 828)

Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, P.R. and Arruda, P.

Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags

Plant Mol. Biol. (2005) In press

Contact: Arruda, P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br.

Location/Qualifiers

1. .828

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="P-352 near isogenic line"

/db\_xref="taxon:4577"

/sex="hermaphrodite"

/tissue\_type="endosperm"

/dev\_stage="multiple stages (10 to 25 days after pollination, see publication for more information)"

/lab\_host="E. coli DH10B"

/clone\_lib="Maize Endosperm cDNA Library"

/notes="Organ: seed; Vector: pSPORT1; Site: 1; Sall; Site 2: NotI; Plant Material and RNA Isolation: Field grown maize plants from inbred line F352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP), seeds were cut from the ear and the upper third of the endosperms, containing only endosperm, aleurone and pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -800 C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according the method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dT. cDNA libraries were constructed using SuperScript plasmid system for cDNA Synthesis and Plasmid Cloning kit as described in Vettore, et al., (2001). The libraries from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, M15, L20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -800 C. Additional information can be found in : Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, P.R. and Arruda, P. (2005)  
Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)"

## FEATURES

## Source

CO460606 828 bp mRNA linear EST 08-JUN-2005  
M2CC120024C02.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA  
Sequence.

CO460606 1 GI:67031857

CO460606

EST.

CO460606

EST.

CO460606

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CO460606

EST.

## ORIGIN

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Pred. No.: 8.24e-24 Length: 828  
Score: 333.00 Matches: 71



Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO460606 (1-828)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAap 20  
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 Db 145 ATGGCGGCTCTGGCCACGTCGACGCTCGCGACCGCGCGCGCTGGCGGTCCTCCGGAC 204  
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QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
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 Db 205 GGTCCACGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 264  
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QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
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 Db 265 GCGGACACGCTCAGCATGGCGGACCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 324  
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QY 61 ArgArgGlyGlyValArgPheProPheProSerLeuValValCys 74  
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RESULT 10  
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 DEFINITION CO456895  
 ACCESSION CO456895  
 VERSION CO456895.1 GI:67028146  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE  
 AUTHORS Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H.,  
 De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and  
 Arruda,P.  
 Endosperm-preferred expression of maize genes as revealed by  
 transcriptome-wide analysis of expressed sequence tags  
 Plant Mol. Biol. (2005) In press

TITLE Centro de Biologia Molecular e Engenharia Genetica  
 JOURNAL Universidade Estadual de Campinas  
 COMMENT Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.

FEATURES  
 source 1..830  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="P-352 near isogenic line"  
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 /sex="hermaphrodite"  
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 /note="Organ: seed; Vector: pSPORT1; Site 1: Sall; Site 2:  
 NotI; Plant Material and RNA Isolation: Field grown maize  
 plants from inbred line P352 were used. Ears were  
 harvested at 10, 15, 20 and 25 days after pollination  
 (DAP), seeds were cut from the ear and the upper third of  
 the endosperms, containing only endosperm, aleurone and  
 pericarpal tissues, was removed, frozen in liquid nitrogen  
 and stored at -800 C. Frozen endosperms were pulverized in  
 liquid nitrogen and total RNA was isolated according the  
 method of Manning (9). Poly(A)+RNA was isolated using  
 Oligotex-dT. cDNA libraries were constructed using

SuperScript Plasmid System for cDNA Synthesis and Plasmid  
 Cloning Kit as described in Vettore, et al., (2001). The  
 libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs  
 ranging from 500 to 800 bp in size were assigned as short  
 libraries (S10, S15, S20), and cDNAs >800 can be assigned as  
 long libraries (L10, L15, L20, L25). Unamplified  
 libraries were plated and individual colonies picked and  
 transferred to 96 well plates containing liquid circle  
 grow (CG) medium supplemented with 100 mg/L of ampicillin  
 and 8% glycerol. Three copies of each cDNA clone were  
 stored at -800 C. Additional information can be found in :  
 Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,  
 Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,  
 A.L., da Silva, F.R. and Arruda, P. (2005)  
 Endosperm-preferred expression of maize genes as revealed  
 by transcriptome-wide analysis of expressed sequence tags.  
 Plant Molecular Biology (/in press/)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 8,268-24 Length: 830  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO456895 (1-830)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAap 20  
 |||||  
 Db 177 ATGGCGGCTCTGGCCACGTCGACGCTCGCGACCGCGCGCGCTGGCGGTCCTCCGGAC 236  
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QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 |||||  
 Db 237 GGTCCACGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 296  
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QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
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 Db 297 GCGGACACGCTCAGCATGGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 356  
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QY 61 ArgArgGlyGlyValArgPheProPheProSerLeuValValCys 74  
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 Db 357 CGCCGCGGGGGGAGG-----TTCCCGTCGCTCGTGTGTC 392  
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RESULT 11  
 CO460923

LOCUS MZCCL15030A05.g 837 bp mRNA linear EST 08-JUN-2005  
 DEFINITION CO460923  
 ACCESSION CO460923  
 VERSION CO460923.1 GI:67032174  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE  
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 837)  
 Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H.,  
 De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and  
 Arruda,P.  
 Endosperm-preferred expression of maize genes as revealed by  
 transcriptome-wide analysis of expressed sequence tags  
 Plant Mol. Biol. (2005) In press

TITLE Centro de Biologia Molecular e Engenharia Genetica  
 JOURNAL Universidade Estadual de Campinas  
 COMMENT Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.  
 Location/Qualifiers



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1. .837
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/lab_host="E. coli DH10B"
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/notes="Organ: seed; Vector: pSPORT1; Site:1: Salt1; Site:2:
NotI; Plant Material and RNA Isolation: Field grown maize
plants from inbred line F352 were used. Ears were
harvested at 10, 15, 20 and 25 days after pollination
(DAP), seeds were cut from the ear and the upper third of
the endosperms, containing only endosperm, aleurone and
pericarpal tissues, was removed, frozen in liquid nitrogen
and stored at -800 C. Frozen endosperms were pulverized in
liquid nitrogen and total RNA was isolated according the
method of Manning (9). Poly(A)+RNA was isolated using
Oligotex-dT. cDNA libraries were constructed using
SuperScript plasmid system for cDNA Synthesis and Plasmid
Cloning Kit as described in Vettore, et al. (2001). The
libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs
ranging from 500 to 800 bp in size were assigned as short
libraries (S10, S15, S20), and cDNAs >800 were assigned as
long libraries (L10, L15, M15, L20, L25). Unamplified
libraries were plated and individual colonies picked and
transferred to 96 well plates containing liquid circle
Grow (CG) medium supplemented with 100 mg/L of ampicillin
and 8% glycerol. Three copies of each cDNA clone were
stored at -800 C. Additional information can be found in :
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,
Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,
A.L., da Silva, P.R. and Arruda, P. (2005)
Endosperm-preferred expression of maize genes as revealed
by transcriptome-wide analysis of expressed sequence tags.
Plant Molecular Biology (/in press/)"

FEATURES
source
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/mol_type="mRNA"
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pollination, see publication for more information)"
/lab_host="E. coli DH10B"
/clone_lib="Maize Endosperm cDNA Library"
/notes="Organ: seed; Vector: pSPORT1; Site:1: Salt1; Site:2:
NotI; Plant Material and RNA Isolation: Field grown maize
plants from inbred line F352 were used. Ears were
harvested at 10, 15, 20 and 25 days after pollination
(DAP), seeds were cut from the ear and the upper third of
the endosperms, containing only endosperm, aleurone and
pericarpal tissues, was removed, frozen in liquid nitrogen
and stored at -800 C. Frozen endosperms were pulverized in
liquid nitrogen and total RNA was isolated according the
method of Manning (9). Poly(A)+RNA was isolated using
Oligotex-dT. cDNA libraries were constructed using
SuperScript plasmid system for cDNA Synthesis and Plasmid
Cloning Kit as described in Vettore, et al. (2001). The
libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs
ranging from 500 to 800 bp in size were assigned as short
libraries (S10, S15, S20), and cDNAs >800 were assigned as
long libraries (L10, L15, M15, L20, L25). Unamplified
libraries were plated and individual colonies picked and
transferred to 96 well plates containing liquid circle
Grow (CG) medium supplemented with 100 mg/L of ampicillin
and 8% glycerol. Three copies of each cDNA clone were
stored at -800 C. Additional information can be found in :
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,
Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,
A.L., da Silva, P.R. and Arruda, P. (2005)
Endosperm-preferred expression of maize genes as revealed
by transcriptome-wide analysis of expressed sequence tags.
Plant Molecular Biology (/in press/)"

ORIGIN
Alignment Scores:
Pred. No.: 8 34e-24 Length: 837
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO465063 (1-837)

QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProApp 20
DB 203 ATGGCGGCTCTGGCCAGCTCGAGCTCTGTCACACGGCGCGGCTGGCGGAC 262
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DB 263 GGTCTCACGTTCCGCGCGCGCGCGGCGGCTGAGGCGCGCGGCGGCGGCG 322
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
DB 323 GCGACACGCTAGCATGCGGACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 382
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB 383 CGCGCGCGGGGGCAGG-----TTCCGCTGCTCTGCTGTGC 418

RESULT 12
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LOCUS MZCCS15035D06.g 844 bp mRNA linear EST 08-JUN-2005
DEFINITION Maize Endosperm cDNA Library Zea mays CDNA, mRNA
sequence.
ACCESSION CO465063

VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 844)
De Rosa, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H.,
De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, P.R. and
Arruda, P.
Endosperm-preferred expression of maize genes as revealed by
transcriptome-wide analysis of expressed sequence tags
Plant Mol. Biol. (2005) In press
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br.
Location/Qualifiers
1. .844
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="P-352 near isogenic line"
/db_xref="taxon:4577"
/sex="hermaphrodite"
/tissue_type="endosperm"
/dev_stage="multiple stages (10 to 25 days after
pollination, see publication for more information)"
/lab_host="E. coli DH10B"
/clone_lib="Maize Endosperm cDNA Library"
/notes="Organ: seed; Vector: pSPORT1; Site:1: Salt1; Site:2:
NotI; Plant Material and RNA Isolation: Field grown maize
plants from inbred line F352 were used. Ears were
harvested at 10, 15, 20 and 25 days after pollination
(DAP), seeds were cut from the ear and the upper third of
the endosperms, containing only endosperm, aleurone and
pericarpal tissues, was removed, frozen in liquid nitrogen
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method of Manning (9). Poly(A)+RNA was isolated using
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Cloning Kit as described in Vettore, et al. (2001). The
libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs
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long libraries (L10, L15, M15, L20, L25). Unamplified
libraries were plated and individual colonies picked and
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Grow (CG) medium supplemented with 100 mg/L of ampicillin
and 8% glycerol. Three copies of each cDNA clone were
stored at -800 C. Additional information can be found in :
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,
Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,
A.L., da Silva, P.R. and Arruda, P. (2005)
Endosperm-preferred expression of maize genes as revealed
by transcriptome-wide analysis of expressed sequence tags.
Plant Molecular Biology (/in press/)"

ORIGIN
Alignment Scores:
Pred. No.: 8 42e-24 Length: 844
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO465063 (1-844)

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QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
 Db 201 ATGGCGGCTCTGGCCAGCTCGAGCTCTGTCGACACGGCGCGGCTGGCGTCCCGGAC 260  
 QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
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 Db 321 GCGACACAGCTCAGCATGCGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 380  
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 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 849)  
 AUTHORS Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,P.T.S., Fisch,P.H.,  
 De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and  
 Arruda,P.  
 TITLE Endosperm-preferred expression of maize genes as revealed by  
 transcriptome-wide analysis of expressed sequence tags  
 JOURNAL Plant Mol. Biol. (2005) In press  
 COMMENT Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.  
 FEATURES  
 source  
 1. 849  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:4577"  
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 /lab\_host="E. coli DH10B"  
 /clone\_lib="Maize Endosperm cDNA Library"  
 /note="Organ: seed; Vector: pSPORT1; Site 1: Sali; Site 2:  
 NotI; Plant Material and RNA Isolation: Field grown maize  
 plants from inbred line F352 were used. Ears were  
 harvested at 10, 15, 20 and 25 days after pollination  
 (DAP), seeds were cut from the ear and the upper third of  
 the endosperms, containing only endosperm, aleurone and  
 pericarpal tissues, was removed, frozen in liquid nitrogen  
 and stored at -80o C. Frozen endosperms were pulverized in  
 liquid nitrogen and total RNA was isolated according the  
 method of Manning (9). Poly(A)+RNA was isolated using  
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 SuperScript Plasmid System for cDNA Synthesis and Plasmid  
 Cloning Kit as described in Vettore, et al., (2001) The  
 libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs  
 ranging from 500 to 800 bp in size were assigned as short  
 libraries (S10, S15, S20), and cDNAs >800 were assigned as  
 long libraries (L10, L15, L20, L25). Unamplified  
 libraries were plated and individual colonies picked and

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 Grow (CG) medium supplemented with 100 mg/l of ampicillin  
 and 8% glycerol. Three copies of each cDNA clone were  
 stored at -80o C. Additional information can be found in :  
 Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, P.T.S.,  
 Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,  
 A.L., da Silva, F.R. and Arruda, P. (2005)  
 Endosperm-preferred expression of maize genes as revealed  
 by transcriptome-wide analysis of expressed sequence tags.  
 Plant Molecular Biology (/in press//)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 8 47e-24 Length: 849  
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 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
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 QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 295 GCGACACAGCTCAGCATGCGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 354  
 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 355 CGCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 390  
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 LOCUS CO456306  
 DEFINITION MZCCL15012E06.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA  
 ACCESSION CO456306  
 VERSION CO456306.1 GI:67027557  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 850)  
 AUTHORS Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,P.T.S., Fisch,P.H.,  
 De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and  
 Arruda,P.  
 TITLE Endosperm-preferred expression of maize genes as revealed by  
 transcriptome-wide analysis of expressed sequence tags  
 JOURNAL Plant Mol. Biol. (2005) In press  
 COMMENT Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.  
 FEATURES  
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 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="F-352 near isogenic line"  
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/dev stage="multiple stages (10 to 25 days after pollination, see publication for more information)"  
 /lab\_host="E. coli DH10B"  
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 Note1: Organ: seed; Vector: pSPORT1; Site 1: SalI; Site 2: NotI; Plant Material and RNA Isolation: Field grown maize plants from inbred line F352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP), seeds were cut from the ear and the upper third of the endosperms, containing only endosperm, aleurone and pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -80o C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according to the method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dT. cDNA libraries were constructed using SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001). The libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, M15, L20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid Circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -80o C. Additional information can be found in : Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005)  
 Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 8 48e-24 Length: 850  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservatives: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO456306 (1-850)

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 Db 197 ATGGCGGCTCTGGCCAGTCGCGAGCTGCTGCACCGCGCGCGCTGGCGGCGTCCGGAC 256  
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 QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
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 Db 257 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 316  
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 QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
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 Db 317 GCGGACACGCTGACATGCGACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 376  
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 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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 Db 377 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412  
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## RESULT 15

LOCUS CO460568  
 DEFINITION MZCCL15027F09.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA  
 853 bp mRNA linear EST 08-JUN-2005  
 sequence.

ACCESSION CO460568

VERSION CO460568.1 GI:67031819

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

1 (bases 1 to 853)

Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H.,  
 De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and  
 Arruda, P.

Endosperm-preferred expression of maize genes as revealed by

transcriptome-wide analysis of expressed sequence tags

Plant Mol. Biol. (2005) in press

Contact: Arruda P

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Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br.

## FEATURES

source

1..853

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="P-352 near isogenic line"

/db\_xref="taxon:4577"

/sex="hermaphrodite"

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/dev\_stage="multiple stages (10 to 25 days after

pollination, see publication for more information)"

/lab\_host="E. coli DH10B"

/clone\_lib="Maize Endosperm cDNA Library"

/notes="Organ: seed; Vector: pSPORT1; Site 1: SalI; Site 2:

NotI; Plant Material and RNA Isolation: Field grown maize

plants from inbred line F352 were used. Ears were

harvested at 10, 15, 20 and 25 days after pollination

(DAP), seeds were cut from the ear and the upper third of

the endosperms, containing only endosperm, aleurone and

pericarpal tissues, was removed, frozen in liquid nitrogen

and stored at -80o C. Frozen endosperms were pulverized in

liquid nitrogen and total RNA was isolated according to the

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Oligotex-dT. cDNA libraries were constructed using

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Cloning Kit as described in Vettore, et al., (2001). The

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Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,

A.L., da Silva, F.R. and Arruda, P. (2005)

Endosperm-preferred expression of maize genes as revealed

by transcriptome-wide analysis of expressed sequence tags.

Plant Molecular Biology (/in press/)"

## ORIGIN

## Alignment Scores:

Pred. No.: 8 52e-24 Length: 853  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservatives: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO460568 (1-853)

QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20

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Db 203 ATGGCGGCTCTGGCCAGTCGCGAGCTGCTGCACCGCGCGCGCTGGCGGCGTCCGGAC 262

|||||

QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40

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Db 263 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 322

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41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
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 323 GGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 382  
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61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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 383 CGCCGCGGGGCGAGG-----TTCCGTCGCTCGTGTGTGC 418  
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RESULT 16  
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 ACCESSION CO464201  
 VERSION CO464201.1 GI:67037361  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 854)  
 Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H.,  
 De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and  
 Arruda,P.  
 Endosperm-preferred expression of maize genes as revealed by  
 transcriptome-wide analysis of expressed sequence tags  
 Plant Mol. Biol. (2005) In press  
 Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.  
 Location/Qualifiers  
 1..854  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
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 NotI; Plant Material and RNA Isolation: Field grown maize  
 plants from inbred line F352 were used. Ears were  
 harvested at 10, 15, 20 and 25 days after pollination  
 (DAP), seeds were cut from the ear and the upper third of  
 the endosperms, containing only endosperm, aleurone and  
 pericarpal tissues, was removed, frozen in liquid nitrogen  
 and stored at -80o C. Frozen endosperms were pulverized in  
 liquid nitrogen and total RNA was isolated according the  
 method of Manning (9). Poly(A)+RNA was isolated using  
 Oligotex-dT. cDNA libraries were constructed using  
 Superscript Plasmid System for cDNA Synthesis and Plasmid  
 Cloning Kit as described in Vettore, et al., (2001) The  
 libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs  
 ranging from 500 to 800 bp in size were assigned as short  
 libraries (S10, S15, S20), and cDNAs >800 were assigned as  
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 Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,  
 A.L., da Silva, F.R. and Arruda, P. (2005)

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 Alignment Scores:  
 Pred. No.: 8,53e-24 Length: 854  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
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 QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
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 Db 316 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 375  
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 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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 Db 376 CGCCGCGGGGCGAGG-----TTCCGTCGCTCGTGTGTGC 411  
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RESULT 17  
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 DEFINITION sequence.  
 ACCESSION CO468515  
 VERSION CO468515.1 GI:67042260  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 858)  
 Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H.,  
 De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and  
 Arruda,P.  
 Endosperm-preferred expression of maize genes as revealed by  
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 Plant Mol. Biol. (2005) In press  
 Contact: Arruda P  
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 Universidade Estadual de Campinas  
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 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.  
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 plants from inbred line F352 were used. Ears were  
 harvested at 10, 15, 20 and 25 days after pollination  
 (DAP), seeds were cut from the ear and the upper third of  
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 pericarpal tissues, was removed, frozen in liquid nitrogen  
 and stored at -80o C. Frozen endosperms were pulverized in  
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 and 8% glycerol. Three copies of each cDNA clone were  
 stored at -80o C. Additional information can be found in :  
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 Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,  
 A.L., da Silva, F.R. and Arruda, P. (2005)

FEATURES  
 source  
 TITLE Endosperm-preferred expression of maize genes as revealed by  
 transcriptome-wide analysis of expressed sequence tags  
 JOURNAL Plant Mol. Biol. (2005) In press  
 COMMENT Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
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 Email: parruda@unicamp.br.  
 Location/Qualifiers  
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 /organism="Zea mays"  
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 NotI; Plant Material and RNA Isolation: Field grown maize  
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 harvested at 10, 15, 20 and 25 days after pollination  
 (DAP), seeds were cut from the ear and the upper third of  
 the endosperms, containing only endosperm, aleurone and  
 pericarpal tissues, was removed, frozen in liquid nitrogen  
 and stored at -80o C. Frozen endosperms were pulverized in  
 liquid nitrogen and total RNA was isolated according the  
 method of Manning (9). Poly(A)+RNA was isolated using  
 Oligotex-dT. cDNA libraries were constructed using  
 Superscript Plasmid System for cDNA Synthesis and Plasmid  
 Cloning Kit as described in Vettore, et al., (2001) The  
 libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs  
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 libraries (S10, S15, S20), and cDNAs >800 were assigned as  
 long libraries (L10, L15, L20, L25). Unamplified  
 libraries were plated and individual colonies picked and  
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 and 8% glycerol. Three copies of each cDNA clone were  
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 Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,  
 A.L., da Silva, F.R. and Arruda, P. (2005)

Endosperm-preferred expression of maize genes as revealed  
 by transcriptome-wide analysis of expressed sequence tags.  
 Plant Molecular Biology (/in press//)"

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## ORIGIN

Alignment Scores:  
 Pred. No.: 8.57e-24 Length: 858  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO468515 (1-858)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
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 Db 216 ATGGCGGCTCTGGCCACGTCGACGCTCGTGCACCGCGCGCGCTGGCGCTCCGGAC 275  
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 QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40  
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 Db 276 GGTCTCACGTTTCGCGCGCGCGCGCGAGGGCTGAGGGGGGCCCGCGCGCGCG 335  
 |||||  
 QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGlnGlnAla 60  
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 Db 336 GCGGACACGCTCAGCATGCGGACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 395  
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 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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 Db 396 CGCGCGCGGGCGAGG-----TTCCGTCGCTCGTGTGTC 431  
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RESULT 18  
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 ACCESSION CO458241.1 GI:67029492  
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 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 860)  
 Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P.  
 Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags  
 Plant Mol. Biol. (2005) In press

## COMMENT

Contact: Arruda P  
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 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.  
 Location/Qualifiers

## FEATURES

## source

1. 860  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="F-352 near isogenic line"  
 /db\_xref="taxon:4577"  
 /sex="hermaphrodite"  
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 /notes="Organ: seed; Vector: pSPORT1; Site 1: SalI; Site 2: NotI; Plant Material and RNA Isolation: Field grown maize plants from inbred line P352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP), seeds were cut from the ear and the upper third of the endosperms, containing only endosperm, aleurone and pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -80o C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according the method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dT. cDNA libraries were constructed using Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001). The libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, L20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid Circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -80o C. Additional information can be found in : Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 8.6e-24 Length: 860  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO458241 (1-860)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
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 Db 201 ATGGCGGCTCTGGCCACGTCGACGCTCGTGCACCGCGCGCGCTGGCGCTCCGGAC 260  
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 QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40  
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 Db 261 GGTCTCACGTTTCGCGCGCGCGCGCGAGGGCTTGGGGGGGCCCGCGCGCGCG 320  
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 QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60  
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 Db 321 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 380  
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 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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Db      381 CGCGCGGGGCGAGG-----TTCCGTCGCTCGTGTGTGC 416
RESULT 19
LOCUS   CO457215                               863 bp   mRNA   linear   EST 08-JUN-2005
DEFINITION MZCCL20013D11.5 Maize Endosperm cDNA Library Zea mays cDNA, mRNA
ACCESSION CO457215
VERSION   CO457215.1   GI:67028466
KEYWORDS EST.
SOURCE   Zea mays
ORGANISM Zea mays
REFERENCE
AUTHORS Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H.,
De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and
Arruda,P.
TITLE   Endosperm-preferred expression of maize genes as revealed by
transcriptome-wide analysis of expressed sequence tags
JOURNAL Plant Mol. Biol. (2005) In press
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br.

FEATURES             source
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        /organism="Zea mays"
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        NotI; Plant Material and RNA Isolation: Field grown maize
        plants from inbred line F352 were used. Ears were
        harvested at 10, 15, 20 and 25 days after pollination
        (DAP), seeds were cut from the ear and the upper third of
        the endosperms, containing only endosperm, aleurone and
        pericarpal tissues, was removed, frozen in liquid nitrogen
        and stored at -80o C. Frozen endosperms were pulverized in
        liquid nitrogen and total RNA was isolated according the
        method of Manning (9). Poly(A)+RNA was isolated using
        Oligotex-dT. cDNA libraries were constructed using
        Superscript Plasmid System for cDNA Synthesis and Plasmid
        Cloning Kit as described in Vettore, et al., (2001) The
        libraries that made SUCSEST. Genet Mol Biol 24: 1-7. cDNAs
        ranging from 500 to 800 bp in size were assigned as short
        libraries (S10, S15, S20), and cDNAs >800 were assigned as
        long libraries (L10, L15, L20, L25). Unamplified
        libraries were plated and individual colonies picked and
        transferred to 96 well plates containing liquid Circle
        Grow (CG) medium supplemented with 100 mg/L of ampicillin
        and 8% glycerol. Three copies of each cDNA clone were
        stored at -80o C. Additional information can be found in :
        Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,
        Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,
        A.L., da Silva, F.R. and Arruda, P. (2005)
        Endosperm-preferred expression of maize genes as revealed
        by transcriptome-wide analysis of expressed sequence tags.
        Plant Molecular Biology (/in press/)"

ORIGIN
Alignment Scores:
Pred. No.:      8.63e-24      Length:      863

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Score:      333.00      Matches:      71
Percent Similarity: 95.9%      Conservative: 0
Best Local Similarity: 95.9%      Mismatches: 1
Query Match: 90.5%      Indels: 2
DB: 7      Gaps: 1

US-10-628-525A-36 (1-74) x CO457215 (1-863)

QY      1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProAap 20
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QY      21 AlaSerThrPheArgGlyValAlaAlaGlnGlyLeuArgGlyValaArgAlaSerAlaAla 40
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Db      270 GGTTCACGTTCCGCGCGCGCGCGCGCGCGCTGAGGGGGGCGCGGGCGTCCGGCGG 329
QY      41 AlaAepThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
      |||
Db      330 GCGGACACGCTCAGCATGCGGACACGCGCGCGCGCGCGCGCCAGGCACCGAGCAGGCG 389
QY      61 ArgArgGlyGlyArgPhePropheProSerLeuValValCys 74
      |||
Db      390 CGCCGCGGGGCGAGG-----TTCCGTCGCTCGTGTGTGC 425

RESULT 20
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DEFINITION MZCCL20033B07.5 Maize Endosperm cDNA Library Zea mays cDNA, mRNA
ACCESSION CO463484
VERSION   CO463484.1   GI:67034951
KEYWORDS EST.
SOURCE   Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
        clade; Panicoideae; Andropogoneae; Zea.
        1 (bases 1 to 873)
        Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H.,
        De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and
        Arruda,P.
        Endosperm-preferred expression of maize genes as revealed by
        transcriptome-wide analysis of expressed sequence tags
        Plant Mol. Biol. (2005) In press
        Contact: Arruda P
        Centro de Biologia Molecular e Engenharia Genetica
        Universidade Estadual de Campinas
        Caixa Postal 6010, 13083-970, Campinas SP, Brazil
        Tel: 55 19 3788 1137
        Fax: 55 19 3788 1089
        Email: parruda@unicamp.br.

FEATURES             source
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        /organism="Zea mays"
        /mol_type="mRNA"
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        pollination, see publication for more information)"
        /lab_host="E. coli DH10B"
        /clone_lib="Maize Endosperm cDNA Library"
        /note="Organ: seed; Vector: pSPORT1; Site 1: SalI; Site 2:
        NotI; Plant Material and RNA Isolation: Field grown maize
        plants from inbred line F352 were used. Ears were
        harvested at 10, 15, 20 and 25 days after pollination
        (DAP), seeds were cut from the ear and the upper third of
        the endosperms, containing only endosperm, aleurone and
        pericarpal tissues, was removed, frozen in liquid nitrogen
        and stored at -80o C. Frozen endosperms were pulverized in
        liquid nitrogen and total RNA was isolated according the
        method of Manning (9). Poly(A)+RNA was isolated using

```



Oligotex-dT. cDNA libraries were constructed using Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001). The libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, L20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -800 C. Additional information can be found in : Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) Endospem-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)

## ORIGIN

Alignment Scores:  
 Pred. No.: 8.74e-24 Length: 873  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO461256 (1-873)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAap 20  
 Db 196 ATGGCGGCTTGGCCACGTGCGAGCTGTCGCAACGCGCGCGCTGGCGCGTCCCGGAC 255  
 QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyValAlaArgAlaSerAlaAla 40  
 Db 256 GCGTCCACGTTCCGCGCGCGCGCGCGAGGCGCTGAGGGGGCGCCGCGGTCCGGCGG 315  
 QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 316 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCCAGGACCCAGCAGCGGCG 375  
 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 376 CGCCGCGGGGCGAGG-----TTCCCGTCGTCGTGTGTC 411

RESULT 21  
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 LOCUS MZCCL15032F10.g Maize Endospem cDNA Library Zea mays cDNA, mRNA EST 08-JUN-2005  
 DEFINITION sequence.  
 ACCESSION CO461256  
 VERSION CO461256.1 GI:67032507  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
 AUTHORS Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P.

TITLE Endospem-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags  
 JOURNAL Plant Mol. Biol. (2005) In press  
 COMMENT Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.

FEATURES  
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Location/Qualifiers  
 1..876  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
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 /lab\_host="E. coli DH10B"  
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## ORIGIN

Alignment Scores:  
 Pred. No.: 8.77e-24 Length: 876  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO461256 (1-876)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAap 20  
 Db 201 ATGGCGGCTTGGCCACGTGCGAGCTGTCGCAACGCGCGCGCTGGCGCGTCCCGGAC 260  
 QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyValAlaArgAlaSerAlaAla 40  
 Db 261 GCGTCCACGTTCCGCGCGCGCGCGAGGCGCTGAGGGGGCGCCGCGGTCCGGCGGCG 320  
 QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 321 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCCAGGACCCAGCAGCAGCGG 380  
 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 381 CGCCGCGGGGCGAGG-----TTCCCGTCGTCGTGTGTC 416

## RESULT 22

CO462929

LOCUS MZCCL20030H11.g Maize Endospem cDNA Library Zea mays cDNA, mRNA EST 08-JUN-2005  
 DEFINITION sequence.



ACCESSION CO462929  
 VERSION CO462929.1 GI:67034379  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

AUTHORS 1 (bases 1 to 880)  
 Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H., De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and Arruda,P.

TITLE Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags

JOURNAL Plant Mol. Biol. (2005) In press

COMMENT Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.

FEATURES  
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 /dev\_stages="multiple stages (10 to 25 days after pollination, see publication for more information)"  
 /lab\_host="E. coli DH108"  
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 /note="Organ: seed; Vector: pSPORT1; Site 1: Sall; Site 2: NotI; Plant Material and RNA Isolation: Field grown maize plants from inbred line P352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP), seeds were cut from the ear and the upper third of the endosperms, containing only endosperm, aleurone and pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -80o C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according to the method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dT. cDNA libraries were constructed using SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001) The libraries that made SUCSEST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, L20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid Circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -80o C. Additional information can be found in : Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 8,82e-24 Length: 880  
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 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO462929 (1-880)

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 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 287 GGGTCCAGTTCGCGCGCGCGCGCGAGGCTGAGGGGGCGCGCGGGCGGCG 346  
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 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
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 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 407 CGCCGCGCGCGCGCGCGG-----TTCCCGTGGTCTCGTGTGTC 442

RESULT 23  
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 LOCUS MZCCL15035D06.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA  
 DEFINITION sequence.  
 CO463816  
 ACCESSION CO463816.1 GI:67035283  
 VERSION  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

AUTHORS 1 (bases 1 to 883)  
 Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H., De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and Arruda,P.

TITLE Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags

JOURNAL Plant Mol. Biol. (2005) In press

COMMENT Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.

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 Location/Qualifiers  
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 /dev\_stages="multiple stages (10 to 25 days after pollination, see publication for more information)"  
 /clone\_lib="Maize Endosperm cDNA Library"  
 /note="Organ: seed; Vector: pSPORT1; Site 1: Sall; Site 2: NotI; Plant Material and RNA Isolation: Field grown maize plants from inbred line F352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP), seeds were cut from the ear and the upper third of the endosperms, containing only endosperm, aleurone and pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -80o C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according to the method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dT. cDNA libraries were constructed using SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001) The libraries that made SUCSEST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, L20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid Circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -80o C. Additional information can be found in : Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)"

libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid Circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -80°C. Additional information can be found in : Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 8.85e-24 Length: 893  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO463816 (1-893)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
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 Db 218 ATGGGGCTCTGGCCAGCTCGCAGCTCTGCGAACGCCGCCCTGGGGCTGCCGGAC 277  
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 QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAa 40  
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 Db 278 GCGTCCACGTTCCGCGCGCGCGCGCAGGGCTGAGGGGGGCCCGGGGCTCGGGCGCG 337  
 |||||  
 QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 |||||  
 Db 338 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCGCCAGGCACCGACGACGCGG 397  
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 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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 Db 398 CGCGCGGGGGGACG-----TTCCCGTCGCTCGTGTGTGC 433  
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## RESULT 24

CO462071  
 LOCUS CO462071.1 GI:67033322  
 DEFINITION MZCCS20028G05.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA  
 ACCESSION CO462071  
 VERSION EST.  
 KEYWORDS Zea mays  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 893)  
 Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P.

TITLE Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags

JOURNAL Plant Mol. Biol. (2005) In press  
 COMMENT Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.

## FEATURES

source  
 1. .893  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="P-352 near isogenic line"  
 /db\_xref="taxon:4577"  
 /sex="hermaphrodite"

/tissue\_type="endosperm"  
 /dev\_stage="multiple stages (10 to 25 days after pollination, see publication for more information)"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="Maize Endosperm cDNA Library"  
 /notes="Organ: seed; Vector: pSPORII; Site: 1: SalI; Site 2: NotI; Plant Material and RNA Isolation: Field grown maize plants from inbred line P352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP). seeds were cut from the ear and the upper third of the endosperms, containing only endosperm, aleurone and pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -80°C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according the method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dT. cDNA libraries were constructed using SuperScript plasmid system for cDNA Synthesis and Plasmid Cloning kit as described in Vettore, et al., (2001) the libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, M15, L20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid Circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -80°C. Additional information can be found in : Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 8.96e-24 Length: 893  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO462071 (1-893)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
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 Db 190 ATGGGGCTCTGGCCAGCTCGCAGCTCTGCGAACGCCGCCCTGGGGCTGCCGGAC 249  
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 QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAa 40  
 |||||  
 Db 250 GCGTCCACGTTCCGCGCGCGCGCGCAGGGCTGAGGGGGGCCCGGGGCTCGGGCGCG 309  
 |||||  
 QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 |||||  
 Db 310 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCCAGGCACCGACGACGCGG 369  
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 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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 Db 370 CGCGCGGGGGGACG-----TTCCCGTCGCTCGTGTGTGC 405  
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## RESULT 25

CO459176  
 LOCUS MZCCS15018E09.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA  
 DEFINITION sequence.  
 ACCESSION CO459176  
 VERSION CO459176.1 GI:67030427  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD



A.L., da Silva, F.R. and Arruda, P. (2005)  
Endosperm-preferred expression of maize genes as revealed  
by transcriptome-wide analysis of expressed sequence tags.  
Plant Molecular Biology (/in press/)"

## ORIGIN

Alignment Scores:  
Pred. No.: 8.98e-24 Length: 895  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x C0463621 (1-895)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
|||||  
Db 227 ATGGCGGCTCTGGCCAGCTCGCAGCTGTGCAACGGCGCGCGCTGGGGCTCCCGGAC 286  
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
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Db 287 GCGTCCACGTTCCGCCGCGCGCGCGCAGGGCTGAGGGGGCGCGGGCTGGCGGCG 346  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
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Db 347 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCCAGGCCACGACGACGAGCG 406  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
|||||  
Db 407 CGCGCGGGGGGACGG-----TTCCCGTCTGCTGTGTGC 442

RESULT 27  
C0456060  
LOCUS MZCCL20018D05.g 903 bp mRNA linear EST 08-JUN-2005  
DEFINITION Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags

ACCESSION C0456060.1 GI:67027311  
VERSION EST.  
KEYWORDS Zea mays  
SOURCE Zea mays

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

AUTHORS Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H.,  
De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and  
Arruda, P.

TITLE Endosperm-preferred expression of maize genes as revealed by

transcriptome-wide analysis of expressed sequence tags

JOURNAL Plant Mol. Biol. (2005) In press

## COMMENT

Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
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Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br.

## FEATURES

## source

1. .903  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="P-352 near isogenic line"  
/db\_xref="taxon:4577"  
/sex="hermaphrodite"  
/tissue\_type="endosperm"  
/dev\_stage="multiple stages (10 to 25 days after  
pollination, see publication for more information)"  
/lab\_host="E. coli DH108"  
/clone\_lib="Maize Endosperm cDNA Library"  
/note="Organ: seed; Vector: pSPORT1; Site: 1: Sali; Site 2:  
NotI; Plant Material and RNA Isolation: Field grown maize

plants from inbred line F352 were used. Ears were  
harvested at 10, 15, 20 and 25 days after pollination  
(DAP). seeds were cut from the ear and the upper third of  
the endosperms, containing only endosperm, aleurone and  
pericarpal tissues, was removed, frozen in liquid nitrogen  
and stored at -800 C. Frozen endosperms were pulverized in  
method of Manning (9). Poly(A)+RNA was isolated according the  
Oligotex-dT. cDNA libraries were constructed using  
Superscript plasmid System for cDNA Synthesis and Plasmid  
Cloning Kit as described in Vettore, et al., (2001) The  
libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs  
ranging from 500 to 800 bp in size were assigned as short  
libraries (S10, S15, S20), and cDNAs >800 were assigned as  
long libraries (L10, L15, M15, L20, L25). Unamplified  
libraries were plated and individual colonies picked and  
transferred to 96 well plates containing liquid Circle  
Grow (CG) medium supplemented with 100 mg/L of ampicillin  
and 8% glycerol. Three copies of each cDNA clone were  
stored at -800 C. Additional information can be found in :  
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,  
Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,  
A.L., da Silva, F.R. and Arruda, P. (2005)

Endosperm-preferred expression of maize genes as revealed  
by transcriptome-wide analysis of expressed sequence tags.  
Plant Molecular Biology (/in press/)"

## ORIGIN

Alignment Scores:  
Pred. No.: 9.07e-24 Length: 903  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x C0456060 (1-903)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
|||||  
Db 228 ATGGCGGCTCTGGCCAGCTCGCAGCTGTGCAACGGCGCGCGCTGGGGCTCCCGGAC 287  
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
|||||  
Db 288 GCGTCCACGTTCCGCCGCGCGCGCGCAGGGCTGAGGGGGCGCGGGCTGGCGGCG 347  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
|||||  
Db 348 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCCAGGCCACGACGACGAGCG 407  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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Db 408 CGCGCGGGGGGACGG-----TTCCCGTCTGCTGTGTGC 443

## RESULT 28

## C0460347

## LOCUS

DEFINITION MZCCL15023D11.g 911 bp mRNA linear EST 08-JUN-2005  
sequence.

## ACCESSION

## C0460347

## VERSION

## EST.

## KEYWORDS

## SOURCE

## ORGANISM

## Zea mays

## Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

## Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

## clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

## AUTHORS

## TITLE

## Endosperm-preferred expression of maize genes as revealed by

## transcriptome-wide analysis of expressed sequence tags

JOURNAL  
COMMENT

Plant Mol. Biol. (2005) In press  
 Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.

## FEATURES

## source

1. .911  
 /location/Qualifiers  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
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 /sex="hermaphrodite"  
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 /dev\_stage="multiple stages (10 to 25 days after  
 pollination, see publication for more information)"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="Maize Endosperm cDNA Library"  
 /note="Organ: seed; Vector: pSPORT1; Site 1: Sall; Site 2:  
 NotI; Plant Material and RNA Isolation: Field grown maize  
 plants from inbred line F352 were used. Ears were  
 harvested at 10, 15, 20 and 25 days after pollination  
 (DAP), seeds were cut from the ear and the upper third of  
 the endosperms, containing only endosperm, aleurone and  
 pericarpal tissues, was removed, frozen in liquid nitrogen  
 and stored at -800 C. Frozen endosperms were pulverized in  
 liquid nitrogen and total RNA was isolated according to the  
 method of Manning (9). Poly(A)+RNA was isolated using the  
 Oligotex-dT. cDNA libraries were constructed using  
 SuperScript Plasmid System for cDNA Synthesis and Plasmid  
 Cloning Kit as described in Vettore, et al., (2001) The  
 libraries that made SUCSEST. Genet Mol Biol 24: 1-7. CDNAS  
 ranging from 500 to 800 bp in size were assigned as short  
 libraries (S10, S15, S20), and CDNAS >800 were assigned as  
 long libraries (L10, L15, M15, L20, L25). Unamplified  
 libraries were plated and individual colonies picked and  
 transferred to 96 well plates containing liquid Circle  
 Grow (CG) medium supplemented with 100 mg/L of ampicillin  
 and 8% glycerol. Three copies of each cDNA clone were  
 stored at -800 C. Additional information can be found in :  
 Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, P.T.S.,  
 Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,  
 A.L., da Silva, F.R. and Arruda, P. (2005)  
 Endosperm-preferred expression of maize genes as revealed  
 by transcriptome-wide analysis of expressed sequence tags.  
 Plant Molecular Biology (/in press//)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 9,16e-24 Length: 911  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO460347 (1-911)

OY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAep 20  
 Db 238 ATGGCGGCTCTGGCCACGTCGCGAGCTGTCGCAACGGCGCGCGCTGGCGTCCGGAC 297  
 OY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaLa 40  
 Db 298 GGTCCACGTTCCGCGCGCGCGCGCGAGGCGCTGAGGGGGCGCGCGTCCGCGCG 357  
 OY 41 AlaAepThrLeuSerMetArgThrSerAlaAlaThrArgAlaAlaProArgHisGlnGlnAla 60  
 Db 358 GCGGACACGCTCAGCATCGGACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 417  
 OY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74

## Db

418 CGCGCGGGGGGAGG-----TCCCGTGGCTGGTGTGTC 453

## RESULT 29

CO464483

## LOCUS

DEFINITION

CO464483 927 bp mRNA linear EST 08-JUN-2005  
 MZCCS15033H11.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA

## ACCESSION

CO464483

## VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS

1 (bases 1 to 927)

Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,P.T.S., Fisch,P.H.,  
 De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and  
 Arruda,P.

Endosperm-preferred expression of maize genes as revealed by  
 transcriptome-wide analysis of expressed sequence tags

Plant Mol. Biol. (2005) In press

COMMENT

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br.

Location/Qualifiers

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/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="F-352 near isogenic line"

/db\_xref="taxon:4577"

/sex="hermaphrodite"

/tissue\_type="endosperm"

/dev\_stage="multiple stages (10 to 25 days after

pollination, see publication for more information)"

/lab\_host="E. coli DH10B"

/clone\_lib="Maize Endosperm cDNA Library"

/note="Organ: seed; Vector: pSPORT1; Site 1: Sall; Site 2:

NotI; Plant Material and RNA Isolation: Field grown maize

plants from inbred line F352 were used. Ears were

harvested at 10, 15, 20 and 25 days after pollination

(DAP), seeds were cut from the ear and the upper third of

the endosperms, containing only endosperm, aleurone and

pericarpal tissues, was removed, frozen in liquid nitrogen

and stored at -800 C. Frozen endosperms were pulverized in

liquid nitrogen and total RNA was isolated according to the

method of Manning (9). Poly(A)+RNA was isolated using

Oligotex-dT. cDNA libraries were constructed using

SuperScript Plasmid System for cDNA Synthesis and Plasmid

Cloning Kit as described in Vettore, et al., (2001) The

libraries that made SUCSEST. Genet Mol Biol 24: 1-7. CDNAS

ranging from 500 to 800 bp in size were assigned as short

libraries (S10, S15, S20), and CDNAS >800 were assigned as

long libraries (L10, L15, M15, L20, L25). Unamplified

libraries were plated and individual colonies picked and

transferred to 96 well plates containing liquid Circle

Grow (CG) medium supplemented with 100 mg/L of ampicillin

and 8% glycerol. Three copies of each cDNA clone were

stored at -800 C. Additional information can be found in :

Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, P.T.S.,

Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,

A.L., da Silva, F.R. and Arruda, P. (2005)

Endosperm-preferred expression of maize genes as revealed

by transcriptome-wide analysis of expressed sequence tags.

Plant Molecular Biology (/in press//)"

## ORIGIN

Alignment Scores:

Pred. No.: 9.34e-24 Length: 927  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO464483 (1-927)

Qy 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
 Db 199 ATGGCGGCTCTGGCCAGCTGTCGCAAGCGCGCGCTGGGGCTCCCGGAC 258  
 Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 Db 259 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCG 318  
 Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 319 GCGGACACGTCAGCATGCGGACGAGCGCGCGCGCGCGCGCGCGCGCGCG 378  
 Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 379 CGCGCGGGGGCAGG-----TTCCCGTCTGCTGCTGTGC 414

RESULT 30  
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 LOCUS MZCCS15011P02.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA  
 DEFINITION sequence.  
 ACCESSION CO457630  
 VERSION CO457630.1 GI:67028881  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 785)  
 Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H.,  
 De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, P.R. and  
 Arruda, P.  
 Endosperm-preferred expression of maize genes as revealed by  
 transcriptome-wide analysis of expressed sequence tags  
 Plant Mol. Biol. (2005) In press  
 Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.  
 Location/Qualifiers  
 1..785  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="P-352 near isogenic line"  
 /db\_xref="taxon:4577"  
 /sex="hermaphrodite"  
 /tissue\_type="endosperm"  
 /dev\_stage="multiple stages (10 to 25 days after  
 pollination, see publication for more information)"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="Maize Endosperm cDNA Library"  
 /notes="Organ: seed; Vector: pSPORT1; Site 1: Salt; Site 2:  
 NotI; Plant Material and RNA Isolation: Field grown maize  
 plants from inbred line F352 were used. Ears were  
 harvested at 10, 15, 20 and 25 days after pollination  
 (DAP), seeds were cut from the ear and the upper third of  
 the endosperms, containing only endosperm, aleurone and  
 pericarpal tissues, was removed, frozen in liquid nitrogen  
 and stored at -80o C. Frozen endosperms were pulverized in  
 liquid nitrogen and total RNA was isolated according the

method of Manning (9). Poly(A)+RNA was isolated using  
 Oligotex-dT. cDNA libraries were constructed using  
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 Cloning Kit as described in Vettore, et al., (2001) The  
 libraries that made SUCSEST. Genet Mol Biol 24: 1-7. cDNAs  
 ranging from 500 to 800 bp in size were assigned as short  
 long libraries (L10, L15, M15, L20, L25). Unamplified  
 libraries were plated and individual colonies picked and  
 transferred to 96 well plates containing liquid Circle  
 Grow (CG) medium supplemented with 100 mg/L of ampicillin  
 and 8% glycerol. Three copies of each cDNA clone were  
 stored at -80o C. Additional information can be found in :  
 Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,  
 Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,  
 A.L., da Silva, P.R. and Arruda, P. (2005)  
 Endosperm-preferred expression of maize genes as revealed  
 by transcriptome-wide analysis of expressed sequence tags.  
 Plant Molecular Biology (/in press/)"

ORIGIN

Alignment Scores:  
 Pred. No.: 1.98e-23 Length: 785  
 Score: 329.00 Matches: 70  
 Percent Similarity: 94.6% Conservative: 0  
 Best Local Similarity: 94.6% Mismatches: 2  
 Query Match: 89.4% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO457630 (1-785)

Qy 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
 Db 211 ATGGCGGCTCTGGCCAGCTGTCGCAAGCGCGCGCTGGGGCTCCCGGAC 270  
 Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 Db 271 GCGTCCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCG 330  
 Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 331 GTGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCG 390  
 Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 391 CGCGCGGGGGCAGG-----TTCCCGTCTGCTGCTGTGC 426

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 Job time : 1196.34 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 31, 2006, 22:47:42 ; Search time 98.966 Seconds  
(without alignments)  
1329.139 Million cell updates/sec

Title: US-10-628-525A-36

Perfect score: 368

Sequence: 1 MAALATSQLVATRAGHVPD.....RHQQQARRGRFFPPLVVC 74

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-Q=/abss/ABSSWEB spool/US10628525/runat\_31032006\_095123\_16858/app\_query.fasta\_1  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=150 -DLOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=30  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abs02p -USER=US10628525 @CGN 1.1.855 @runat\_31032006\_095123\_16858  
-NCPUs=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length  | ID | Description         |
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| 2          | 333   | 90.5        | 4800    | 3  | US-08-941-445A-4    |
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| 4          | 128.5 | 34.9        | 2542    | 3  | US-08-941-445A-6    |
| 5          | 98.5  | 26.8        | 1714    | 3  | US-10-104-047-1085  |
| 6          | 88.5  | 24.0        | 6776    | 3  | US-09-104-047-884   |
| 7          | 87    | 23.6        | 49315   | 3  | US-09-902-540-884   |
| 8          | 86    | 23.4        | 3785    | 3  | US-09-949-016-13016 |
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| 12 | 84   | 22.8 | 109519 | 3 | US-09-758-759-1      | Sequence 1, Appli |
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| 16 | 82   | 22.3 | 25709  | 3 | US-09-949-016-13338  | Sequence 13338, A |
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| c  | 78.5 | 21.3 | 1458   | 3 | US-09-252-991A-1112  | Sequence 1112, Ap |
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126 74.5 20.2 3030 3 US-09-232-149A-333 Sequence 333, App
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133 74.5 20.2 3030 3 US-09-657-279-333 Sequence 333, App
134 74.5 20.2 3030 3 US-10-012-896-333 Sequence 333, App
135 74.5 20.2 3801 3 US-09-252-991A-14280 Sequence 14280, A
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137 74.5 20.2 7007 3 US-09-949-016-13645 Sequence 13645, A
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139 74.5 20.2 8820 3 US-09-902-540-974 Sequence 974, App
140 74 20.1 1032 3 US-09-252-991A-9565 Sequence 9565, Ap
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143 74 20.1 1614 3 US-09-252-991A-9523 Sequence 9523, Ap
144 74 20.1 18551 3 US-09-902-540-1187 Sequence 1187, Ap
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ALIGNMENTS

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US-09-731-166-3
; Sequence 3, Application US/09731166
; Patent No. 6639126
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent J. H.
; APPLICANT: Singletary, George W.
; TITLE OF INVENTION: Production of Modified Polysaccharides
; FILE REFERENCE: 35718/206348
; CURRENT APPLICATION NUMBER: US/09/731,166
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/169,993
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1818
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: UDP-glucose starch glycosyl transferase -- Genbank
; NAME/KEY: CDS
; LOCATION: (1)...(1818)
US-09-731-166-3

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Pred. No.: 4,868-25 Length: 1818
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Percent Similarity: 95.9% Conservative: 0
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Query Match: 90.5% Indels: 2
DB: 3 Gaps: 1

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RESULT 2
US-08-941-445A-4
; Sequence 4, Application US/08941445A
; Patent No. 6107050
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanning
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/941.445A  
FILING DATE: 30-SEP-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026,855  
FILING DATE: 30-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Winner, Ellen P  
REGISTRATION NUMBER: 28,547  
REFERENCE/DOCKET NUMBER: 89-97  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4800 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: not relevant  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1449..1553, 1685..1765, 1860..1958, 2055  
LOCATION: ..2144, 2226..2289, 2413..2513, 2651..2760, 2858  
LOCATION: ..3101, 3212..3394, 3490..3681, 3793..3879, 3977  
LOCATION: ..4105, 4227..4343)  
US-08-941-445A-4

Alignment Scores:  
Pred. No.: 1-5e-24 Length: 4800  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 3 Gaps: 1

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QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40  
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Db 1413 CGCGCGCGGGGCGAGG-----TTCCCGTCTGCTGCTGTCG 1448

## RESULT 3

US-08-679-645-25  
Sequence 25, Application US/08679645  
Patent No. 6350934  
GENERAL INFORMATION:  
APPLICANT: Zwick, Michael G.  
APPLICANT: Edington, Brent E.  
APPLICANT: McSwiggen, James A.  
APPLICANT: Merlo, Patricia Ann Owens  
APPLICANT: Guo, Lining  
APPLICANT: Skokut, Thomas A.  
APPLICANT: Young, Scott A.  
APPLICANT: Folkerts, Otto  
APPLICANT: Merlo, Donald J.

TITLE OF INVENTION: COMPOSITION AND METHODS FOR  
TITLE OF INVENTION: MODULATION OF GENE EXPRESSION  
NUMBER OF SEQUENCES: 1263  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/679,645  
FILING DATE: July 12, 1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/001,135  
FILING DATE: July 13, 1995  
APPLICATION NUMBER: 08/300,726  
FILING DATE: September 2, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 219/247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2267 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-679-645-25

Alignment Scores:  
Pred. No.: 1-98e-20 Length: 2267  
Score: 289.00 Matches: 64  
Percent Similarity: 85.9% Conservative: 3  
Best Local Similarity: 82.1% Mismatches: 5  
Query Match: 78.5% Indels: 6  
DB: 3 Gaps: 2

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## RESULT 4

US-08-941-445A-6  
Sequence 6, Application US/08941445A  
Patent No. 6107060

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; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Haining
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 453..2282
; US-08-941-445A-6

Alignment Scores:
Pred. No.: 0.00583 Length: 2542
Score: 128.50 Matches: 35
Percent Similarity: 60.3% Conservative: 12
Best Local Similarity: 44.9% Mismatches: 24
Query Match: 34.9% Indels: 7
DB: 3 Gaps: 4

US-10-628-525A-36 (1-74) x US-08-941-445A-6 (1-2542)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProasp 20
Db 453 ATGTGGCTCTCACCAGCTCCCGCCAGCTCGGCCACCGGCTTCAGGCGCTCAAG---CCCGCGCAGC 512

QY 21 -----AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAla 37
Db 513 AGGTGGCGCGCTGTCGTGCTCGGCCACGGGTTCCAGGGCTCAAG---CCCGCGCAGC 569

QY 38 SerAlaAlaAlaAsp-----ThrLeuSerMetArgThrSerAlaArgAlaAlaProArg 55
Db 570 CCCGCGCGCGCGCGCGCGCGCTCGCTCAGCGTGCAGCAGCAGCGCGCGCGCGCGCGCGCG 629

QY 56 HisGlnGlnAlaAlaArgGlyGlyArgPheProPheProSerLeuValVal 73
Db 630 CAGCAGCGGTGCTGTCAGCGTGGCAGCGG---AGTTCCCTTCGTGCTGTTG 680

RESULT 5
; Sequence 1085, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1085
; LENGTH: 1714
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1085

Alignment Scores:
Pred. No.: 0.432 Length: 1714
Score: 98.50 Matches: 31
Percent Similarity: 44.6% Conservative: 6
Best Local Similarity: 37.3% Mismatches: 28
Query Match: 26.8% Indels: 18
DB: 3 Gaps: 3

US-10-628-525A-36 (1-74) x US-10-104-047-1085 (1-1714)

QY 6 ThrSerGlnLeuValAla---ThrArgAlaGlyHisGlyValProaspAlaSerThrPhe 24
Db 784 TCCAAGATGCTGTGTGGCCCGGTGAGTCTGCCATTGGTCTGCCAGGTCCTCTGCACGTG 843

QY 25 Arg-ArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAspThrIle 44
Db 844 AGGCAGGGGAGGCCAGCAAGGACTTCAGGGCTGCAGAGCCTTCCTCGCAGTTCCTACCTT 903

QY 44 u-----SerMetArgThrSerAlaArgAlaAlaPr 54
Db 904 ACAACACAGGATCTAATCCCTAACCTGGGGTACGTGTGAGCACACAGGGAGAGGCCCTC 963

QY 54 oArgHisGlnGlnAlaAlaArg-----ArgGlyGlyArgPheProPh 68
Db 964 GAGGCATGGGCACCATGCCAGGCTGTAGGCACCTTCTCTGCAGCAGGAGCAGAAATCCCTT 1023

QY 68 eProSer 70
Db 1024 CCCAAGT 1030

RESULT 6
US-09-902-540-884/C
; Sequence 884, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 884
; LENGTH: 6776
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-884

Alignment Scores:
Pred. No.: 22.3 Length: 6776
```



```
Pred. No.: 1.01e+05 Length: 4403765
Score: 84.50 Matches: 27
Percent Similarity: 39.5% Conservative: 3
Best Local Similarity: 35.5% Mismatches: 31
Query Match: 23.0% Indels: 15
DB: 3 Gaps: 2

US-10-628-525A-36 (1-74) x US-09-103-840A-2 (1-4403765)

QY 2 AlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAla 21
Db 1387044 GCGGCAACTGCTGGCGCTCAACGAGTCCCGCGTGTGGACACACCGCCCTGAT--- 1387100
QY 22 SerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyValaArgAlaSerAlaAla 41
Db 1387101 -----CGGATCGCGCGCCAGGTGGCGGGGGCGACCCCGCGCGGTGGC 1387148
QY 42 AspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAlaArg 61
Db 1387149 CCGCGCTGGCTCGCGACACCCGCTGGGACGTTGAGCGCGCACGAGCGTCCGGTGA 1387208
QY 62 ArgGly-----GlyArgPhePro 67
Db 1387209 CCGGATGACACACCGCGTGGCGGAACACCTTCGGCGCGCTTTCCT 1387256

RESULT 10
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: TUBERCULOSIS
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 1.01e+05 Length: 4411529
Score: 84.50 Matches: 27
Percent Similarity: 39.5% Conservative: 3
Best Local Similarity: 35.5% Mismatches: 31
Query Match: 23.0% Indels: 15
DB: 3 Gaps: 2

US-10-628-525A-36 (1-74) x US-09-103-840A-1 (1-4411529)

QY 2 AlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAla 21
Db 1387574 GCGGCAACTGCTGGCGCTCAACGAGTCCCGCGTGTGGACACACCGCCCTGAT--- 1387630
QY 22 SerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyValaArgAlaSerAlaAla 41
Db 1387631 -----CGGATCGCGCGCCAGGTGGCGGGGGCGACCCCGCGCGGTGGC 1387678
QY 42 AspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAlaArg 61
Db 1387679 CCGCGCTGGCTCGCGACACCCGCTGGGACGTTGAGCGCGCACGAGCGTCCGGTGA 1387738
QY 62 ArgGly-----GlyArgPhePro 67
Db 1387739 CCGGATGACACACCGCGTGGCGGAACACCTTCGGCGCGCTTTCCT 1387786
```

```
RESULT 11
US-09-758-759-82
; Sequence 82, Application US/09758759
; Patent No. 6861513
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas J.
; APPLICANT: Wang, Tim X.
; APPLICANT: Horan, Ann C.
; TITLE OF INVENTION: Everminomicin Biosynthetic Genes
; FILE REFERENCE: ID0983K US
; CURRENT APPLICATION NUMBER: US/09/758,759
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/175,751
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Micromonospora carbonacea
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(666)
; OTHER INFORMATION: evaC
US-09-758-759-82

Alignment Scores:
Pred. No.: 4.39 Length: 666
Score: 84.00 Matches: 25
Percent Similarity: 55.6% Conservative: 5
Best Local Similarity: 46.3% Mismatches: 18
Query Match: 22.8% Indels: 6
DB: 3 Gaps: 3

US-10-628-525A-36 (1-74) x US-09-758-759-82 (1-666)

QY 15 GlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGly 34
Db 153 GGAGCTGGCCCGCCCTGAAGCGCGAGCGGTCTCGCGCGCTCGCCGCC-----GTCGCGC 206
QY 35 AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaPro 54
Db 207 CGAGCGAGCGGACGCTGGTGCT-----CGGCTGGACCTCGCTTCGACCG 257
QY 55 ArgHisGlnGlnAlaAla---ArgArgGlyGlyArgPhePro 67
Db 258 CGAGATTCTCGCAACCGCGCGCGAGCGAGCGGACGCTACCCG 299

RESULT 12
US-09-758-759-1
; Sequence 1, Application US/09758759
; Patent No. 6861513
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas J.
; APPLICANT: Wang, Tim X.
; APPLICANT: Horan, Ann C.
; TITLE OF INVENTION: Everminomicin Biosynthetic Genes
; FILE REFERENCE: ID0983K US
; CURRENT APPLICATION NUMBER: US/09/758,759
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/175,751
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 109519
; TYPE: DNA
; ORGANISM: Micromonospora carbonacea
US-09-758-759-1

Alignment Scores:
Pred. No.: 1.61e+03 Length: 109519
```





Score: 82.00 Matches: 29  
Percent Similarity: 53.0% Conservative: 6  
Best Local Similarity: 43.9% Mismatches: 24  
Query Match: 22.3% Indels: 7  
DB: 3 Gaps: 3

US-10-628-525A-36 (1-74) x US-09-949-016-14168 (1-21490)

QY 10 ValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAla 29  
Db 1416 GTGTGGGCGCGAAGGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1475  
QY 30 GInGlyLeuArg---GlyAlaArgAlaSerAlaAlaAspThrLeuSerMetArgThr 48  
Db 1476 AAGGAGCGCGGTGGCGGCACTTGTGCGCGCGCGCTTGATGGCTGGCG-----CCC 1529  
QY 49 SerAlaArgAlaAla-ProArgHisGlnGlnAlaArgArgGlyGlyArgPhe----- 66  
Db 1530 CCTCGCGCTCGCTCTCTCCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1589  
QY 67 ---ProPheProSer 70  
Db 1590 GGGCCGGCACCTTCG 1605

## RESULT 16

US-09-949-016-13338  
; Sequence 13338, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13338  
; LENGTH: 25709  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-13338

## Alignment Scores:

Pred. No.: 482 Length: 25709  
Score: 82.00 Matches: 29  
Percent Similarity: 53.0% Conservative: 6  
Best Local Similarity: 43.9% Mismatches: 24  
Query Match: 22.3% Indels: 7  
DB: 3 Gaps: 3

US-10-628-525A-36 (1-74) x US-09-949-016-13338 (1-25709)

QY 10 ValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAla 29  
Db 1416 GTGTGGGCGCGAAGGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1475  
QY 30 GInGlyLeuArg---GlyAlaArgAlaSerAlaAlaAspThrLeuSerMetArgThr 48  
Db 1476 AAGGAGCGCGGTGGCGGCACTTGTGCGCGCGCGCTTGATGGCTGGCG-----CCC 1529  
QY 49 SerAlaArgAlaAla-ProArgHisGlnGlnAlaArgArgGlyGlyArgPhe----- 66  
Db 1530 CCTCGCGCTCGCTCTCTCCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1589  
QY 67 ---ProPheProSer 70  
Db 1590 GGGCCGGCACCTTCG 1605

Db 1590 GGGCCGGCACCTTCG 1605

## RESULT 17

US-09-252-991A-15592/c  
; Sequence 15592, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 15592  
; LENGTH: 1008  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-15592

## Alignment Scores:

Pred. No.: 14.4 Length: 1008  
Score: 81.00 Matches: 24  
Percent Similarity: 48.4% Conservative: 6  
Best Local Similarity: 38.7% Mismatches: 30  
Query Match: 22.0% Indels: 2  
DB: 3 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-252-991A-15592 (1-1008)

QY 5 AlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPhe 24  
Db 315 GCGCCTCGCGAAGGCTTGCCTGTCGAGCGCGGTTGGAGCTGGCGGTGGAGACCGTGT 256  
QY 25 ArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAspThrLeu 44  
Db 255 CGGCGCGGATCTGCAGCGCGGCTTCTGTCGACGGCTTCGACGGGCTCGCCCTGGCGCGCTT 196  
QY 45 SerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAlaArgArgGlyGly 64  
Db 195 CGGCAAGGCGGAGCTGCGCTGCTCAGCCCGC-----TCGCGGAGCGCGACGGCGC 142  
QY 65 ArgPhe 66  
Db 141 CCGTTC 136

## RESULT 18

US-09-252-991A-15755  
; Sequence 15755, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 15755  
; LENGTH: 1266  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-15755  
Alignment Scores:

```
Pred. No.: 18.7 Length: 1266
Score: 81.00 Matches: 24
Percent Similarity: 48.4% Conservative: 6
Best Local Similarity: 38.7% Mismatches: 30
Query Match: 22.0% Indels: 2
DB: 3 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-252-991A-15755 (1-1266)
QY 5 AlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPhe 24
DB 559 GCCTCGCCGAGGCTTGGCTGTCAGAGCCGGTTGGAGCTGGCGTGGAGACCGTGTCT 618
QY 25 ArgArgGlyAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAspThrLeu 44
DB 619 CGCGCGGATCTGAGCGGCTTGTGTGACGGCTTCGACGGGCTTCGCCCTGGCCGGCTT 678
QY 45 SerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAlaArgArgGlyGly 64
DB 679 CGCGAGGCGAGCTGCGCTGCTCAGCCCGC-----TCGCGAGCCCGAGCGCGGC 732
QY 65 ArgPhe 66
DB 733 CGGTTT 738

RESULT 19
US-08-656-393-1/c
; Sequence 1, Application US/08656393
; Patent No. 5837258
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; TITLE OF INVENTION: METHODS AND USES OF CONNECTIVE TISSUE
; TITLE OF INVENTION: GROWTH FACTOR AS AN INDUCTION AGENT
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,393
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2541 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-656-393-1

Alignment Scores:
Pred. No.: 41.9 Length: 2541
Score: 81.00 Matches: 23
Percent Similarity: 49.2% Conservative: 6
Best Local Similarity: 39.0% Mismatches: 20
Query Match: 22.0% Indels: 10
```

```
DB: 2 Gaps: 2
US-10-628-525A-36 (1-74) x US-08-656-393-1 (1-2541)
QY 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31
DB 2264 ACACGCCGATCTTGGCGTTGGCCGGGAGCCGAAGTCACAGAGAGGCCCTTGTGCGGCT 2205
QY 32 LeuArgGly-----AlaArgAlaSerAlaAlaAlaAspThrLeuSerMet 46
DB 2204 CGCAGGGTGGCGTGGTGCACAGCTGCCACAGTGTCTGGCGAGAC-----2157
QY 47 ArgThrSerAlaArgAlaAlaProArgHisGlnGlnAlaArgArgGlyGlyArg 65
DB 2156 ---GCGGAGCAGCCGCGCTCCAGCAGAGCTTCAGCCCGCGGCGAGCGCG 2103

RESULT 20
US-09-252-991A-15560/c
; Sequence 15560, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15560
; LENGTH: 3402
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15560

Alignment Scores:
Pred. No.: 58.8 Length: 3402
Score: 81.00 Matches: 24
Percent Similarity: 48.4% Conservative: 6
Best Local Similarity: 38.7% Mismatches: 30
Query Match: 22.0% Indels: 2
DB: 3 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-252-991A-15560 (1-3402)
QY 5 AlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPhe 24
DB 1552 GCGCTCGCCGAGGCTTGGTGTGAGCCGGTTGGAGCTGGCGTGGAGACCGTGTCT 1493
QY 25 ArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAspThrLeu 44
DB 1492 CGCGCGGATCTGACGGCGCTTGTGTGACCGGCTTCGACGGGCTTCGCCCTGGCCGGCTT 1433
QY 45 SerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAlaArgArgGlyGly 64
DB 1432 CGCGAGGCGGAGCTGGCTGCTCAGCCCGC-----TCGCGAGAGCCGAGCGCGGC 1379
QY 65 ArgPhe 66
DB 1378 CGGTTT 1373

RESULT 21
US-09-252-991A-15688
; Sequence 15688, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
```

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; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15688
; LENGTH: 3606
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15688

Alignment Scores:
Pred. No.:          62.9      Length:      3606
Score:              81.00     Matches:    24
Percent Similarity: 48.4%     Conservative: 6
Best Local Similarity: 38.7%  Mismatches: 30
Query Match:        22.0%     Indels:    2
DB:                 3        Gaps:        1

US-10-628-525A-36 (1-74) x US-09-252-991A-15688 (1-3606)

QY 5 AlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPhe 24
   |||
   :::
   |||
Db 1689 GCGCCTCGCGGAGGCTTCGGTGTGAGCGCGGTTGGGAGCTGGCGGTGGAGACCGTGCT 1748
QY 25 ArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAspThrLeu 44	
Db 1749 CGGCGGAGATCGCAGCGGCTTGTGAGCGGCTTCGACGGCTTCGACGGGCTCGCCCTGGCGGCTT 1808	
QY 45 SerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAlaArgArgGlyGly 64	
Db 1809 CGGCAAGGCGAGTGGCTGCTAGCCCCCGC-----TCGCGAGGCGCGCAGCGCGGC 1862	
QY 65 ArgPhe 66	
Db 1863 CGGTTTC 1868

RESULT 22
US-09-724-797-27
; Sequence 27, Application US/09724797
; Patent No. 6733998
; GENERAL INFORMATION:
; APPLICANT: Jon S. THORSON
; TITLE OF INVENTION: MICRONOSPORA ECHINOSPORA GENES
; TITLE OF INVENTION: ENCODING FOR BIOSYNTHESIS OF
; TITLE OF INVENTION: CALICHEAMICIN AND SELF-RESISTANCE THEREO
; FILE REFERENCE: 2653-40
; CURRENT APPLICATION NUMBER: US/09/724,797
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/111,325
; PRIOR FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Bacteria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(993)
US-09-724-797-27

Alignment Scores:
Pred. No.:          15.9      Length:      993
Score:              80.50     Matches:    26
Percent Similarity: 46.4%     Conservative: 6
Best Local Similarity: 37.7%  Mismatches: 32
Query Match:        21.9%     Indels:    5
DB:                 3        Gaps:        1

US-10-628-525A-36 (1-74) x US-09-724-797-27 (1-993)

; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15688
; LENGTH: 3606
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15688

Alignment Scores:
Pred. No.:          62.9      Length:      3606
Score:              81.00     Matches:    24
Percent Similarity: 48.4%     Conservative: 6
Best Local Similarity: 38.7%  Mismatches: 30
Query Match:        22.0%     Indels:    2
DB:                 3        Gaps:        1

US-10-628-525A-36 (1-74) x US-09-252-991A-15688 (1-3606)

QY 5 AlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPhe 24
   |||
   :::
   |||
Db 1689 GCGCCTCGCGGAGGCTTCGGTGTGAGCGCGGTTGGGAGCTGGCGGTGGAGACCGTGCT 1748
QY 25 ArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAspThrLeu 44	
Db 1749 CGGCGGAGATCGCAGCGGCTTGTGAGCGGCTTCGACGGCTTCGACGGGCTCGCCCTGGCGGCTT 1808	
QY 45 SerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAlaArgArgGlyGly 64	
Db 1809 CGGCAAGGCGAGTGGCTGCTAGCCCCCGC-----TCGCGAGGCGCGCAGCGCGGC 1862	
QY 65 ArgPhe 66	
Db 1863 CGGTTTC 1868

RESULT 23
US-09-232-279-1/c
; Sequence 1, Application US/09232279
; Patent No. 6376473
; GENERAL INFORMATION:
; APPLICANT: Audoneet et al.
; TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE FORMULA, PARTICULARLY FOR
; TITLE OF INVENTION: TREATING BOVINE RESPIRATORY DISEASE
; FILE REFERENCE: 454313-2250
; CURRENT APPLICATION NUMBER: US/09/232,279
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2799
; TYPE: DNA
; ORGANISM: Bovine herpesvirus 2
US-09-232-279-1

Alignment Scores:
Pred. No.:          52.7      Length:      2799
Score:              80.50     Matches:    28
Percent Similarity: 51.6%     Conservative: 4
Best Local Similarity: 45.2%  Mismatches: 18
Query Match:        21.9%     Indels:    12
DB:                 3        Gaps:        2

US-10-628-525A-36 (1-74) x US-09-232-279-1 (1-2799)

QY 7 SerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArg 26
Db 1833 GCCCAGCTCGTGGCAGTAGCTCAGCGCCATGCGGTCCCC-----CAA 1792	
QY 27 GlyAlaAlaGlnGlyLeu-ArgGlyAlaArgAlaSerAlaAlaAspThrLeuSerMe 46	
Db 1791 CATGCGCGCGCGCGCGCGGTCCAGCGCAGCGTCCGCGCGCTGGCGCTGGGTGAGCTT 1732	
QY 46 tArgThrSerAlaArgAlaAla-----ProArgHisGlnGlnAlaAla 61	
Db 1731 AGCCGCTCGGCCACACAGGCGCGCTCTTGTCTGCAGCAGCACGACGAGGTGGCCAG 1672	
QY 61 gArg 62	
Db 1671 GCGG 1668

RESULT 24
US-10-085-519-1/c
; Sequence 1, Application US/10085519
; Patent No. 6818628
; GENERAL INFORMATION:
; APPLICANT: Audoneet et al.
; TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE FORMULA, PARTICULARLY FOR
; TITLE OF INVENTION: TREATING BOVINE RESPIRATORY DISEASE
; FILE REFERENCE: 454313-2250
; CURRENT APPLICATION NUMBER: US/10/085,519
; CURRENT FILING DATE: 2002-02-28
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; PRIOR APPLICATION NUMBER: 09/232,279
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2799
; TYPE: DNA
; ORGANISM: Bovine herpesvirus 2
US-10-085-519-1

Alignment Scores:
Pred. No.: 52.7 Length: 2799
Score: 80.50 Matches: 28
Percent Similarity: 51.6% Conservative: 4
Best Local Similarity: 45.2% Mismatches: 18
Query Match: 21.9% Indels: 12
DB: 3 Gaps: 2

US-10-628-525A-36 (1-74) x US-10-085-519-1 (1-2799)
QY 7 SerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArg 26
Db 1833 GCCCAGCTGTGGCAGTACGTACGGCCATGGGTCCCC-----CAA 1792
QY 27 GlyAlaAlaGlnGlyLeu-ArgGlyAlaArgAlaSerAlaAlaAlaAspThrLeuSerMe 46
Db 1791 CATGCGCGCGCGCGCGCGGTCACGCGAGCGCTGCGCGCGCTGGGGTTGAGCTT 1732
QY 46 tArgThrSerAlaArgAlaAala-----ProArgHisGlnGlnAlaAr 61
Db 1731 AGCGGCTCGGCCACAGGCGCGCTCTTGTTCGACGACGACGACGACGACGTCGCCAG 1672
QY 61 gArg 62
Db 1671 GCGG 1668

RESULT 25
US-08-682-847-1/c
; Sequence 1, Application US/08682847
; Patent No. 5858989
; GENERAL INFORMATION:
; APPLICANT: BABIUK, LORNE
; APPLICANT: VAN DEN HURK, SYLVIA
; APPLICANT: ZAMB, TIM
; APPLICANT: FITZPATRICK, DAVID
; TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE 1
; TITLE OF INVENTION: POLYPEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,847
; FILING DATE: 12-JUL-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: PARK, FREDDIE K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 29310-20005.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 3382 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 432..3230
US-08-682-847-1

Alignment Scores:
Pred. No.: 65.7 Length: 3382
Score: 80.50 Matches: 28
Percent Similarity: 51.6% Conservative: 4
Best Local Similarity: 45.2% Mismatches: 18
Query Match: 21.9% Indels: 12
DB: 2 Gaps: 2

US-10-628-525A-36 (1-74) x US-08-682-847-1 (1-3382)
QY 7 SerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArg 26
Db 2267 GCCCAGCTGTGGCAGTACGTACGGCCATGGGTCCCC-----CAA 2226
QY 27 GlyAlaAlaGlnGlyLeu-ArgGlyAlaArgAlaSerAlaAlaAlaAspThrLeuSerMe 46
Db 2225 CATGCGCGCGCGCGCGGTCACGCGAGCGCTGCGCGCGCTGGGGTTGAGCTT 2166
QY 46 tArgThrSerAlaArgAlaAala-----ProArgHisGlnGlnAlaAr 61
Db 2165 AGCGGCTCGGCCACAGGCGCGCTCTTGTTCGACGACGACGACGACGACGTCGCCAG 2106
QY 61 gArg 62
Db 2105 GCGG 2102

RESULT 26
US-09-252-991A-6863/c
; Sequence 6863, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6863
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6863

Alignment Scores:
Pred. No.: 11.3 Length: 666
Score: 80.00 Matches: 32
Percent Similarity: 45.6% Conservative: 9
Best Local Similarity: 35.6% Mismatches: 30
Query Match: 21.7% Indels: 19
DB: 3 Gaps: 3

US-10-628-525A-36 (1-74) x US-09-252-991A-6863 (1-666)
QY 2 AlaAlaLeuAlaThrSerGlnLeuValAlaThr-----ArgAlaGlyHisGlyVal 18
Db 392 GCAGCACTGCGCGCGGATCGGTAGTGTGATCGGTGCGCGCGGTGCAGTCGCGG 333
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QY 19 ProAspAlaSerThr-----PheArgArgGlyValAlaGlnGlyLeuArgGlyAlaArg 36
Db 332 CCGACGGCGCACAGACGAGCGGCGATCGCGCGGCGCTCGGTGGCGAGCGCGCA 273
QY 37 AlaSerAlaAla-AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHi 56
Db 272 AGCTCATCGCGCGCAGATCGGTGGCAGCACCGGTGGCTGATCGCGCGCGCTCGCGG 213
QY 56 sGlnGlnGlnAlaArgGlyGly----- 64
Db 212 GCGCGCGCGCGCGCGCTGGCGCAACCATATTATGGCGAGCGCAACCGCGCTAGCAGCAG 153
QY 65 ----ArgPheProPheSerLeuVal 72
Db 152 ATGACGACTACCGCGACCGTGCCTACTA 125
RESULT 27
US-09-902-540-7146
; Sequence 7146, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 7146
; LENGTH: 813
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-7146
Alignment Scores:
Pred. No.: 14.2 Length: 813
Score: 80.00 Matches: 27
Percent Similarity: 42.6% Conservative: 2
Best Local Similarity: 39.7% Mismatches: 25
Query Match: 21.7% Indels: 14
DB: 3 Gaps: 3
US-10-628-525A-36 (1-74) x US-09-902-540-7146 (1-813)
QY 8 GlnLeuValAlaThrArgAlaGlyHis-----GlyValPro 19
Db 12 CGCCTACTTCTTACAGGAAGAGCCACCGCGGACGCGCGCGGGCGGCGGAGTCCCC 71
QY 20 AspAlaSerThrPheArgArgGlyAlaGlnGlyLeuArgGlyAlaArgAlaSerAla 39
Db 72 GGTGCTGGA-----AGAGGTGCTGCCAAGGCCTCGCGCTGGCGGTGCGCGCGT 122
QY 40 AlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGln 59
Db 123 GCGCAACCAATGACACACAGCGCTGTGGAAGGTGGGGGACACCGCCCATCCAGGTGGC 182
QY 60 Ala-----ArgArgGlyGly 64
Db 183 GCGCGTGGAGTAGCAGAGGTGGC 206
RESULT 28
US-09-252-991A-6763
; Sequence 6763, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
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; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6763
; LENGTH: 1164
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6763
Alignment Scores:
Pred. No.: 21.5 Length: 1164
Score: 80.00 Matches: 32
Percent Similarity: 45.6% Conservative: 9
Best Local Similarity: 35.6% Mismatches: 30
Query Match: 21.7% Indels: 19
DB: 3 Gaps: 3
US-10-628-525A-36 (1-74) x US-09-252-991A-6763 (1-1164)
QY 2 AlaAlaLeuAlaThr-SerGlnLeuValAlaThr-----ArgAlaGlyHisGlyVal 18
Db 785 GCAGCACTGGCGCGCGCATCGGTAGTCATCGGTGGCGCTCGGGCGGTGCAGTCGGCG 844
QY 19 ProAspAlaSerThr-----PheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArg 36
Db 845 CCGGACGGCGCAACAGACCGAAGCGGCGATCGCGCGGCGCTCGGTGGCGCGCGCA 904
QY 37 AlaSerAlaAla-AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHi 56
Db 905 AGTCATCGCGCGCGCAGATCGGTGGCAGCACCGGTGGCTGATCGCGCGCGCTCGCGCG 964
QY 56 sGlnGlnGlnAlaArgArgGlyGly----- 64
Db 965 GCGCGCGCGCGCGCGCTGGCGCAACCATATTATGGCGAGCGCAACCGCGCTAGCAGCAG 1024
QY 65 ----ArgPheProPheSerLeuVal 72
Db 1025 ATGACGACTACCGCGACCGTGCCTACTA 1052
RESULT 29
US-09-902-540-656
; Sequence 656, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 656
; LENGTH: 5163
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-656
Alignment Scores:
Pred. No.: 121 Length: 5163
Score: 80.00 Matches: 27
Percent Similarity: 42.6% Conservative: 2
Best Local Similarity: 39.7% Mismatches: 25
Query Match: 21.7% Indels: 14
DB: 3 Gaps: 3
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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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| 3               | 333   | 90.5        | 2263   | 6  | US-10-272-291-1      |
| 4               | 333   | 90.5        | 2263   | 6  | US-10-272-291-2      |
| 5               | 333   | 90.5        | 4800   | 6  | US-10-272-291-5      |
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| 7               | 333   | 90.5        | 4800   | 8  | US-10-628-525-4      |
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22.3 81.5 22.1 3503 6

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Sequence 6610, Ap  
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Sequence 54101, A  
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Sequence 3212, Ap  
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Sequence 80269, A  
Sequence 114, App  
Sequence 190, App  
Sequence 76, Appli  
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Sequence 1, Appli

US-10-156-761-1  
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US-10-723-860-8239  
US-10-229-1488-1

ALIGNMENTS

RESULT 1  
US-10-877-645-2  
; Sequence 2, Application US/10877645  
; Publication No. US20050005327A1  
; GENERAL INFORMATION:  
; APPLICANT: Ravanello, Monica P  
; APPLICANT: Foley, Terry J  
; APPLICANT: LeDeaux, John R  
; APPLICANT: Wyrick, Annette E  
; APPLICANT: Savage, Thomas J  
; TITLE OF INVENTION: Elevation of Oil Levels in Plants  
; FILE REFERENCE: REN-00-119  
; CURRENT APPLICATION NUMBER: US/10/877,645  
; CURRENT FILING DATE: 2004-06-25  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 2  
; LENGTH: 1818  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-10-877-645-2  
Alignment Scores:  
Pred. No.: 4,9e-31 Length: 1818  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 8 Gaps: 1  
US-10-628-525A-36 (1-74) x US-10-877-645-2 (1-1818)  
QY 1 MetAlaLaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProApp 20  
Db 1 ATGGCGGCTCTGGCCACGCTCGCAGCTCGTGCACGCGCGCGGCTGGCGCTCGCGGAC 60  
QY 21 AlaSerThrPheArgGlyValAlaGlnGlyLeuArgGlyValAlaArgAlaSerAlaLa 40  
Db 61 GCGTCCAGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 121 GCGGACACGCTCAGCATGCGGACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 181 CGCCCGCGGGCGAGG-----TTCCCGTGGCTCGTGTGC 216  
RESULT 2  
US-10-425-115-155307  
; Sequence 155307, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 155307  
; LENGTH: 2111  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_7321C.1  
US-10-425-115-155307

Alignment Scores:

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Pred. No.: 5.67e-31 Length: 2111
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-425-115-155307 (1-2111)

Qy 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 1 ATGGCGGCTCTGGCCAGCTCGCAGCTCGTGCACAGCGCGCGGCTGGGGCTCCCGGAC 60
Qy 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 61 GCGTCCACGTTCCG 120
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 121 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 181 CGCGCGCGGGGCGAGG-----TTCCCGTCTGCTGTGTGTC 216

RESULT 3
US-10-272-291-1
; Sequence 1, Application US/10272291
; Publication No. US20030150023A1
; GENERAL INFORMATION:
; APPLICANT: ExSeed Genetics
; TITLE OF INVENTION: Starch
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/272,291
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/329,525
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The mutation is at position 1643 in the sequence,
; OTHER INFORMATION: 1450 bp after the start codon.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The change is a "G" in the wild type (EX385) to an
; OTHER INFORMATION: "A" in the mutant
US-10-272-291-2

Alignment Scores:
Pred. No.: 6.07e-31 Length: 2263
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 6 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-272-291-2 (1-2263)

Qy 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 194 ATGGCGGCTCTGGCCAGCTCGCAGCTCGTGCACAGCGCGCGGCTGGGGCTCCCGGAC 253
Qy 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 254 GCGTCCACGTTCCG 313
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 314 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 373
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 374 CGCGCGGGGGGCGAGG-----TTCCCGTCTGCTGTGTGTC 409

RESULT 5
US-10-272-291-5
; Sequence 5, Application US/10272291
; Publication No. US20030150023A1
; GENERAL INFORMATION:
; APPLICANT: ExSeed Genetics
; TITLE OF INVENTION: Starch
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/272,291
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/329,525
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4800
; TYPE: DNA
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Pred. No.: 5.67e-31 Length: 2111
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-425-115-155307 (1-2111)

Qy 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 1 ATGGCGGCTCTGGCCAGCTCGCAGCTCGTGCACAGCGCGCGGCTGGGGCTCCCGGAC 60
Qy 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 61 GCGTCCACGTTCCG 120
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 121 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 181 CGCGCGGGGGGCGAGG-----TTCCCGTCTGCTGTGTGTC 216

RESULT 3
US-10-272-291-1
; Sequence 1, Application US/10272291
; Publication No. US20030150023A1
; GENERAL INFORMATION:
; APPLICANT: ExSeed Genetics
; TITLE OF INVENTION: Starch
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/272,291
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/329,525
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The mutation is at position 1643 in the sequence,
; OTHER INFORMATION: 1450 bp after the start codon.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The change is a "G" in the wild type (EX385) to an
; OTHER INFORMATION: "A" in the mutant
US-10-272-291-2

Alignment Scores:
Pred. No.: 6.07e-31 Length: 2263
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 6 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-272-291-1 (1-2263)

Qy 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 194 ATGGCGGCTCTGGCCAGCTCGCAGCTCGTGCACAGCGCGCGGCTGGGGCTCCCGGAC 253
Qy 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 254 GCGTCCACGTTCCG 313
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 314 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 373
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 374 CGCGCGGGGGGCGAGG-----TTCCCGTCTGCTGTGTGTC 409
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; ORGANISM: Zea mays
; NAME/KEY: transit_peptide
; LOCATION: (1233)..(1448)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1554)..(1684)
; OTHER INFORMATION: number 2
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1766)..(1859)
; OTHER INFORMATION: number 3
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1959)..(2054)
; OTHER INFORMATION: number 4
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2145)..(2225)
; OTHER INFORMATION: number 5
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2290)..(2412)
; OTHER INFORMATION: number 6
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2514)..(2650)
; OTHER INFORMATION: number 7
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; NAME/KEY: intron
; LOCATION: (2761)..(2857)
; OTHER INFORMATION: number 8
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; NAME/KEY: intron
; LOCATION: (3102)..(3211)
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; NAME/KEY: intron
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; FEATURE:
; NAME/KEY: intron
; LOCATION: (3682)..(3792)
; OTHER INFORMATION: number 11
; FEATURE:
; NAME/KEY: intron
; LOCATION: (3880)..(3976)
; OTHER INFORMATION: number 12
; FEATURE:
; NAME/KEY: intron
; LOCATION: (4106)..(4226)
; OTHER INFORMATION: number 13
US-10-272-291-5

Alignment Scores:
Pred. No.: 1.27e-30 Length: 4800
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 6 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-272-291-5 (1-4800)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 1233 ATGGCGGCTCTGGCCAGCTCGTCGCAACGCGCGCGCTGGGGCTCCCGGAC 1292
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 1293 GCGTCCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCTCGGGCGG 1352

US-10-628-525A-36 (1-74) x US-10-109-048-1141 (1-4800)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 1233 ATGGCGGCTCTGGCCAGCTCGTCGCAACGCGCGCGCTGGGGCTCCCGGAC 1292
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 1293 GCGTCCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCTCGGGCGG 1352
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 1353 GCGGACACGCTACGATCGGACACGCGCGCGCGCGCGCGCCAGCCAGCCAGCCAGCGG 1412
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 1413 CGCCGGGGGGCAGG-----TTCCCGTCTGCTGCTGTGC 1448

RESULT 7
US-10-628-525-4
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:

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Alignment Scores:  
Pred. No.: 1,27e-30 Length: 4800  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 80.5% Indels: 2  
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-628-525-4 (1-4800)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 1233 ATGGCGGCTCTGGCCACGTCGACGCTGTCGCAACCGCGCGCTGGCGTCCCGGAC 1292

QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaGlnAla 40  
DB 1293 GCGTCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1352

QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaThrArgAlaAlaProArgHisGlnGlnAla 60  
DB 1353 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1412

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 1413 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1448

RESULT 8  
US-10-425-114-17713  
; Sequence 17713, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 17713  
; LENGTH: 1406  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3075-006-H11\_FLI

US-10-425-114-17713  
; Sequence 17713, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 17713  
; LENGTH: 1406  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3075-006-H11\_FLI

Alignment Scores:  
Pred. No.: 2,76e-30 Length: 1406  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-425-114-17713 (1-1406)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 172 ATGGCGGCTCTGGCCACGTCGACGCTGTCGCAACCGCGCGCTGGCGTCCCGGAC 231

QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaGlnAla 40  
DB 232 GCGTCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 291

QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaThrArgAlaAlaProArgHisGlnGlnAla 60  
DB 292 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 351

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 352 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 387

RESULT 9  
US-10-425-114-16641  
; Sequence 16641, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 16641  
; LENGTH: 1409  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3066-030-H5\_FLI

Alignment Scores:  
Pred. No.: 2,76e-30 Length: 1409  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-425-114-16641 (1-1409)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 175 ATGGCGGCTCTGGCCACGTCGACGCTGTCGCAACCGCGCGCTGGCGTCCCGGAC 234

QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaGlnAla 40  
DB 235 GCGTCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 294

QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaThrArgAlaAlaProArgHisGlnGlnAla 60  
DB 295 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 354











```
; APPLICANT: Eric B. Kniec
; APPLICANT: Howard B. Gampier
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Using Modified Single Stranded Oligonucleotides
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2054
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Zea mays
US-10-307-005-2054

Alignment Scores:
Pred. No.:      8,91e-14      Length:      121
Score:          183.00      Matches:     38
Percent Similarity: 97.4%      Conservative: 0
Best Local Similarity: 97.4%      Mismatches:  1
Query Match:    49.7%      Indels:      0
DB:             6          Gaps:         0

US-10-628-525A-36 (1-74) x US-10-307-005-2054 (1-121)

QY 19 ProAspAlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaArgAlaSer 38
Db 119 CCGGACGGCTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTAG 60
QY 39 AlaAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHsgln 57
Db 59 GCGGCGCGCGGACACGCTCAGCATGCGGACCAACGCGCGCGCGCGCGCGCGCGCGCCAG 3

RESULT 22
US-10-307-005-2049
; Sequence 2049, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kniec
; APPLICANT: Howard B. Gampier
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Using Modified Single Stranded Oligonucleotides
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2049
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Zea mays
US-10-307-005-2049

Alignment Scores:
Pred. No.:      8,91e-14      Length:      121
Score:          183.00      Matches:     38
Percent Similarity: 97.4%      Conservative: 0
Best Local Similarity: 97.4%      Mismatches:  1
Query Match:    49.7%      Indels:      0
DB:             6          Gaps:         0

US-10-628-525A-36 (1-74) x US-10-307-005-2054 (1-121)

QY 19 ProAspAlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaArgAlaSer 38
Db 119 CCGGACGGCTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTAG 60
QY 39 AlaAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHsgln 57
Db 59 GCGGCGCGCGGACACGCTCAGCATGCGGACCAACGCGCGCGCGCGCGCGCGCGCGCCAG 3

RESULT 22
US-10-307-005-2049
; Sequence 2049, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kniec
; APPLICANT: Howard B. Gampier
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Using Modified Single Stranded Oligonucleotides
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2049
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Zea mays
US-10-307-005-2049

Alignment Scores:
Pred. No.:      8,91e-13      Length:      121
Score:          175.00      Matches:     38
Percent Similarity: 95.0%      Conservative: 0
Best Local Similarity: 95.0%      Mismatches:  2
Query Match:    47.6%      Indels:      0
DB:             6          Gaps:         0

US-10-628-525A-36 (1-74) x US-10-307-005-2050 (1-121)

QY 10 ValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgGlyAlaAla 29
Db 121 GTCCGAACGCGCGCGCGCGCTGGCGCTCCCGGACGGCTCCACGTTCCGCGCGCGCGCG 62
QY 30 GlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSer 49
Db 61 TAGGGCCTGAGGGGGCGCGCGCGTCCGCGCGCGCGGACACGCTCAGCATGCGGACCCAGC 2

RESULT 24
US-10-425-115-148056
; Sequence 148056, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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Alignment Scores:
Pred. No.:      8,55e-13      Length:      121
Score:          175.00      Matches:     38
Percent Similarity: 95.0%      Conservative: 0
Best Local Similarity: 95.0%      Mismatches:  2
Query Match:    47.6%      Indels:      0
DB:             6          Gaps:         0

US-10-628-525A-36 (1-74) x US-10-307-005-2049 (1-121)

QY 10 ValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgGlyAlaAla 29
Db 1  GTCCGAACGCGCGCGCGCTGGCGCTCCCGGACGGCTCCACGTTCCGCGCGCGCGCGCG 60
QY 30 GlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSer 49
Db 61 TAGGGCCTGAGGGGGCGCGCGCGTCCGCGCGCGCGGACACGCTCAGCATGCGGACCCAGC 120

RESULT 23
US-10-307-005-2050/c
; Sequence 2050, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kniec
; APPLICANT: Howard B. Gampier
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Using Modified Single Stranded Oligonucleotides
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2050
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Zea mays
US-10-307-005-2050
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```
Alignment Scores:
Pred. No.:      8,55e-13      Length:      121
Score:          175.00      Matches:     38
Percent Similarity: 95.0%      Conservative: 0
Best Local Similarity: 95.0%      Mismatches:  2
Query Match:    47.6%      Indels:      0
DB:             6          Gaps:         0

US-10-628-525A-36 (1-74) x US-10-307-005-2050 (1-121)

QY 10 ValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgGlyAlaAla 29
Db 121 GTCCGAACGCGCGCGCGCTGGCGCTCCCGGACGGCTCCACGTTCCGCGCGCGCGCG 62
QY 30 GlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSer 49
Db 61 TAGGGCCTGAGGGGGCGCGCGCGTCCGCGCGCGCGGACACGCTCAGCATGCGGACCCAGC 2

RESULT 24
US-10-425-115-148056
; Sequence 148056, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; TITLE OF INVENTION: Using Modified Single Stranded Oligonucleotides
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/818,875
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2061
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Zea mays
US-10-307-005-2061

Alignment Scores:
Pred. No.:          2,44e-10      Length:      121
Score:              155.00        Matches:     34
Percent Similarity: 91.9%         Conservative: 0
Best Local Similarity: 91.9%      Mismatches:  1
Query Match:        42.1%         Indels:      2
DB:                  6            Gaps:        1

US-10-628-525A-36 (1-74) x US-10-307-005-2061 (1-121)

QY 38 SerAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln 57
Db 1 TCGGCGCGCGGACACACGCTCAGCATGCGGACGCGCGCGCGCGCCAGGCACACAG 60
QY 58 GlnGlnAlaArgGlyGlyArgPheProPheSerLeuValValCys 74
Db 61 TAGCAGCGCGCGCGCGCGGAGG-----TTCCCGTCGCTCGTGTGTC 105

RESULT 28
US-10-307-005-2062/c
; Sequence 2062, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; TITLE OF INVENTION: Using Modified Single Stranded Oligonucleotides
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2062
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Zea mays
US-10-307-005-2062

Alignment Scores:
Pred. No.:          2,44e-10      Length:      121
Score:              155.00        Matches:     34
Percent Similarity: 91.9%         Conservative: 0
Best Local Similarity: 91.9%      Mismatches:  1
Query Match:        42.1%         Indels:      2
DB:                  6            Gaps:        1

US-10-628-525A-36 (1-74) x US-10-307-005-2061 (1-121)

QY 38 SerAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln 57
Db 1 TCGGCGCGCGGACACACGCTCAGCATGCGGACGCGCGCGCGCGCCAGGCACACAG 60
QY 58 GlnGlnAlaArgGlyGlyArgPheProPheSerLeuValValCys 74
Db 61 TAGCAGCGCGCGCGCGGAGG-----TTCCCGTCGCTCGTGTGTC 105

RESULT 28
US-10-307-005-2062/c
; Sequence 2062, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; TITLE OF INVENTION: Using Modified Single Stranded Oligonucleotides
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2061
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Zea mays
US-10-307-005-2061

Alignment Scores:
Pred. No.:          2,44e-10      Length:      121
Score:              155.00        Matches:     34
Percent Similarity: 91.9%         Conservative: 0
Best Local Similarity: 91.9%      Mismatches:  1
Query Match:        42.1%         Indels:      2
DB:                  6            Gaps:        1

US-10-628-525A-36 (1-74) x US-10-307-005-2061 (1-121)

QY 38 SerAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln 57
Db 121 TCGGCGCGCGGACACACGCTCAGCATGCGGACGCGCGCGCGCGCCAGGCACACAG 62
QY 58 GlnGlnAlaArgGlyGlyArgPheProPheSerLeuValValCys 74
Db 61 TAGCAGCGCGCGCGCGGAGG-----TTCCCGTCGCTCGTGTGTC 17

RESULT 29
US-10-425-115-26578
; Sequence 26578, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 26578
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_124248C.1
US-10-425-115-26578

Alignment Scores:
Pred. No.:          4.13e-07      Length:      315
Score:              132.00        Matches:     29
Percent Similarity: 73.9%         Conservative:  5
Best Local Similarity: 63.0%      Mismatches: 12
Query Match:        35.9%         Indels:      0
DB:                  8            Gaps:        0

US-10-628-525A-36 (1-74) x US-10-425-115-26578 (1-315)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProApp 20
Db 178 ATGGCAGCTATGGCCACTTAGCAGCTGTTTAAACGCCGCGGACTGGCGGTACATGAC 237
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 238 GCATCCAGTTTCGACGTGGCCCTCACAGGCCCTGAAGGGGGTCCAGGCATATGTGACG 297

QY 41 AlaAspThrLeuSerMet 46
Db 298 GTTGACACTCTTATTATG 315

RESULT 30
US-10-437-963-99960
; Sequence 99960, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
```

```
Pred. No.:          2,44e-10      Length:      121
Score:              155.00        Matches:     34
Percent Similarity: 91.9%         Conservative:  0
Best Local Similarity: 91.9%      Mismatches:  1
Query Match:        42.1%         Indels:      2
DB:                  6            Gaps:        1

US-10-628-525A-36 (1-74) x US-10-307-005-2062 (1-121)

QY 38 SerAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln 57
Db 121 TCGGCGCGCGGACACACGCTCAGCATGCGGACGCGCGCGCGCGCCAGGCACACAG 62
QY 58 GlnGlnAlaArgGlyGlyArgPheProPheSerLeuValValCys 74
Db 61 TAGCAGCGCGCGCGCGGAGG-----TTCCCGTCGCTCGTGTGTC 17

RESULT 29
US-10-425-115-26578
; Sequence 26578, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 26578
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_124248C.1
US-10-425-115-26578

Alignment Scores:
Pred. No.:          4.13e-07      Length:      315
Score:              132.00        Matches:     29
Percent Similarity: 73.9%         Conservative:  5
Best Local Similarity: 63.0%      Mismatches: 12
Query Match:        35.9%         Indels:      0
DB:                  8            Gaps:        0

US-10-628-525A-36 (1-74) x US-10-425-115-26578 (1-315)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProApp 20
Db 178 ATGGCAGCTATGGCCACTTAGCAGCTGTTTAAACGCCGCGGACTGGCGGTACATGAC 237
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 238 GCATCCAGTTTCGACGTGGCCCTCACAGGCCCTGAAGGGGGTCCAGGCATATGTGACG 297

QY 41 AlaAspThrLeuSerMet 46
Db 298 GTTGACACTCTTATTATG 315

RESULT 30
US-10-437-963-99960
; Sequence 99960, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
```



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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 2, 2006, 01:09:48 ; Search time 231.07 Seconds  
(without alignments)  
1278.753 Million cell updates/sec

Title: US-10-628-525A-36  
Perfect score: 368  
Sequence: 1 MAALATSQLVATRAGHVPD.....RHQQARRGRPPFPLVVC 74

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Command line parameters:

-MODEL=frame+p2n.model -DRV=xlh  
-Q=/abs/ABSSWEB\_spool/US10628525/runat\_31032006\_095139\_17270/app\_query.fasta.1  
-DB=Published Applications NA New -QPM=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62  
-TRANS=human40 cdi -LIST=150 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abs05h  
-USER=US10628525 @CGN 1 1 2249 @runat\_31032006\_095139\_17270 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New:  
1: /SIDSS/ptodata/2/pubpna/US06 NEW PUB seq:  
2: /SIDSS/ptodata/2/pubpna/US06 NEW PUB seq:  
3: /SIDSS/ptodata/2/pubpna/US07 NEW PUB seq:  
4: /SIDSS/ptodata/2/pubpna/US07 NEW PUB seq:  
5: /SIDSS/ptodata/2/pubpna/US09 NEW PUB seq:  
6: /SIDSS/ptodata/2/pubpna/US09 NEW PUB seq:  
7: /SIDSS/ptodata/2/pubpna/US10 NEW PUB seq:  
8: /SIDSS/ptodata/2/pubpna/US10 NEW PUB seq:  
9: /SIDSS/ptodata/2/pubpna/US10 NEW PUB seq:  
10: /SIDSS/ptodata/2/pubpna/US10 NEW PUB seq:  
11: /SIDSS/ptodata/2/pubpna/US11 NEW PUB seq:  
12: /SIDSS/ptodata/2/pubpna/US11 NEW PUB seq:  
13: /SIDSS/ptodata/2/pubpna/US11 NEW PUB seq:  
14: /SIDSS/ptodata/2/pubpna/US11 NEW PUB seq:  
15: /SIDSS/ptodata/2/pubpna/US60 NEW PUB seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No.        | Score | Query Match | ID   | Description        |
|-------------------|-------|-------------|------|--------------------|
| 1                 | 98.5  | 26.8        | 1714 | US-11-072-512-1085 |
| 2                 | 97.5  | 26.5        | 2886 | US-10-504-599A-15  |
| Sequence 1085, Ap |       |             |      |                    |
| Sequence 15, Appl |       |             |      |                    |

|    |      |      |        |    |                       |                   |
|----|------|------|--------|----|-----------------------|-------------------|
| 3  | 82   | 22.3 | 153376 | 14 | US-11-121-086-5       | Sequence 5, Appl  |
| 4  | 80.5 | 21.9 | 1472   | 6  | US-09-925-065A-711806 | Sequence 711806,  |
| 5  | 78.5 | 21.3 | 1072   | 11 | US-11-096-568A-13501  | Sequence 13501, A |
| 6  | 77.5 | 21.1 | 1239   | 9  | US-10-330-773-285     | Sequence 285, App |
| 7  | 77.5 | 21.1 | 21239  | 9  | US-10-330-773-284     | Sequence 284, App |
| 8  | 76.5 | 20.8 | 861    | 8  | US-10-750-185-54914   | Sequence 54914, A |
| 9  | 76.5 | 20.8 | 861    | 8  | US-10-750-623-54914   | Sequence 54914, A |
| 10 | 75.5 | 20.8 | 7006   | 8  | US-10-821-234-218     | Sequence 218, App |
| 11 | 75   | 20.4 | 807    | 11 | US-11-096-568A-3539   | Sequence 3539, Ap |
| 12 | 75   | 20.4 | 1069   | 9  | US-10-921-793-57      | Sequence 57, Appl |
| 13 | 75   | 20.4 | 1069   | 9  | US-10-931-198-57      | Sequence 57, Appl |
| 14 | 75   | 20.4 | 1069   | 9  | US-10-942-042-57      | Sequence 57, Appl |
| 15 | 75   | 20.4 | 1534   | 11 | US-11-096-568A-8024   | Sequence 8024, Ap |
| 16 | 75   | 20.4 | 2272   | 14 | US-11-094-519A-12     | Sequence 12, Appl |
| 17 | 75   | 20.4 | 2292   | 8  | US-10-821-234-168     | Sequence 168, App |
| 18 | 75   | 20.4 | 2294   | 14 | US-11-094-519A-21     | Sequence 21, Appl |
| 19 | 75   | 20.4 | 2312   | 9  | US-10-921-793-55      | Sequence 55, Appl |
| 20 | 75   | 20.4 | 2312   | 9  | US-10-931-198-55      | Sequence 55, Appl |
| 21 | 75   | 20.4 | 2312   | 10 | US-10-942-042-55      | Sequence 91, Appl |
| 22 | 75   | 20.4 | 2312   | 11 | US-11-245-147-91      | Sequence 240, App |
| 23 | 75   | 20.4 | 2312   | 11 | US-11-245-147-91      | Sequence 1, Appl  |
| 24 | 75   | 20.4 | 88421  | 14 | US-11-205-109-1       | Sequence 5, Appl  |
| 25 | 75   | 20.4 | 153376 | 14 | US-11-121-086-5       | Sequence 680636,  |
| 26 | 75   | 20.4 | 172543 | 14 | US-11-121-086-6       | Sequence 18, Appl |
| 27 | 74.5 | 20.2 | 656    | 6  | US-09-925-065A-680636 | Sequence 164, App |
| 28 | 74.5 | 20.2 | 1781   | 14 | US-11-091-883-18      | Sequence 24055, A |
| 29 | 74.5 | 20.2 | 1781   | 14 | US-11-091-883-164     | Sequence 333, App |
| 30 | 74.5 | 20.2 | 1848   | 11 | US-11-096-568A-24055  | Sequence 337172,  |
| 31 | 74.5 | 20.2 | 3030   | 14 | US-11-234-786-333     | Sequence 410437,  |
| 32 | 73.5 | 20.0 | 361    | 6  | US-09-925-065A-337172 | Sequence 410438,  |
| 33 | 73.5 | 20.0 | 361    | 6  | US-09-925-065A-337173 | Sequence 1023846, |
| 34 | 73.5 | 20.0 | 370    | 10 | US-10-301-480-410437  | Sequence 1023847, |
| 35 | 73.5 | 20.0 | 370    | 10 | US-10-301-480-410438  | Sequence 937187,  |
| 36 | 73.5 | 20.0 | 370    | 10 | US-10-301-480-1023846 | Sequence 937195,  |
| 37 | 73.5 | 20.0 | 370    | 10 | US-10-301-480-1023847 | Sequence 953796,  |
| 38 | 73.5 | 20.0 | 635    | 6  | US-09-925-065A-937187 | Sequence 18374, A |
| 39 | 73.5 | 20.0 | 635    | 6  | US-09-925-065A-937195 | Sequence 42352, A |
| 40 | 73.5 | 20.0 | 635    | 6  | US-09-925-065A-953796 | Sequence 42352, A |
| 41 | 73.5 | 20.0 | 1181   | 11 | US-11-096-568A-18374  | Sequence 2, Appl  |
| 42 | 73.5 | 20.0 | 1498   | 8  | US-10-750-185-42352   | Sequence 2, Appl  |
| 43 | 73.5 | 20.0 | 1498   | 8  | US-10-750-623-42352   | Sequence 7399, Ap |
| 44 | 73.5 | 20.0 | 6462   | 5  | US-09-889-325-2       | Sequence 25, Appl |
| 45 | 73.5 | 20.0 | 6462   | 5  | US-09-889-325-2       | Sequence 23, Appl |
| 46 | 73   | 19.8 | 600    | 14 | US-11-136-527-7399    | Sequence 3303, Ap |
| 47 | 73   | 19.8 | 1295   | 9  | US-10-978-927-25      | Sequence 19, Appl |
| 48 | 73   | 19.8 | 1354   | 11 | US-11-096-568A-16245  | Sequence 1, Appl  |
| 49 | 73   | 19.8 | 1729   | 9  | US-10-978-927-23      | Sequence 1, Appl  |
| 50 | 73   | 19.8 | 2479   | 14 | US-11-136-527-3303    | Sequence 948409,  |
| 51 | 73   | 19.8 | 9710   | 8  | US-10-655-872-1       | Sequence 17682, A |
| 52 | 73   | 19.8 | 12263  | 9  | US-10-978-927-19      | Sequence 2572, Ap |
| 53 | 73   | 19.8 | 88421  | 14 | US-11-205-109-1       | Sequence 3454, Ap |
| 54 | 72.5 | 19.7 | 556    | 6  | US-09-925-065A-948409 | Sequence 84, Appl |
| 55 | 72.5 | 19.7 | 2092   | 11 | US-11-096-568A-17682  | Sequence 49, Appl |
| 56 | 72.5 | 19.7 | 6269   | 14 | US-11-136-527-2572    | Sequence 58, Appl |
| 57 | 72   | 19.6 | 1966   | 14 | US-11-136-527-3454    | Sequence 59834, A |
| 58 | 72   | 19.6 | 3695   | 14 | US-11-169-041-84      | Sequence 161072,  |
| 59 | 72   | 19.6 | 121736 | 11 | US-11-114-798-49      | Sequence 26033, A |
| 60 | 72   | 19.6 | 318488 | 11 | US-11-114-798-58      | Sequence 21916, A |
| 61 | 71.5 | 19.4 | 656    | 6  | US-09-925-065A-59834  | Sequence 26, Appl |
| 62 | 71.5 | 19.4 | 656    | 6  | US-10-301-480-161072  | Sequence 36, Appl |
| 63 | 71.5 | 19.4 | 656    | 9  | US-10-301-480-774481  | Sequence 2, Appl  |
| 64 | 71.5 | 19.4 | 656    | 11 | US-11-096-568A-26033  | Sequence 18, Appl |
| 65 | 71.5 | 19.4 | 943    | 11 | US-11-096-568A-21916  | Sequence 17149, A |
| 66 | 71.5 | 19.4 | 1825   | 11 | US-11-096-568A-21916  | Sequence 17, Appl |
| 67 | 71.5 | 19.4 | 2561   | 14 | US-11-127-877-26      | Sequence 17, Appl |
| 68 | 71.5 | 19.4 | 5679   | 14 | US-11-075-185-36      | Sequence 17, Appl |
| 69 | 71.5 | 19.4 | 37507  | 8  | US-10-522-037-2       | Sequence 17, Appl |
| 70 | 71.5 | 19.4 | 78869  | 14 | US-11-075-185-1       | Sequence 40, Appl |
| 71 | 71   | 19.3 | 175023 | 14 | US-11-121-086-18      |                   |
| 72 | 71   | 19.3 | 1202   | 11 | US-11-096-568A-17149  |                   |
| 73 | 71   | 19.3 | 2133   | 14 | US-11-087-100-17      |                   |
| 74 | 71   | 19.3 | 2133   | 14 | US-11-087-084-17      |                   |
| 75 | 71   | 19.3 | 2133   | 14 | US-11-087-085-17      |                   |
|    |      |      | 4680   | 11 | US-11-228-659-40      |                   |

|                                                        |      |                                                                |      |    |                      |                   |
|--------------------------------------------------------|------|----------------------------------------------------------------|------|----|----------------------|-------------------|
| 149                                                    | 68.5 | 18.6                                                           | 1240 | 11 | US-11-096-568A-20045 | Sequence 20045, A |
| 150                                                    | 68.5 | 18.6                                                           | 1283 | 11 | US-11-096-568A-25832 | Sequence 25832, A |
| ALIGNMENTS                                             |      |                                                                |      |    |                      |                   |
| RESULT 1                                               |      |                                                                |      |    |                      |                   |
| US-11-072-512-1085                                     |      |                                                                |      |    |                      |                   |
| ; Sequence 1085, Application US/11072512               |      |                                                                |      |    |                      |                   |
| ; Publication No. US20060029945A1                      |      |                                                                |      |    |                      |                   |
| ; GENERAL INFORMATION:                                 |      |                                                                |      |    |                      |                   |
| ; APPLICANT: ISOGAI, TAKAO                             |      |                                                                |      |    |                      |                   |
| ; APPLICANT: SUGIYAMA, TOMOYASU                        |      |                                                                |      |    |                      |                   |
| ; APPLICANT: OTSUKI, TETSUJI                           |      |                                                                |      |    |                      |                   |
| ; APPLICANT: WAKAMATSU, AI                             |      |                                                                |      |    |                      |                   |
| ; APPLICANT: SATO, HIROYUKI                            |      |                                                                |      |    |                      |                   |
| ; APPLICANT: ISHII, SHIZUKO                            |      |                                                                |      |    |                      |                   |
| ; APPLICANT: YAMAMOTO, JUN-ICHI                        |      |                                                                |      |    |                      |                   |
| ; APPLICANT: ISONO, YUUKO                              |      |                                                                |      |    |                      |                   |
| ; APPLICANT: HIO, YURI                                 |      |                                                                |      |    |                      |                   |
| ; APPLICANT: OTSUKA, KAORU                             |      |                                                                |      |    |                      |                   |
| ; APPLICANT: NAGAI, KEIICHI                            |      |                                                                |      |    |                      |                   |
| ; APPLICANT: IRIE, RYOTARO                             |      |                                                                |      |    |                      |                   |
| ; APPLICANT: TAMECHIKA, ICHIRO                         |      |                                                                |      |    |                      |                   |
| ; APPLICANT: SEKI, NAOHIKO                             |      |                                                                |      |    |                      |                   |
| ; APPLICANT: YOSHIKAWA, TSUTOMU                        |      |                                                                |      |    |                      |                   |
| ; APPLICANT: OTSUKA, MOTOUYUKI                         |      |                                                                |      |    |                      |                   |
| ; APPLICANT: NAGAHARI, KENJI                           |      |                                                                |      |    |                      |                   |
| ; APPLICANT: MASUHO, YASUHIKO                          |      |                                                                |      |    |                      |                   |
| ; TITLE OF INVENTION: Novel full length cDNA           |      |                                                                |      |    |                      |                   |
| ; FILE REFERENCE: 084335-0191                          |      |                                                                |      |    |                      |                   |
| ; CURRENT APPLICATION NUMBER: US/11/072,512            |      |                                                                |      |    |                      |                   |
| ; CURRENT FILING DATE: 2005-03-07                      |      |                                                                |      |    |                      |                   |
| ; PRIOR APPLICATION NUMBER: US 60/350,978              |      |                                                                |      |    |                      |                   |
| ; PRIOR FILING DATE: 2002-01-25                        |      |                                                                |      |    |                      |                   |
| ; PRIOR APPLICATION NUMBER: JP 2001-379298             |      |                                                                |      |    |                      |                   |
| ; PRIOR FILING DATE: 2001-11-05                        |      |                                                                |      |    |                      |                   |
| ; NUMBER OF SEQ ID NOS: 4096                           |      |                                                                |      |    |                      |                   |
| ; SOFTWARE: PatentIn Ver. 2.1                          |      |                                                                |      |    |                      |                   |
| ; SEQ ID NO 1085                                       |      |                                                                |      |    |                      |                   |
| ; LENGTH: 1714                                         |      |                                                                |      |    |                      |                   |
| ; TYPE: DNA                                            |      |                                                                |      |    |                      |                   |
| ; ORGANISM: Homo sapiens                               |      |                                                                |      |    |                      |                   |
| US-11-072-512-1085                                     |      |                                                                |      |    |                      |                   |
| Alignment Scores:                                      |      |                                                                |      |    |                      |                   |
| Pred. No.: 0.279 Length: 1714                          |      |                                                                |      |    |                      |                   |
| Score: 98.50 Matches: 31                               |      |                                                                |      |    |                      |                   |
| Percent Similarity: 44.6% Conservative: 6              |      |                                                                |      |    |                      |                   |
| Best Local Similarity: 37.3% Mismatches: 28            |      |                                                                |      |    |                      |                   |
| Query Match: 26.8% Indels: 18                          |      |                                                                |      |    |                      |                   |
| DB: 11 Gaps: 3                                         |      |                                                                |      |    |                      |                   |
| US-10-628-525A-36 (1-74) x US-11-072-512-1085 (1-1714) |      |                                                                |      |    |                      |                   |
| Qy                                                     | 6    | ThrsSerGlnLeuValAlaA---ThrArgAlaGlyHisGlyValProAspAlaSerThrPhe | 24   |    |                      |                   |
| Db                                                     | 784  | TCCAAGATGCTGGTGGCCCGGTGAGGTCTGCCATTGTTGCCAGGTCCCTCTGCACGTG     | 843  |    |                      |                   |
| Qy                                                     | 25   | Arg-ArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaArgAlaSerAlaAlaAAspThrLe  | 44   |    |                      |                   |
| Db                                                     | 844  | AGGCAGGGGAGCCAGCAAGCACTTCAGGGCTGCAGACCTTCCTCCCTGCAGTTTCTACCTT  | 903  |    |                      |                   |
| Qy                                                     | 44   | u-----SerMetArgThrSerAlaArgAlaAlaApr                           | 54   |    |                      |                   |
| Db                                                     | 904  | ACAAACAGGGATCTTAATCCCTAACCTGGGGTACGTGTGAGACCAACAGGGAGAGCCCTC   | 963  |    |                      |                   |
| Qy                                                     | 54   | oArGHisGlnGlnAlaAAsq-----ArgGlyGlyArgPheProPh                  | 68   |    |                      |                   |
| Db                                                     | 964  | GAGGATGGGACCATGATCCAGGCCTGTAGGACACCTTCTTCGACGAGGAGATCCCTT      | 1023 |    |                      |                   |
| Qy                                                     | 68   | eProSer 70                                                     |      |    |                      |                   |

```

Db      1024  CCCAAGT 1030

RESULT 2
US-10-504-599A-15
; Sequence 15, Application US/10504599A
; Publication No. US2005027033A1
; GENERAL INFORMATION:
; APPLICANT: YAMAKAWA, HIROHITO
; APPLICANT: SUZUKI, ERIKO
; APPLICANT: MIYATAKE, KIYOKO
; APPLICANT: HAYAKAWA, KATSUYUKI
; TITLE OF INVENTION: WHEAT DETECTING METHOD
; FILE REFERENCE: 8036-1018
; CURRENT APPLICATION NUMBER: US/10/504,599A
; CURRENT FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: PCT/JP02/09983
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: JP 2002-39040
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: JP 2002-132119
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 15
; LENGTH: 2886
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-504-599A-15

Alignment Scores:
Pred. No.:      0.581      Length:      2886
Score:          97.50      Matches:      30
Percent Similarity: 54.5%      Conservative: 6
Best Local Similarity: 45.5%      Mismatches: 25
Query Match:    26.5%      Indels:      5
DB:             8      Gaps:        3

US-10-628-525A-36 (1-74) x US-10-504-599A-15 (1-2886)
QY      1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProasp 20
      |||||
Db      13 ATGGCGGCTCTGGTCAGTCCAGCTCCGACCTCCGGCACCGTCTCGGCATCACCGAC 72
      |||||
QY      21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
      |||||
Db      73 -----AGGTTCCGGCGTGTCAGGTTTCCAGGGCGTGAGGCCCGGAGCCCGGGATGCG 126
      |||||
QY      41 AlaAspThrLeuSerMetArgThr-----SerAlaArgAlaAlaProArgHisGlnGln 59
      |||||
Db      127 GCT-----CTCGCATGAGGACCGTTCGGAGCTAGCGCCGCCCCCAACGCAACCGCGAAA 180
      |||||
QY      60 AlaArgGlyGlyArg 65
      |||||
Db      181 GCGCACCGCGGACCCCG 198

RESULT 3
US-11-121-086-5
; Sequence 5, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 153376
; TYPE: DNA

; ORGANISM: Homo sapiens
US-11-121-086-5

Alignment Scores:
Pred. No.:      1.15e+03      Length:      153376
Score:          82.00      Matches:      29
Percent Similarity: 53.0%      Conservative: 6
Best Local Similarity: 43.9%      Mismatches: 24
Query Match:    22.3%      Indels:      7
DB:             14      Gaps:        3

US-10-628-525A-36 (1-74) x US-11-121-086-5 (1-153376)
QY      10 ValAlaThrArgAlaGlyHisGlyValProaspAlaSerThrPheArgGlyAlaAla 29
      |||||
Db      56868 GTGTGGGGCGCGAAGGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 56927
      |||||
QY      30 GlnGlyLeuArg--GlyAlaArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThr 48
      :|||
Db      56928 AAGGGAGCGCGGTGGCGGCACTTGTCCCGCGCTTGTGATGGGTGGGC-----CCC 56981
      |||||
QY      49 SerAlaArgAlaAla--ProArgHisGlnGlnGlnAlaArgAlaArgGlyGlyArgPhe----- 66
      |||||
Db      56982 CCTCGCGGCTCCCGCTCTCTCCACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 57041
      |||||
QY      67 ----ProPheProSer 70
      |||||
Db      57042 GGGCCCGGCACCTTCG 57057

RESULT 4
US-09-925-065A-711806/c
; Sequence 711806, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 711806
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-711806

Alignment Scores:
Pred. No.:      22.9      Length:      1472
Score:          80.50      Matches:      28
Percent Similarity: 51.6%      Conservative: 4
Best Local Similarity: 45.2%      Mismatches: 17
Query Match:    21.9%      Indels:      13
DB:             6      Gaps:        2

US-10-628-525A-36 (1-74) x US-09-925-065A-711806 (1-1472)
QY      5 AlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProaspAlaSerThrPhe 24
      |||||
Db      839 GCGGGGGCGAGGTTCCAGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 792
      |||||
QY      25 ArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAspThrLeu 44
      |||||

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Db 6500 TTACGCCCGCGCGCCCGCGCCCGCGCCAGGGGTTTGGCGCGAGGGCGGAGGGGGCG 6559
QY 36 ArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSerAlaArg-----51
Db 6560 CGGGCGGGCGGCGCTCCCTCCACCCCTTGGCCCGCCCGCCCGATCAGCGTCCCT 6619
QY 52 -----AlaAla 53
Db 6620 CGGGCCCGCGGTGGGAAGTCCGGGAGCCCGCGGGGCGAGCACCGCTCGGGGGCG 6679
QY 54 ProArg-----HisGlnGlnAlaAlaArgGlyGlyArgPheProPhe 68
Db 6680 CGCGCGCTCCCGCGCTCTGGGCTCTGAGGATGCCCGCGC---GGCGGTGGCGGCC 6736
QY 69 ProSerLeuValValCys 74
Db 6737 CCTCTCCCGCGGTCTGCG 6754

RESULT 11
US-11-096-568A-3539
; Sequence 3539, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 3539
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(807)
; OTHER INFORMATION: Ceres Seq. ID no. 12611403
US-11-096-568A-3539

Alignment Scores:
Pred. No.: 52.9 Length: 807
Score: 75.00 Matches: 30
Percent Similarity: 46.3% Conservative: 8
Best Local Similarity: 36.6% Mismatches: 25
Query Match: 20.4% Indels: 19
DB: 11 Gaps: 4

US-10-628-525A-36 (1-74) x US-11-096-568A-3539 (1-807)
QY 2 AlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProAspAla 21
Db 541 GCCCGCGTCAGCGGCGACCCCATATGCGCCGACAG---GGCCGTGCGGCCCGAGCGGG 597
QY 22 SerThr-----PheArgArgGlyAlaAlaGlnGly 31
Db 598 GAGGTGGAGTGGAGCGGGGGAAGGAGGATCCGCGCGCGCGCGCGCGCGAAGGGA 657
QY 32 LeuArgGlyAlaAlaAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSerAlaArg 51
Db 658 GGAGGGCGCGGAGGCGCGCGCGCGCGGGGGTGGCGGGCGGCGGACCGCGCGCAAGA 717
QY 52 -----AlaAlaProArgHis-----GlnGlnGlnAla-ArgArgGlyCl 64
Db 718 ACGGTGGGAGCGACGCGCGCGCGCGCCATGCTAGGTTTCAGCGGAGGAGGAGGGT 777
QY 64 YArg 65
Db 778 GAGG 781

RESULT 12
US-10-921-793-57/c
; Sequence 57, Application US/10921793
```

```
; Publication No. US20060039949A1
; GENERAL INFORMATION:
; APPLICANT: Nycz, Jeffrey
; TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated
; FILE REFERENCE: 64118.000087
; CURRENT APPLICATION NUMBER: US/10/921,793
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 1069
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-921-793-57

Alignment Scores:
Pred. No.: 68.6 Length: 1069
Score: 75.00 Matches: 21
Percent Similarity: 49.1% Conservative: 6
Best Local Similarity: 38.2% Mismatches: 27
Query Match: 20.4% Indels: 1
DB: 9 Gaps: 0

US-10-628-525A-36 (1-74) x US-10-921-793-57 (1-1069)
QY 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31
Db 205 ACACGCCGATCTTGGCGTTCGGCCGGGAGCCGAACTCAGAAAGAGGCCCTTTGTGCGGT 146
QY 32 LeuArgGly-AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAlaAr 51
Db 145 CGCAGGGTTCGGCTCGGTGCACAGCTGCCCAGCTGCTTGGCGCAGCGCGCAGCAGC 86
QY 51 gAlaAlaProArgHisGlnGlnAlaArgGlyGlyArg 65
Db 85 CGCAGCGCTCCAGCAGCAGGCTCAGCCCGCGCGCGCGCGCG 43

RESULT 13
US-10-931-198-57/c
; Sequence 57, Application US/10931198
; Publication No. US20060045902A1
; GENERAL INFORMATION:
; APPLICANT: Nycz, Jeffrey
; TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated
; FILE REFERENCE: 64118.000087
; CURRENT APPLICATION NUMBER: US/10/931,198
; CURRENT FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 1069
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-931-198-57

Alignment Scores:
Pred. No.: 68.6 Length: 1069
Score: 75.00 Matches: 21
Percent Similarity: 49.1% Conservative: 6
Best Local Similarity: 38.2% Mismatches: 27
Query Match: 20.4% Indels: 1
DB: 9 Gaps: 0

US-10-628-525A-36 (1-74) x US-10-931-198-57 (1-1069)
QY 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31
Db 205 ACACGCCGATCTTGGCGTTCGGCCGGGAGCCGAACTCAGAAAGAGGCCCTTTGTGCGGT 146
QY 32 LeuArgGly-AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAlaAr 51
```

Db 145 CGCAGGGGTCGGTCCGACAGCTCGCCAGCTCTTGGCGCAGACGGCGGAGCAGC 86  
Qy 51 gAlaAlaProArgHisGlnGlnAlaArgArgGlyArg 65  
Db 85 CGCAGCGCTCCAGCAGCGAGCTCAGCGCCGCGCGGAGCGCGG 43

## RESULT 14

US-10-942-042-57/c  
; Sequence 57, Application US/10942042  
; Publication No. US20060057184A1  
; GENERAL INFORMATION:  
; APPLICANT: NYCZ, Jeffrey  
; TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated  
; TITLE OF INVENTION: Osteoinductive Material  
; FILE REFERENCES: 6418.000087  
; CURRENT APPLICATION NUMBER: US/10/942,042  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 57  
; LENGTH: 1069  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-942-042-57

Alignment Scores:  
Pred. No.: 68.6 Length: 1069  
Score: 75.00 Matches: 21  
Percent Similarity: 49.1% Conservative: 6  
Best Local Similarity: 38.2% Mismatches: 27  
Query Match: 20.4% Indels: 1  
DB: 10 Gaps: 0

US-10-628-525A-36 (1-74) x US-10-942-042-57 (1-1069)

Qy 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31  
Db 205 ACACGCCGATCTTGGCGTGGCGGGAGCCGAAGTCACAGAAGAGGCCCTTGTGCGGGT 146  
Qy 32 LeuArgGly-AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAlaAr 51  
Db 145 CGCAGGGGTCGGCTCGGTGCACAGCTCGCCAGCTCTTGGCGCAGACGGCGGAGCAGC 86  
Qy 51 gAlaAlaProArgHisGlnGlnAlaArgArgGlyArg 65  
Db 85 CGCAGCGCTCCAGCAGCGAGCTCAGCGCCGCGCGGAGCGCGG 43

## RESULT 15

US-11-096-568A-8024  
; Sequence 8024, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; TITLE OF INVENTION: Therby  
; FILE REFERENCES: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 8024  
; LENGTH: 1534  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(1534)  
; OTHER INFORMATION: Ceres Seq. ID no. 15177270  
US-11-096-568A-8024

Alignment Scores:  
Pred. No.: 95.7 Length: 1534  
Score: 75.00 Matches: 29  
Percent Similarity: 38.8% Conservative: 4

Best Local Similarity: 34.1% Mismatches: 29  
Query Match: 20.4% Indels: 23  
DB: 11 Gaps: 3  
US-10-628-525A-36 (1-74) x US-11-096-568A-8024 (1-1534)

Qy 13 ArgAlaGlyHisGlyValProAspAla-----SerThr 23  
Db 773 CGCCGAGGAGCGCGGTTCCTCGTGCAGGCAACGGCGGAGTCCGCCGCGTGTGTC 832  
Qy 24 PheArgArg-----GlyAlaAlaGlnGlyLeuArg 33  
Db 833 TACCGCGCGCGCGCGCGACCTGGCTGAGTTGGAATCTTTCAGCCGCGAGCAGCTCCGGCA 892  
Qy 34 GlyAlaArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSerAlaAlaAla 53  
Db 893 GGGTCCGGGTGTCCGCTTCTCAGCGATTCGATGCAAGTACCGCGCGCGGAGGTGCA 952  
Qy 54 ProArg-----HisGlnGlnAlaAlaArgGlyArgGlyArgPhe-ProPheProSe 70  
Db 953 CCCTCGAGAGCTGTTCATGCGGAGTGTTCGCGCGCGGCGGCTTCGCGCGGACCGG 1012  
Qy 70 rLeuValValCys 74  
Db 1013 GCTGAGACTCTGT 1025

## RESULT 16

US-11-094-519A-12/c  
; Sequence 12, Application US/11094519A  
; Publication No. US20050281810A1  
; GENERAL INFORMATION:  
; APPLICANT: BERNSTEIN, Jeanne  
; APPLICANT: LEVINE, Zurit  
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING  
; FILE REFERENCES: 2786-0140P  
; CURRENT APPLICATION NUMBER: US/11/094,519A  
; PRIOR FILING DATE: 2005-03-31  
; PRIOR APPLICATION NUMBER: US/09/695,293  
; PRIOR FILING DATE: 2000-10-25  
; PRIOR APPLICATION NUMBER: IL 132558  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 2272  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-094-519A-12

Alignment Scores:  
Pred. No.: 138 Length: 2272  
Score: 75.00 Matches: 21  
Percent Similarity: 49.1% Conservative: 6  
Best Local Similarity: 38.2% Mismatches: 27  
Query Match: 20.4% Indels: 1  
DB: 14 Gaps: 0

US-10-628-525A-36 (1-74) x US-11-094-519A-12 (1-2272)

Qy 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31  
Db 471 ACACGCCGATCTTGGCGTGGCGGGAGCCGAAGTCACAGAAGAGGCCCTTGTGCGGGT 412  
Qy 32 LeuArgGly-AlaArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSerAlaAr 51  
Db 411 CGCAGGGGTCGCGCTCGGTGCACAGCTCGCCAGCTTGGCGCAGACGGCGGAGCAGC 352  
Qy 51 gAlaAlaProArgHisGlnGlnAlaArgArgGlyArg 65  
Db 351 CGCAGCGCTCCAGCAGCGAGGCTCAGCGCCGCGCGGAGCGCGG 309

RESULT 17  
US-10-821-234-168



```
; Sequence 168, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 168
; LENGTH: 2292
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-168

Alignment Scores:
Pred. No.: 139 Length: 2292
Score: 75.00 Matches: 21
Percent Similarity: 49.1% Conservatve: 6
Best Local Similarity: 38.2% Mismatches: 27
Query Match: 20.4% Indels: 1
DB: 8 Gaps: 0

US-10-628-525A-36 (1-74) x US-10-821-234-168 (1-2292)
QY 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31
Db 1865 ACACGCCGATCTTGGCGTGGCGGGGACCGAAGTCACAGAAGAGCCCTTGTGGCGGT 1924

QY 32 LeuArgGly-AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAla 51
Db 1925 CGCAGGGTTCGGCTCGGTGCACAGCTGCCCGACAGTCTTGGCGCAGCGCGGCGAGC 1984

QY 51 gAlaAlaProArgHisGlnGlnAlaArgArgGlyGlyArg 65
Db 1985 CGCAGCGCTCCAGCAGAGGCTCACGCCCGCGCGGCGCGG 2027

RESULT 18
US-11-094-519A-21/c
; Sequence 21, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 2294
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-094-519A-21

Alignment Scores:
Pred. No.: 139 Length: 2294
Score: 75.00 Matches: 21
Percent Similarity: 49.1% Conservatve: 6
Best Local Similarity: 38.2% Mismatches: 27
Query Match: 20.4% Indels: 1
DB: 14 Gaps: 0

; Sequence 168, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 168
; LENGTH: 2292
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-168

Alignment Scores:
Pred. No.: 139 Length: 2292
Score: 75.00 Matches: 21
Percent Similarity: 49.1% Conservatve: 6
Best Local Similarity: 38.2% Mismatches: 27
Query Match: 20.4% Indels: 1
DB: 8 Gaps: 0

US-10-628-525A-36 (1-74) x US-10-821-234-168 (1-2292)
QY 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31
Db 1865 ACACGCCGATCTTGGCGTGGCGGGGACCGAAGTCACAGAAGAGCCCTTGTGGCGGT 1924

QY 32 LeuArgGly-AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAla 51
Db 1925 CGCAGGGTTCGGCTCGGTGCACAGCTGCCCGACAGTCTTGGCGCAGCGCGGCGAGC 1984

QY 51 gAlaAlaProArgHisGlnGlnAlaArgArgGlyGlyArg 65
Db 1985 CGCAGCGCTCCAGCAGAGGCTCACGCCCGCGCGGCGCGG 2027

RESULT 18
US-11-094-519A-21/c
; Sequence 21, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 2294
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-094-519A-21

Alignment Scores:
Pred. No.: 139 Length: 2294
Score: 75.00 Matches: 21
Percent Similarity: 49.1% Conservatve: 6
Best Local Similarity: 38.2% Mismatches: 27
Query Match: 20.4% Indels: 1
DB: 14 Gaps: 0

US-10-628-525A-36 (1-74) x US-11-094-519A-21 (1-2294)
QY 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31
Db 483 ACACGCCGATCTTGGCGTGGCGGGGACCGAAGTCACAGAAGAGCCCTTGTGGCGGT 424

QY 32 LeuArgGly-AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAla 51
Db 423 CGCAGGGTTCGGCTCGGTGCACAGCTGCCCGACAGTCTTGGCGCAGCGCGGCGAGC 364

QY 51 gAlaAlaProArgHisGlnGlnAlaArgArgGlyGlyArg 65
Db 363 CGCAGCGCTCCAGCAGAGGCTCACGCCCGCGCGGCGCGG 321

RESULT 19
US-10-921-793-55/c
; Sequence 55, Application US/10921793
; Publication No. US20060039949A1
; GENERAL INFORMATION:
; APPLICANT: Nycz, Jeffrey
; TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated
; FILE REFERENCE: 64118.000087
; CURRENT APPLICATION NUMBER: US/10/921,793
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 2312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-921-793-55

Alignment Scores:
Pred. No.: 140 Length: 2312
Score: 75.00 Matches: 21
Percent Similarity: 49.1% Conservatve: 6
Best Local Similarity: 38.2% Mismatches: 27
Query Match: 20.4% Indels: 1
DB: 9 Gaps: 0

US-10-628-525A-36 (1-74) x US-10-921-793-55 (1-2312)
QY 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31
Db 428 ACACGCCGATCTTGGCGTGGCGGGGACCGAAGTCACAGAAGAGCCCTTGTGGCGGT 369

QY 32 LeuArgGly-AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAla 51
Db 368 CGCAGGGTTCGGCTCGGTGCACAGCTGCCCGACAGTCTTGGCGCAGCGCGGCGAGC 309

QY 51 gAlaAlaProArgHisGlnGlnAlaArgArgGlyGlyArg 65
Db 308 CGCAGCGCTCCAGCAGAGGCTCACGCCCGCGCGGCGCGG 266

RESULT 20
US-10-931-198-55/c
; Sequence 55, Application US/10931198
; Publication No. US20060045902A1
; GENERAL INFORMATION:
; APPLICANT: Nycz, Jeffrey
; TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated
; FILE REFERENCE: 64118.000087
; CURRENT APPLICATION NUMBER: US/10/931,198
; CURRENT FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 2312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-931-198-55/c
```

US-10-931-198-55

Alignment Scores:  
 Pred. No.: 140 Length: 2312  
 Score: 75.00 Matches: 21  
 Percent Similarity: 49.1% Conservative: 6  
 Best Local Similarity: 38.2% Mismatches: 27  
 Query Match: 20.4% Indels: 1  
 DB: 9 Gaps: 0

US-10-628-525A-36 (1-74) x US-10-931-198-55 (1-2312)

Qy 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31  
 Db 428 ACACGCCGATCTTGGCGTTGGCGGGGAGCCGAGTCAACAGAGGCGCTTGTGCGGGT 369

Qy 32 LeuArgGly-AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAlaAr 51  
 Db 368 CGCAGGGGTCCGCTCGTGCACAGCTCCGCCAGCTGTGGCGCAGACGGCGGCGAGC 309

Qy 51 gAlaAlaProArgHisGlnGlnAlaArgArgGlyGlyArg 65  
 Db 308 CGCAGCGGTCCAGCAGCGAGCTCACGCCCGCGGCGGCGGCGG 266

RESULT 21

US-10-942-042-55/c  
 ; Sequence 55, Application US/10942042  
 ; Publication No. US20060057184A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nycz, Jeffrey  
 ; TITLE OF INVENTION: Osteoinductive Device with Porous Substrate and Impregnated  
 ; FILE REFERENCE: 64118.000087  
 ; CURRENT APPLICATION NUMBER: US/10/942,042  
 ; CURRENT FILING DATE: 2004-09-16  
 ; NUMBER OF SEQ ID NOS: 84  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 55  
 ; LENGTH: 2312  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-942-042-55

Alignment Scores:  
 Pred. No.: 140 Length: 2312  
 Score: 75.00 Matches: 21  
 Percent Similarity: 49.1% Conservative: 6  
 Best Local Similarity: 38.2% Mismatches: 27  
 Query Match: 20.4% Indels: 1  
 DB: 10 Gaps: 0

US-10-628-525A-36 (1-74) x US-10-942-042-55 (1-2312)

Qy 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31  
 Db 428 ACACGCCGATCTTGGCGTTGGCGGGGAGCCGAGTCAACAGAGGCGCTTGTGCGGGT 369

Qy 32 LeuArgGly-AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAlaAr 51  
 Db 368 CGCAGGGGTCCGCTCGTGCACAGCTCCGCCAGCTGTGGCGCAGACGGCGGCGAGC 309

Qy 51 gAlaAlaProArgHisGlnGlnAlaArgArgGlyGlyArg 65  
 Db 308 CGCAGCGGTCCAGCAGCGAGCTCACGCCCGCGGCGGCGGCGG 266

RESULT 22

US-11-245-147-91/c  
 ; Sequence 91, Application US/11245147  
 ; Publication No. US20060030541A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GARCIA, TERESA  
 ; APPLICANT: ROMAN ROMAN, SERGIO  
 ; APPLICANT: BARON, ROLAND  
 ; APPLICANT: CALL, KATHERINE  
 ; APPLICANT: THEILHABER, JOACHIM  
 ; APPLICANT: CONNOLLY, TIMOTHY  
 ; APPLICANT: JACKSON, AMANDA  
 ; APPLICANT: BUSHNELL, STEVEN  
 ; APPLICANT: RAWADI, GEORGES  
 ; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE  
 ; FILE REFERENCE: 37991-0023  
 ; CURRENT APPLICATION NUMBER: US/11/245,147  
 ; CURRENT FILING DATE: 2005-10-07  
 ; PRIOR APPLICATION NUMBER: PCT/IB02/02211  
 ; PRIOR FILING DATE: 2002-04-05  
 ; PRIOR APPLICATION NUMBER: 60/281,400  
 ; PRIOR FILING DATE: 2001-04-05  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SOFTWARE: PatentIn Ver. 3.2  
 ; SEQ ID NO 240  
 ; LENGTH: 2312  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:

; OTHER INFORMATION: Homo sapiens connective tissue growth factor  
 ; OTHER INFORMATION: (CTGF), mRNA  
 US-11-245-147-240

|                        |       |
|------------------------|-------|
| Alignment Scores:      |       |
| Pred. No.:             | 140   |
| Score:                 | 75.00 |
| Percent Similarity:    | 49.1% |
| Best Local Similarity: | 38.2% |
| Query Match:           | 20.4% |
| DB:                    | 11    |
| Length:                | 2312  |
| Matches:               | 21    |
| Conservative:          | 6     |
| Mismatches:            | 27    |
| Indels:                | 1     |
| Gaps:                  | 0     |

US-10-628-525A-36 (1-74) x US-11-245-147-240 (1-2312)

|    |     |                                                              |     |
|----|-----|--------------------------------------------------------------|-----|
| Qy | 12  | ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly | 31  |
|    |     |                                                              |     |
| Db | 428 | ACACGCCGATCTTCGGTGTGGCCGGGAGCCGAAGTCACAGAGAGSCCTTGTGCGGT     | 369 |
|    |     |                                                              |     |
| Qy | 32  | LeuArgGly-AlaArgAlaSerAlaAlaAspThrIeuSerMetArgThrSerIaIar    | 51  |
|    |     |                                                              |     |
| Db | 368 | CGCAGGGGTTCGGCTCGGTGCACAGCTCGCCAGCTGCTTGGCGCAGACGCGCAGCAGC   | 309 |
|    |     |                                                              |     |
| Qy | 51  | gAlaAlaProArgHisGlnGlnGlnAlaArgArgGlyArg                     | 65  |
|    |     |                                                              |     |
| Db | 308 | CGCAGCCGTTCAGCAGCAGGGCTCAGCCCGCCGGCAGCCGG                    | 266 |
|    |     |                                                              |     |

## RESULT 24

```

US-11-205-109-1
; Sequence 1, Application US/11205109
; Publication No. US20050287641a1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Zazopoulos, Emmanuel
; APPLICANT: Staffa, Alfredo
; TITLE OF INVENTION: GENE CLUSTER FOR RAMOPLANIN BIOSYNTHESIS
; FILE REFERENCE: 3002-2US
; CURRENT APPLICATION NUMBER: US/11/205,109
; CURRENT FILING DATE: 2005-08-17
; PRIOR APPLICATION NUMBER: US/09/976,059
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/239,924
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 88421
; TYPE: DNA
; ORGANISM: Actinoplanes sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (207)..(3078)
; OTHER INFORMATION: ORF 1; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3118)..(4032)
; OTHER INFORMATION: ORF 2; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4038)..(5048)
; OTHER INFORMATION: ORF 3; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6665)..(5814)
; OTHER INFORMATION: ORF 4; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7703)..(6693)
; OTHER INFORMATION: ORF 5; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9464)..(8130)
; OTHER INFORMATION: ORF 6; negative strandedness
; FEATURE:

```

```
; LOCATION: (79864)..(78107)
; OTHER INFORMATION: ORF 25; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (81624)..(79861)
; OTHER INFORMATION: ORF 26; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (81909)..(81682)
; OTHER INFORMATION: ORF 27; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (82346)..(82062)
; OTHER INFORMATION: ORF 28; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (82587)..(84446)
; OTHER INFORMATION: ORF 29; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (84481)..(85548)
; OTHER INFORMATION: ORF 30; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (85556)..(86845)
; OTHER INFORMATION: ORF 31; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (87372)..(86803)
; OTHER INFORMATION: ORF 32; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (87494)..(88420)
; OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
US-11-205-109-1

Alignment Scores:
Pred. No.: 4.05e+03 Length: 88421
Score: 75.00 Matches: 28
Percent Similarity: 44.1% Conservative: 2
Best Local Similarity: 41.2% Mismatches: 26
Query Match: 20.4% Indels: 12
DB: 14 Gaps: 3

US-10-628-525A-36 (1-74) x US-11-205-109-1 (1-88421)
QY 5 AlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPhe 24
Db 57238 GCTCGATCCGGTATCCGCGCCCGCTGGC-----CCGATGTCGAGGACGC 57288
QY 25 ArgArgGlyAlaAlaGlnGly-----LeuArgGlyAlaAlaAlaAlaAla 41
Db 57289 CGCGCGGCGCTGCTGTGCCACGCGCGCACCGGAGCGCTGCCCGCGCGCA 57348
QY 42 AspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAlaArg 61
Db 57349 GCGACT-----GCTGTGGACGACCCCGGACCGCGCGGAGTGGC 57390
QY 62 ArgGlyGlyArgPheProPhePro 69
Db 57391 CCGGCTGGACGGGACCGGATCCG 57414

RESULT 25
US-11-121-086-5/c
; Sequence 5, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 153376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-5

Alignment Scores:
Pred. No.: 7.51e+03 Length: 172543
Score: 75.00 Matches: 27
Percent Similarity: 49.2% Conservative: 5
Best Local Similarity: 41.5% Mismatches: 18
Query Match: 20.4% Indels: 15
DB: 14 Gaps: 3

US-10-628-525A-36 (1-74) x US-11-121-086-6 (1-172543)
QY 7 SerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArg 26
Db 3395 ACCAGTTCACGGTCAACCGCGTGAAGGGGAGTGCC-----CGG 3354
QY 27 GlyAlaAlaGlnGlyLeuArgGly-AlaArgAlaSerAlaAlaAlaAspThrLeuSerMe 46
Db 3395 ACCAGTTCACGGTCAACCGCGTGAAGGGGAGTGCC-----CGG 3354

; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 153376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-5

Alignment Scores:
Pred. No.: 6.74e+03 Length: 153376
Score: 75.00 Matches: 27
Percent Similarity: 49.2% Conservative: 5
Best Local Similarity: 41.5% Mismatches: 18
Query Match: 20.4% Indels: 15
DB: 14 Gaps: 3

US-10-628-525A-36 (1-74) x US-11-121-086-5 (1-153376)
QY 7 SerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArg 26
Db 99969 AACCACTTCACGGTCAACCGCGTGAAGGGGAGTGCC-----CGG 99928
QY 27 GlyAlaAlaGlnGlyLeuArgGly-AlaArgAlaSerAlaAlaAlaAspThrLeuSerMe 46
Db 99927 GGGGCGGGCGGGGGCTGAGGTCCGCCAGGGCGGCTGCG----- 99882
QY 46 tangThrSerAlaArgAlaAlaProArgHisGlnGlnGlnAlaArgGlyArgPh 66
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Db 99831 CCCCAGTCCCTCC 99819

RESULT 26
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; Sequence 6, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 172543
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-6

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Job time : 284.07 secs

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QY 29 AlaGlnGlyLeu-----ArgGly 34  
DB 589 GCGCGGGGACCTACTCTCCGTGGACCTGCCCGCGCTGAGGAGCGTGACGTGGG 648  
QY 35 AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaPro 54  
DB 649 GCGCTGCGGGAGCGCTGCTGGATGATGCCG-----GCCGCTCTTCGAGCGATACCG 702  
QY 55 ArgHis-----GlnGlnGlnAlaArgArgGlyArg 65  
DB 703 CGCATGTTCGCCCTGCGCAACGCGGAGCGAGGAGCGCGC 744

## RESULT 30

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; Sequence 24055, Application US/11096568A  
; Publication No. US2006048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
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; FEATURE:  
; NAME/KEY: misc feature  
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; OTHER INFORMATION: Ceres Seq. ID no. 12418208  
US-11-096-568A-24055

## Alignment Scores:

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US-10-628-525A-36 (1-74) x US-11-096-568A-24055 (1-1848)

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QY 31 -----GlyLeuArg----- 33  
DB 393 CCGGCGCTACACGACGAGGAGTTCGAGTTTACCTCTCCGACTCGAGGCGCGCTCCT 452  
QY 34 -----GlyAlaArgAlaSerAlaAlaAspThrLeuSerMetArgThr 48  
DB 453 CGTCACCAACGCGGAGGCGCAACGCGGAGCGGAGGCTGC-----CGCTGC 497  
QY 49 SerAlaArgAlaAlaProArgHisGlnGlnAlaArgArgGlyArgPhePro 67  
DB 498 CAAGCTCGGGCTGCGCCAGCCACCGCCCTCCACGACGCGCGCGCTGTCCA 554

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

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Listing first 150 summaries

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| 9  | 333   | 90.5 | 1818 | 3  | PCT-US04-20582-2     | Sequence 2, Appli   | 82  | 288   | 78.3 | 400  | 28 | US-09-619-643-16655  | Sequence 16655, A  |
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| 49 | 326   | 88.6 | 1409 | 51 | US-10-425-114-16641  | Sequence 16641, A   | 122 | 183   | 49.7 | 121  | 48 | US-10-307-005-2054   | Sequence 2054, Ap  |
| 50 | 326   | 88.6 | 1409 | 51 | US-10-425-114-16641  | Sequence 16641, A   | 123 | 183   | 49.7 | 121  | 48 | US-10-307-005-2054   | Sequence 2054, Ap  |
| 51 | 326   | 88.6 | 1409 | 82 | US-09-634-779-9      | Sequence 9, Appli   | 124 | 183   | 49.7 | 121  | 53 | US-10-623-107-6393   | Sequence 6393, Ap  |
| 52 | 326   | 88.6 | 1416 | 43 | US-10-219-999-7933   | Sequence 7933, Ap   | 125 | 183   | 49.7 | 121  | 53 | US-10-623-107-6393   | Sequence 6393, Ap  |
| 53 | 326   | 88.6 | 1416 | 51 | US-10-425-114-19555  | Sequence 19555, A   | 126 | 183   | 49.7 | 121  | 62 | US-10-861-178-6393   | Sequence 6393, Ap  |
| 54 | 326   | 88.6 | 1416 | 51 | US-10-425-114-19555  | Sequence 19555, A   | 127 | 183   | 49.7 | 121  | 62 | US-10-861-178-6393   | Sequence 6393, Ap  |
| 55 | 326   | 88.6 | 2401 | 72 | US-09-619-643-19076  | Sequence 19076, Ap  | 128 | 175   | 47.6 | 121  | 1  | PCT-US03-31862-2049  | Sequence 2049, Ap  |
| 56 | 326   | 88.6 | 2401 | 72 | US-09-619-643-19076  | Sequence 19076, Ap  | 129 | 175   | 47.6 | 121  | 1  | PCT-US03-31862-2049  | Sequence 2049, Ap  |
| 57 | 323   | 87.8 | 408  | 28 | US-10-425-115-155340 | Sequence 155340, A  | 130 | 175   | 47.6 | 121  | 48 | US-10-307-005-2050   | Sequence 2050, Ap  |
| 58 | 323   | 87.8 | 408  | 28 | US-09-619-643-19022  | Sequence 19022, A   | 131 | 175   | 47.6 | 121  | 48 | US-10-307-005-2050   | Sequence 2050, Ap  |
| 59 | 323   | 87.8 | 408  | 28 | US-09-619-643-19022  | Sequence 19022, A   | 132 | 175   | 47.6 | 121  | 48 | US-10-307-005-2050   | Sequence 2050, Ap  |
| 60 | 323   | 87.8 | 408  | 28 | US-09-619-643-19022  | Sequence 19022, A   | 133 | 175   | 47.6 | 121  | 48 | US-10-307-005-2050   | Sequence 2050, Ap  |
| 61 | 316.5 | 86.0 | 1818 | 1  | PCT-US02-27129-7     | Sequence 7, Appli   | 134 | 175   | 47.6 | 121  | 62 | US-10-861-178-6393   | Sequence 6393, Ap  |
| 62 | 316.5 | 86.0 | 1818 | 3  | PCT-US04-07182A-7    | Sequence 7, Appli   | 135 | 162   | 44.0 | 360  | 29 | US-09-619-643-18231  | Sequence 18231, A  |
| 63 | 316.5 | 86.0 | 1818 | 43 | US-10-228-063-7      | Sequence 7, Appli   | 136 | 162   | 44.0 | 360  | 29 | US-09-619-643-18231  | Sequence 18231, A  |
| 64 | 316.5 | 86.0 | 4207 | 3  | PCT-US04-20582-7     | Sequence 7, Appli   | 137 | 162   | 44.0 | 360  | 29 | US-09-619-643-18231  | Sequence 18231, A  |
| 65 | 316.5 | 86.0 | 4207 | 62 | US-10-877-645-7      | Sequence 7, Appli   | 138 | 162   | 44.0 | 360  | 29 | US-09-619-643-18231  | Sequence 18231, A  |
| 66 | 314   | 85.3 | 408  | 28 | US-09-619-643-19289  | Sequence 7, Appli   | 139 | 160   | 43.5 | 369  | 23 | US-09-304-517A-89175 | Sequence 89175, A  |
| 67 | 314   | 85.3 | 408  | 75 | US-09-619-643-19289  | Sequence 19289, A   | 140 | 160   | 43.5 | 369  | 23 | US-09-304-517A-89175 | Sequence 89175, A  |
| 68 | 313.5 | 85.2 | 1170 | 3  | PCT-US04-07182A-77   | Sequence 77, Appl   | 141 | 160   | 43.5 | 369  | 23 | US-09-371-146A-89175 | Sequence 89175, A  |
| 69 | 313.5 | 85.2 | 1425 | 3  | PCT-US04-07182A-77   | Sequence 77, Appl   | 142 | 160   | 43.5 | 369  | 23 | US-09-371-146A-89175 | Sequence 89175, A  |
| 70 | 306.5 | 83.3 | 1863 | 3  | PCT-US04-20582-105   | Sequence 105, App   | 143 | 160   | 43.5 | 369  | 29 | US-09-654-617-292592 | Sequence 292592, A |
| 71 | 306.5 | 83.3 | 1863 | 62 | US-10-877-645-11     | Sequence 11, Appl   | 144 | 160   | 43.5 | 369  | 29 | US-09-654-617-292592 | Sequence 292592, A |
| 72 | 306.5 | 83.3 | 4470 | 3  | PCT-US04-20582-1     | Sequence 1, Appl    | 145 | 160   | 43.5 | 369  | 29 | US-09-654-617-292592 | Sequence 292592, A |
| 73 | 306.5 | 83.3 | 4470 | 62 | US-10-877-645-1      | Sequence 1, Appl    | 146 | 160   | 43.5 | 369  | 29 | US-09-654-617-292592 | Sequence 292592, A |
| 74 | 302   | 82.1 | 386  | 75 | US-09-619-643-20077  | Sequence 20077, A   | 147 | 159   | 43.2 | 121  | 1  | PCT-US03-31862-2057  | Sequence 2057, Ap  |
| 75 | 302   | 82.1 | 386  | 75 | US-09-619-643-20077  | Sequence 20077, A   | 148 | 159   | 43.2 | 121  | 1  | PCT-US03-31862-2057  | Sequence 2057, Ap  |
| 76 | 295   | 80.2 | 431  | 23 | US-09-394-745-22672  | Sequence 22672, A   | 149 | 159   | 43.2 | 121  | 48 | US-10-307-005-2057   | Sequence 2057, Ap  |
| 77 | 295   | 80.2 | 431  | 23 | US-09-394-745-22672  | Sequence 22672, A   | 150 | 159   | 43.2 | 121  | 48 | US-10-307-005-2057   | Sequence 2057, Ap  |
| 78 | 293   | 78.6 | 1101 | 72 | US-11-218-305-19766  | Sequence 19766, A   | 151 | 159   | 43.2 | 121  | 48 | US-10-307-005-2057   | Sequence 2057, Ap  |
| 79 | 289   | 78.5 | 2267 | 13 | US-08-300-726-1      | Sequence 1, Appli   | 152 | 159   | 43.2 | 121  | 48 | US-10-307-005-2057   | Sequence 2057, Ap  |
| 80 | 289   | 78.5 | 2267 | 13 | US-08-300-726A-1     | Sequence 1, Appli   | 153 | 159   | 43.2 | 121  | 48 | US-10-307-005-2057   | Sequence 2057, Ap  |



1 NUMBER OF SEQ ID NOS: 295529  
2 SEQ ID NO 87805  
3 LENGTH: 414  
4 TYPE: DNA  
5 ORGANISM: Zea mays  
6 US-09-985-678-87805

Alignment Scores:  
Pred. No.: 3.6e-33 Length: 414  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 39 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-985-678-87805 (1-414)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProApp 20  
DB 169 ATGGCGGCTCTGGCCACGTCGCAGCTCGTCCCAACGCGCGCGCTGGCGCTCCCGGAC 228  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40  
DB 229 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCGCG 288  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60  
DB 289 GCGGACACGCTAGCATGTCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 348  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 349 CGCGCGGCTGGCAGG-----TTCCGTCGCTCGTGTGTGC 384

RESULT 5

US-60-130-180-74  
1 Sequence 74, Application US/60130180  
2 GENERAL INFORMATION:  
3 APPLICANT: Andersen, Scott E.  
4 TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
5 FILE REFERENCE: 38-21(15503)A  
6 CURRENT APPLICATION NUMBER: US/60/130,180  
7 CURRENT FILING DATE: 1999-04-22  
8 NUMBER OF SEQ ID NOS: 5164  
9 SEQ ID NO 74  
10 LENGTH: 414  
11 TYPE: DNA  
12 ORGANISM: Zea mays  
13 FEATURE:  
14 OTHER INFORMATION: Clone ID: LIB3061-001-Q1-K2-E5  
15 US-60-130-180-74

Alignment Scores:  
Pred. No.: 3.6e-33 Length: 414  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 75 Gaps: 1

US-10-628-525A-36 (1-74) x US-60-130-180-74 (1-414)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProApp 20  
DB 169 ATGGCGGCTCTGGCCACGTCGCAGCTCGTCCCAACGCGCGCGCTGGCGCTCCCGGAC 228  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40  
DB 229 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCGCG 288  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60

DB 289 GCGGACACGCTCAGCATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 348  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 349 CGCGCGGCTGGCAGG-----TTCCGTCGCTCGTGTGTGC 384

RESULT 6

US-09-865-419A-36190  
1 Sequence 36190, Application US/09865419A  
2 GENERAL INFORMATION:  
3 APPLICANT: Conner, Timothy W.  
4 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
5 FILE REFERENCE: 38-21(51935)B  
6 CURRENT APPLICATION NUMBER: US/09/865,419A  
7 PRIOR FILING DATE: 2001-05-29  
8 PRIOR APPLICATION NUMBER: US 60/208,063  
9 PRIOR FILING DATE: 2000-05-31  
10 NUMBER OF SEQ ID NOS: 54020  
11 SEQ ID NO 36190  
12 LENGTH: 609  
13 TYPE: DNA  
14 ORGANISM: Zea mays  
15 FEATURE:  
16 OTHER INFORMATION: Clone ID: LIB3600-059-Q1-K6-B7  
17 US-09-865-419A-36190

Alignment Scores:  
Pred. No.: 6.44e-33 Length: 609  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 33 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-865-419A-36190 (1-609)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProApp 20  
DB 36 ATGGCGGCTCTGGCCACGTCGCAGCTCGTCCCAACGCGCGCGCTGGCGCTCCCGGAC 95  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40  
DB 96 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCGCG 155  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60  
DB 156 GCGGACACGCTCAGCATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 215  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 216 CGCGCGGCTGGCAGG-----TTCCGTCGCTCGTGTGTGC 251

RESULT 7

US-60-208-063-19249  
1 Sequence 19249, Application US/60208063  
2 GENERAL INFORMATION:  
3 APPLICANT: Andersen, Scott E.  
4 APPLICANT: Conner, Timothy W.  
5 APPLICANT: La Rosa, Thomas J.  
6 APPLICANT: Lalquidj, Raghunath V.  
7 APPLICANT: Ruff, Thomas G.  
8 APPLICANT: Shukla, Hridayabhiranjan  
9 APPLICANT: Wu, Kunsheng  
10 APPLICANT: Xu, Nanfei  
11 TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
12 FILE REFERENCE: 38-21(51935)A  
13 CURRENT APPLICATION NUMBER: US/60/208,063  
14 CURRENT FILING DATE: 2000-05-31  
15 NUMBER OF SEQ ID NOS: 25021  
16 SEQ ID NO 19249

; LENGTH: 609  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; OTHER INFORMATION: Clone ID: LIB3600-059-Q1-K6-B7  
 US-60-208-063-19249

Alignment Scores:  
 Pred. No.: 6.44e-33 Length: 609  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 76 Gaps: 1

US-10-628-525A-36 (1-74) x US-60-208-063-19249 (1-609)

QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
 DB 36 ATGGCGGCTCTGGCCACGTCGACGTCGTCGAACGGCGCGCGGCTGGCGCTCCGGAC 95  
 QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 DB 96 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 155  
 QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 DB 156 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 215  
 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 DB 216 CGCGCGGGGGGAGG-----TTCCCGTCGCTCGTGTGTGC 251

RESULT 8

US-09-553-094-11949  
 ; Sequence 11949, Application US/09553094  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Andersen, Scott E.  
 ; APPLICANT: Fisher, Dane K.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants  
 ; FILE REFERENCE: 38-21(15503)B  
 ; CURRENT APPLICATION NUMBER: US/09/553,094  
 ; CURRENT FILING DATE: 2000-04-18  
 ; NUMBER OF SEQ ID NOS: 18831  
 ; SEQ ID NO 11949  
 ; LENGTH: 634  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; OTHER INFORMATION: Clone ID: LIB3061-091-Q1-K6-G11  
 US-09-553-094-11949

Alignment Scores:  
 Pred. No.: 6.84e-33 Length: 634  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 27 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-553-094-11949 (1-634)

QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
 DB 150 ATGGCGGCTCTGGCCACGTCGACGTCGTCGAACGGCGCGCGGCTGGCGCTCCGGAC 209  
 QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 DB 210 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 269  
 QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 DB 270 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 329

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 DB 330 CGCGCGGGGGGAGG-----TTCCCGTCGCTCGTGTGTGC 365

RESULT 9

PCT-US04-20582-2  
 ; Sequence 2, Application PC/TUS0420582  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ravanello, Monica P  
 ; APPLICANT: Foley, Terry J  
 ; APPLICANT: LeDeaux, John R  
 ; APPLICANT: Wyrick, Annette E  
 ; APPLICANT: Savage, Thomas J  
 ; TITLE OF INVENTION: Elevation of Oil Levels in Plants  
 ; FILE REFERENCE: REN-00-119  
 ; CURRENT APPLICATION NUMBER: PCT/US04/20582  
 ; CURRENT FILING DATE: 2004-07-06  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: Patent in version 3.2  
 ; SEQ ID NO 2  
 ; LENGTH: 1818  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 PCT-US04-20582-2

Alignment Scores:  
 Pred. No.: 3.34e-32 Length: 1818  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 3 Gaps: 1

US-10-628-525A-36 (1-74) x PCT-US04-20582-2 (1-1818)

QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
 DB 1 ATGGCGGCTCTGGCCACGTCGACGTCGTCGAACGGCGCGGCTGGCGCTCCGGAC 60  
 QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 DB 61 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120  
 QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 DB 121 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 DB 181 CGCGCGGGGGGAGG-----TTCCCGTCGCTCGTGTGTGC 216

RESULT 10

US-10-877-645-2  
 ; Sequence 2, Application US/10877645  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ravanello, Monica P  
 ; APPLICANT: Foley, Terry J  
 ; APPLICANT: LeDeaux, John R  
 ; APPLICANT: Wyrick, Annette E  
 ; APPLICANT: Savage, Thomas J  
 ; TITLE OF INVENTION: Elevation of Oil Levels in Plants  
 ; FILE REFERENCE: REN-00-119  
 ; CURRENT APPLICATION NUMBER: US/10/877,645  
 ; CURRENT FILING DATE: 2004-06-25  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: Patent in version 3.2  
 ; SEQ ID NO 2  
 ; LENGTH: 1818  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 US-10-877-645-2

Alignment Scores:

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Pred. No.: 3.34e-32 Length: 1818
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 62 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-877-645-2 (1-1818)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 1 ATGGCGGCTCTGGCCACGTCGACGTCGTCGCAACGCGCGCGCTGGCGCGTCCGGAC 60
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyValAlaSerAlaAla 40
Db 61 GGTCCACGTTCCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCGG 120
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 121 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 181 CGCCGCGGGGGGAGG-----TTCCGCTCGCTCGTGTGTC 216

RESULT 11
US-10-425-115-155307
; Sequence 155307, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 155307
; LENGTH: 2111
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MR74577_7321C.1
US-10-425-115-155307

Alignment Scores:
Pred. No.: 4.19e-32 Length: 2111
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 51 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-425-115-155307 (1-2111)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 1 ATGGCGGCTCTGGCCACGTCGACGTCGTCGCAACGCGCGCGCTGGCGCGTCCGGAC 60
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyValAlaSerAlaAla 40
Db 61 GGTCCACGTTCCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGG 120
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 121 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 181 CGCCGCGGGGGGAGG-----TTCCGCTCGCTCGTGTGTC 216
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```
RESULT 12
PCT-US02-33122-1
; Sequence 1, Application PC/TUS0233122
; GENERAL INFORMATION:
; APPLICANT: ExSeed Genetics
; TITLE OF INVENTION: Starch
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: PCT/US02/33122
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/329,525
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Wild type sequence EX385
PCT-US02-33122-1

Alignment Scores:
Pred. No.: 4.65e-32 Length: 2263
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 1 Gaps: 1

US-10-628-525A-36 (1-74) x PCT-US02-33122-1 (1-2263)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 194 ATGGCGGCTCTGGCCACGTCGACGTCGTCGCAACGCGCGCGCTGGCGCGTCCGGAC 253
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyValAlaSerAlaAla 40
Db 254 GGTCCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGG 313
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 314 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCG 373
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 374 CGCCGCGGGGGGAGG-----TTCCGCTCGCTCGTGTGTC 409
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```
RESULT 13
PCT-US02-33122-2
; Sequence 2, Application PC/TUS0233122
; GENERAL INFORMATION:
; APPLICANT: ExSeed Genetics
; TITLE OF INVENTION: Starch
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: PCT/US02/33122
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/329,525
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The mutation is at position 1643 in the sequence,
; OTHER INFORMATION: 1450 bp after the start codon.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The change is a "G" in the wild type (EX385) to an
```

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; OTHER INFORMATION: "A" in the mutant
PCT-US02-33122-2

Alignment Scores:
Pred. No.: 4.65e-32 Length: 2263
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 1 Gaps: 1

US-10-628-525A-36 (1-74) x PCT-US02-33122-2 (1-2263)
QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 194 ATGGCGGCTCTGGCCACGTCGACGTCGTCGCAACGCGCGCCGCGCTCCCGGAC 253
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
DB 254 GCGTCCACGTTCCG 313
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
DB 314 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 373
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB 374 CG 409

RESULT 14
US-10-628-525A-36 (1-74) x PCT-US02-33122-2 (1-2263)
; Sequence 1, Application US/10272291
; GENERAL INFORMATION:
; APPLICANT: ExSeed Genetics
; TITLE OF INVENTION: Starch
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/272,291
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/329,525
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The mutation is at position 1643 in the sequence,
; OTHER INFORMATION: 1450 bp after the start codon.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The change is a "G" in the wild type (EX385) to an
; OTHER INFORMATION: "A" in the mutant
US-10-628-525A-36 (1-74) x US-10-628-525A-36 (1-74)
Alignment Scores:
Pred. No.: 4.65e-32 Length: 2263
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 1 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-628-525A-36 (1-2263)
QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 194 ATGGCGGCTCTGGCCACGTCGACGTCGTCGCAACGCGCGCCGCGCTCCCGGAC 253
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
DB 254 GCGTCCACGTTCCG 313
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
DB 314 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 373
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB 374 CG 409

RESULT 15
US-10-628-525A-36 (1-74) x PCT-US02-33122-2 (1-2263)
; Sequence 2, Application US/10272291
; GENERAL INFORMATION:
; APPLICANT: ExSeed Genetics
; TITLE OF INVENTION: Starch
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/272,291
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/329,525
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The mutation is at position 1643 in the sequence,
; OTHER INFORMATION: 1450 bp after the start codon.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The change is a "G" in the wild type (EX385) to an
; OTHER INFORMATION: "A" in the mutant
US-10-628-525A-36 (1-74) x US-10-628-525A-36 (1-2263)
QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 194 ATGGCGGCTCTGGCCACGTCGACGTCGTCGCAACGCGCGCCGCGCTCCCGGAC 253
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
DB 254 GCGTCCACGTTCCG 313
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
DB 314 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 373
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB 374 CG 409

RESULT 16
PCT-US02-33122-5
; Sequence 5, Application PC/TUS0233122
; GENERAL INFORMATION:
; APPLICANT: ExSeed Genetics
; TITLE OF INVENTION: Starch
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: PCT/US02/33122
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/329,525
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4800
```



```

; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1233)..(1448)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1554)..(1684)
; OTHER INFORMATION: number 2
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1766)..(1859)
; OTHER INFORMATION: number 3
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1959)..(2054)
; OTHER INFORMATION: number 4
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2145)..(2225)
; OTHER INFORMATION: number 5
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2290)..(2412)
; OTHER INFORMATION: number 6
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2514)..(2650)
; OTHER INFORMATION: number 7
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2761)..(2857)
; OTHER INFORMATION: number 8
; FEATURE:
; NAME/KEY: intron
; LOCATION: (3102)..(3211)
; OTHER INFORMATION: number 9
; FEATURE:
; NAME/KEY: intron
; LOCATION: (3395)..(3489)
; OTHER INFORMATION: number 10
; NAME/KEY: intron
; LOCATION: (3682)..(3792)
; OTHER INFORMATION: number 11
; NAME/KEY: intron
; LOCATION: (3880)..(3976)
; OTHER INFORMATION: number 12
; NAME/KEY: intron
; LOCATION: (4106)..(4226)
; OTHER INFORMATION: number 13
PCT-US02-33122-5

Alignment Scores:
Pred. No.: 1 44e-31 Length: 4800
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 1 Gaps: 1

US-10-628-525A-36 (1-74) x PCT-US02-33122-5 (1-4800)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAep 20
Db 1233 ATGGCGGCTCTGGCCAGCTCGCTCGTCCACACGGCGCGCTGGCGCTGGCGGAC 1292

Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 1293 GCGTCCAGTTCCGCGCGCGCGCGCGCGCGCTGAGGGGGGCGCGCGCGCGCGG 1352

; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1233)..(1448)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1554)..(1684)
; OTHER INFORMATION: number 2
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1766)..(1859)
; OTHER INFORMATION: number 3
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1959)..(2054)
; OTHER INFORMATION: number 4
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2145)..(2225)
; OTHER INFORMATION: number 5
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2290)..(2412)
; OTHER INFORMATION: number 6
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2514)..(2650)
; OTHER INFORMATION: number 7
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2761)..(2857)
; OTHER INFORMATION: number 8
; FEATURE:
; NAME/KEY: intron
; LOCATION: (3102)..(3211)
; OTHER INFORMATION: number 9
; FEATURE:
; NAME/KEY: intron
; LOCATION: (3395)..(3489)
; OTHER INFORMATION: number 10
; NAME/KEY: intron
; LOCATION: (3682)..(3792)
; OTHER INFORMATION: number 11
; NAME/KEY: intron
; LOCATION: (3880)..(3976)
; OTHER INFORMATION: number 12
; NAME/KEY: intron
; LOCATION: (4106)..(4226)
; OTHER INFORMATION: number 13
PCT-US02-33122-5

Alignment Scores:
Pred. No.: 1 44e-31 Length: 4800
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 1 Gaps: 1

US-10-628-525A-36 (1-74) x PCT-US02-33122-5 (1-4800)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAep 20
Db 1233 ATGGCGGCTCTGGCCAGCTCGCTCGTCCACACGGCGCGCTGGCGCTGGCGGAC 1292

Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 1293 GCGTCCAGTTCCGCGCGCGCGCGCGCGCTGAGGGGGGCGCGCGCGCGCGG 1352

Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 1353 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1412

Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 1413 CG 1448

RESULT 17
US-09-625-406-4
; Sequence 4, Application US/09625406
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanning
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Greenlee, Winner and Sullivan, P.C.
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/625,406
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/941,445
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4800 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1449..1553, 1685..1765, 1860..1958, 2055
; LOCATION: ..2144, 2226..2289, 2413..2513, 2651..2760, 2858
; LOCATION: ..3101, 3212..3394, 3490..3681, 3793..3879, 3977
; LOCATION: ..4105, 4227..4343)
; US-09-625-406-4

Alignment Scores:
Pred. No.: 1 44e-31 Length: 4800
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 28 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-625-406-4 (1-4800)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAep 20
Db 1233 ATGGCGGCTCTGGCCAGCTCGCTCGTCCACACGGCGCGCGCTGGCGCTGGCGGAC 1292
```

Qy 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 1293 GCCTCCACGTTCCCGCCGCGCGCGCGCGCTGAGGGGGGCGCGCGCGCTGCGCGCGC 1352  
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 1353 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1412  
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 1413 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGC 1448

## RESULT 18

US-10-109-048-1141  
; Sequence 1141, Application US/10109048  
; GENERAL INFORMATION:  
; APPLICANT: COMMURI, PADMA  
; APPLICANT: KEELING, PETER L.  
; APPLICANT: RAMIREZ, NONA  
; APPLICANT: MCKEAN, ANGELA  
; APPLICANT: GAO, ZHONG  
; APPLICANT: GUAN, HANPING  
; TITLE OF INVENTION: GLUCAN CHAIN LENGTH DOMAINS  
; FILE REFERENCE: 2461-76  
; CURRENT APPLICATION NUMBER: US/10/109,048  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: 60/279,720  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 1154  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1141  
; LENGTH: 4800  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-10-109-048-1141

Alignment Scores:  
Pred. No.: 1.44e-31 Length: 4800  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservativity: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 42 Gaps: 1

US-10-628-525a-36 (1-74) x US-10-109-048-1141 (1-4800)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProApp 20  
Db 1233 ATGGCGGCTCTGGCCACGTCGCAGCTCGTCGCAACGCGCGCGCTGCGCGCTCCCGGAC 1292  
Qy 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 1293 GCGTCCACGTTCCCGCCGCGCGCGCGCGCGCGCTGAGGGGGGCGCGCGCTGCGCGCGC 1352  
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 1353 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1412  
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 1413 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGC 1448

## RESULT 19

US-10-272-291-5  
; Sequence 5, Application US/10272291  
; GENERAL INFORMATION:  
; APPLICANT: Exseed Genetics  
; TITLE OF INVENTION: Starch  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/272,291  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: 60/329,525

; PRIOR FILING DATE: 2001-10-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 4800  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: transit\_peptide  
; LOCATION: (1233)..(1448)  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (1554)..(1684)  
; OTHER INFORMATION: number 2  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (1766)..(1859)  
; OTHER INFORMATION: number 3  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (1959)..(2054)  
; OTHER INFORMATION: number 4  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (2145)..(2225)  
; OTHER INFORMATION: number 5  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (2290)..(2412)  
; OTHER INFORMATION: number 6  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (2514)..(2650)  
; OTHER INFORMATION: number 7  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (2761)..(2857)  
; OTHER INFORMATION: number 8  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (3102)..(3211)  
; OTHER INFORMATION: number 9  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (3395)..(3489)  
; OTHER INFORMATION: number 10  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (3682)..(3792)  
; OTHER INFORMATION: number 11  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (3880)..(3976)  
; OTHER INFORMATION: number 12  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (4106)..(4226)  
; OTHER INFORMATION: number 13  
US-10-272-291-5

Alignment Scores:  
Pred. No.: 1.44e-31 Length: 4800  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservativity: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 43 Gaps: 1

US-10-628-525a-36 (1-74) x US-10-272-291-5 (1-4800)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProApp 20  
Db 1233 ATGGCGGCTCTGGCCACGTCGCAGCTCGTCGCAACGCGCGCGCTGCGCGCTCCCGGAC 1292



DB: 53 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-628-525A-4 (1-4800)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
 Db 1233 ATGGCGGCTCTGGCCACGTCGACCTGTCGCAACGCGCGCCGCTGGGGCGTCCCGGAC 1292

Qy 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 Db 1293 GCGTCCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGGCCCGGGCGTCCGGCGCG 1352

Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 1353 GCGGACACGCTCAGCATGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1412

Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 1413 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGCTGTGTGC 1449

RESULT 22

US-09-304-517A-91115  
 ; Sequence 91115, Application US/09304517A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheikh, Nordine  
 ; APPLICANT: Liu, Jingdong  
 ; TITLE OF INVENTION: Annotated Plant Genes  
 ; FILE REFERENCE: 38-21(15097)B  
 ; CURRENT APPLICATION NUMBER: US/09/304,517A  
 ; CURRENT FILING DATE: 1999-05-06  
 ; NUMBER OF SEQ ID NOS: 295529  
 ; SEQ ID NO 91115  
 ; LENGTH: 418  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 US-09-304-517A-91115

Alignment Scores:  
 Pred. No.: 1,68e-32 Length: 418  
 Score: 328.00 Matches: 70  
 Percent Similarity: 94.6% Conservative: 0  
 Best Local Similarity: 94.6% Mismatches: 2  
 Query Match: 89.1% Indels: 2  
 DB: 23 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-304-517A-91115 (1-418)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
 Db 179 ATGGCGGCTCTGGCCACGTCGACCTGTCGCAACGCGCGCCGCTGGGGCGTCCCGGAC 238

Qy 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 Db 239 GCGTCCACGTTCCGCGCGCGCGCGCGCTGAGGGGGGCCCGGGCGTCCGGCGCG 298

Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 299 GCGGACACGCTCAGCATGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 358

Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 359 CGCGCGGGTGGCAGG-----TTCCCGTCGCTCGCTGTGTGC 394

RESULT 23

US-09-371-146A-91115  
 ; Sequence 91115, Application US/09371146A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheikh, Nordine  
 ; APPLICANT: Liu, Jingdong  
 ; TITLE OF INVENTION: ANNOTATED PLANT GENES  
 ; FILE REFERENCE: 38-21(15097)C  
 ; CURRENT APPLICATION NUMBER: US/09/371,146A  
 ; CURRENT FILING DATE: 1999-08-09

Db 299 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCCAGGACACAGCAGCAGGCG 358  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 359 CGCCGCGGTGGCAGG-----TTCCCGTCGCTCGTGTGTC 394

## RESULT 25

US-09-985-678-91115  
; Sequence 91115, Application US/09985678  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; TITLE OF INVENTION: Annotated Plant Genes  
; FILE REFERENCE: 16517.255/38-21(15097)P  
; CURRENT APPLICATION NUMBER: US/09/985,678  
; CURRENT FILING DATE: 2001-11-05  
; PRIOR APPLICATION NUMBER: US 09/304,517  
; PRIOR FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 295529  
; SEQ ID NO 91115  
; LENGTH: 418  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-985-678-91115

## Alignment Scores:

Pred. No.: 1,68e-32 Length: 418  
Score: 328.00 Matches: 70  
Percent Similarity: 94.6% Conservatives: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 89.1% Indels: 2  
DB: 39 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-985-678-91115 (1-418)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 179 ATGGCGGCTCTGGCCACGTCGAGCTCGTCGCAACGCGCGCGCTGGCGTCCCGGAC 238  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 239 GCGTCCACGTTCCGCGCGCGCGCGCATGTCCTGAGGGGGCGCGCGCTCGCGCGCG 298  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 299 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCCAGGACCCAGCAGCAGGCG 358  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 359 CGCCGCGGTGGCAGG-----TTCCCGTCGCTCGTGTGTC 394

## RESULT 26

US-60-130-180-4602  
; Sequence 4602, Application US/60130180  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Fisher, Dane K.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(15503)A  
; CURRENT APPLICATION NUMBER: US/60/130,180  
; CURRENT FILING DATE: 1999-04-22  
; NUMBER OF SEQ ID NOS: 5164  
; SEQ ID NO 4602  
; LENGTH: 418  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: L1B3061-052-Q1-K1-F7  
US-60-130-180-4602

## Alignment Scores:

Pred. No.: 1,68e-32 Length: 418  
Score: 328.00 Matches: 70  
Percent Similarity: 94.6% Conservatives: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 89.1% Indels: 2  
DB: 75 Gaps: 1

US-10-628-525A-36 (1-74) x US-60-130-180-4602 (1-418)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 179 ATGGCGGCTCTGGCCACGTCGAGCTCGTCGCAACGCGCGCGCTGGCGTCCCGGAC 238  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 239 GCGTCCACGTTCCGCGCGCGCGCGCATGTCCTGAGGGGGCGCGCGCTCGCGCGCG 298  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 299 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCCAGGACCCAGCAGCAGGCG 358  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 359 CGCCGCGGTGGCAGG-----TTCCCGTCGCTCGTGTGTC 394

## RESULT 27

US-09-619-643-19435  
; Sequence 19435, Application US/09619643  
; GENERAL INFORMATION:  
; APPLICANT: Fisher, Dane K.  
; APPLICANT: Lalquid, Raghunath V.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(51230)B  
; CURRENT APPLICATION NUMBER: US/09/619,643  
; CURRENT FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 19435  
; LENGTH: 339  
; TYPE: DNA  
; ORGANISM: Zea mays  
; OTHER INFORMATION: Clone ID: L1B3151-045-Q1-K1-D7  
US-09-619-643-19435

## Alignment Scores:

Pred. No.: 2,25e-32 Length: 339  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservatives: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 28 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-619-643-19435 (1-339)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 65 ATGGCGGCTCTGGCCACGTCGAGCTCGTCGCAACGCGCGCGCGCTGGCGTCCCGGAC 124  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 125 GCGTCCACGTTCCGCGCGCGCGCGCATGTCCTGAGGGGGCGCGCGCTCGCGCGCG 184  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 185 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCCAGGACCCAGCAGCAGGCG 244  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 245 CGCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTC 280

## RESULT 28

US-60-145-148-3000  
; Sequence 3000, Application US/60145148

GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Deng, Mollan  
; APPLICANT: Fisher, Dane K.  
; APPLICANT: Miller, Philip W.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; TITLE OF INVENTION: PLANTS  
; FILE REFERENCE: 38-21(51230)A  
; CURRENT APPLICATION NUMBER: US/60/145,148  
; CURRENT FILING DATE: 1999-07-22  
; SEQ ID NO 3000  
; LENGTH: 339  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-045-Q1-K1-D7  
US-60-145-148-3000

Alignment Scores:  
Pred. No.: 2,25e-32 Length: 339  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 75 Gaps: 1

US-10-628-525A-36 (1-74) x US-60-145-148-3000 (1-339)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 65 ATGGGGCTCTGGCCAGCTCGAGCTCGTGCACAGCCCGCGGCTGGGGCTCCCGGAC 124  
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 125 GCGTCCACGTTCCCGCGCGCGCGCGAGCGCTGAGGGGGCGCCGGGGGTGGCGGCG 184  
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 185 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCCAGGACACGAGCAGCGCG 244  
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 245 CGCCGGGGGGGAGG-----TTCCCGTCGCTCGTGTGTGC 280

RESULT 29  
US-09-619-643-19534  
; Sequence 19534, Application US/09619643  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath V.  
; APPLICANT: Fisher, Dane K.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(51230)B  
; CURRENT APPLICATION NUMBER: US/09/619,643  
; CURRENT FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 19534  
; LENGTH: 386  
; TYPE: DNA  
; ORGANISM: Zea mays  
; OTHER INFORMATION: Clone ID: LIB3151-046-Q1-K1-F12  
US-09-619-643-19534

Alignment Scores:  
Pred. No.: 2,74e-32 Length: 386  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 28 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-619-643-19534 (1-386)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 146 ATGGGGCTCTGGCCAGCTCGAGCTCGTGCACAGCCCGCGGCTGGGGCTCCCGGAC 205  
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 206 GCGTCCACGTTCCCGCGCGCGCGCGAGGCTGAGGGGGCGCCGGGGGTGGCGGCG 265  
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 266 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCCAGGACACGAGCAGCGCG 325  
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 326 CGCCGGGGGGGAGG-----TTCCCGTCGCTCGTGTGTGC 361

#### RESULT 30

US-60-145-148-3100  
; Sequence 3100, Application US/60145148  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Deng, Mollan  
; APPLICANT: Fisher, Dane K.  
; APPLICANT: Miller, Philip W.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; TITLE OF INVENTION: PLANTS  
; FILE REFERENCE: 38-21(51230)A  
; CURRENT APPLICATION NUMBER: US/60/145,148  
; CURRENT FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 3994  
; SEQ ID NO 3100  
; LENGTH: 386  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-046-Q1-K1-F12  
US-60-145-148-3100

Alignment Scores:  
Pred. No.: 2,74e-32 Length: 386  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 75 Gaps: 1

US-10-628-525A-36 (1-74) x US-60-145-148-3100 (1-386)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 146 ATGGGGCTCTGGCCAGCTCGAGCTCGTGCACAGCCCGCGGCTGGGGCTCCCGGAC 205  
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 206 GCGTCCACGTTCCCGCGCGCGCGCGAGGCTGAGGGGGCGCCGGGGGTGGCGGCG 265  
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 266 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCCAGGACACGAGCAGCGCG 325  
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 326 CGCCGGGGGGGAGG-----TTCCCGTCGCTCGTGTGTGC 361

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Job time : 2029.88 secs

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 21:21:57 ; Search time 138.391 Seconds  
(without alignments)  
1603.719 Million cell updates/sec

Title: US-10-628-525A-36  
Perfect score: 368  
Sequence: 1 MAALATSQLVATRAGHGVDP.....RHQQQARRGRFFPPLVVC 74

Scoring table: BLOSUM62 Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6698573 seqs, 1499593917 residues

Total number of hits satisfying chosen parameters: 13397146

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Command line parameters:  
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-Q=/abs/ABSWEB.spool/US10628525/runat\_31032006\_095132\_17106/app.query.fasta\_1  
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-LOOPCL=0 -LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=150 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR\_MIN=0 -ALIGN=30 -MODES=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abes06h  
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA.New:\*

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4: /SID55/ptodata/2/pna/US08 NEW COMB.seq:\*  
5: /SID55/ptodata/2/pna/US09 NEW COMB.seq:\*  
6: /SID55/ptodata/2/pna/US10 NEW COMB.seq:\*  
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12: /SID55/ptodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                            |
|------------|-------|-------------|--------|----|----------------------------------------|
| 1          | 333   | 90.5        | 414    | 8  | US-11-329-388-4757 Sequence 4757, Ap   |
| 2          | 333   | 90.5        | 634    | 8  | US-11-329-388-11949 Sequence 11949, A  |
| 3          | 328   | 89.1        | 418    | 8  | US-11-329-388-1278 Sequence 1278, Ap   |
| 4          | 326   | 88.6        | 339    | 10 | US-11-227-183A-19435 Sequence 19435, A |
| 5          | 326   | 88.6        | 386    | 10 | US-11-227-183A-19534 Sequence 19534, A |

|       |    |                       |                    |
|-------|----|-----------------------|--------------------|
| 415   | 10 | US-11-227-183A-18500  | Sequence 18500, A  |
| 428   | 8  | US-11-353-150-45112   | Sequence 45112, A  |
| 449   | 10 | US-11-227-183A-17085  | Sequence 17085, A  |
| 561   | 10 | US-11-227-183A-20738  | Sequence 20738, A  |
| 1409  | 8  | US-11-398-234A-9      | Sequence 9, Appli  |
| 1915  | 8  | US-11-330-822-50      | Sequence 50, Appli |
| 408   | 10 | US-11-227-183A-19022  | Sequence 19022, A  |
| 420   | 10 | US-11-227-183A-19076  | Sequence 19076, A  |
| 408   | 10 | US-11-227-183A-19289  | Sequence 19289, A  |
| 386   | 10 | US-11-227-183A-20077  | Sequence 20077, A  |
| 431   | 8  | US-11-353-150-45136   | Sequence 45136, A  |
| 400   | 10 | US-11-227-183A-16655  | Sequence 16655, A  |
| 388   | 10 | US-11-227-183A-18495  | Sequence 18495, A  |
| 625   | 8  | US-11-329-388-8047    | Sequence 8047, Ap  |
| 649   | 8  | US-11-329-388-8026    | Sequence 8026, Ap  |
| 432   | 8  | US-11-329-388-1754    | Sequence 1754, Ap  |
| 422   | 10 | US-11-227-183A-17758  | Sequence 17758, A  |
| 354   | 10 | US-11-227-183A-19448  | Sequence 19448, A  |
| 363   | 8  | US-11-329-388-3077    | Sequence 3077, Ap  |
| 365   | 10 | US-11-227-183A-18014  | Sequence 18014, A  |
| 371   | 10 | US-11-227-183A-18823  | Sequence 18823, A  |
| 338   | 10 | US-11-227-183A-32098  | Sequence 32098, A  |
| 203   | 10 | US-11-227-183A-18999  | Sequence 18999, A  |
| 519   | 10 | US-11-227-183A-20737  | Sequence 20737, A  |
| 360   | 10 | US-11-227-183A-18231  | Sequence 18231, A  |
| 369   | 8  | US-11-329-388-1751    | Sequence 1751, Ap  |
| 297   | 10 | US-11-227-183A-28810  | Sequence 28810, A  |
| 283   | 10 | US-11-227-183A-18478  | Sequence 18478, A  |
| 304   | 10 | US-11-227-183A-17248  | Sequence 17248, A  |
| 315   | 8  | US-11-353-150-62704   | Sequence 62704, A  |
| 291   | 10 | US-11-227-183A-17794  | Sequence 17794, A  |
| 283   | 10 | US-11-227-183A-20080  | Sequence 20080, A  |
| 360   | 10 | US-11-227-183A-18826  | Sequence 18826, A  |
| 266   | 10 | US-11-227-183A-26235  | Sequence 26235, A  |
| 150   | 10 | US-11-227-183A-20693  | Sequence 20693, A  |
| 241   | 10 | US-11-227-183A-26412  | Sequence 26412, A  |
| 251   | 10 | US-11-227-183A-20324  | Sequence 20324, A  |
| 146   | 8  | US-11-329-388-4836    | Sequence 4836, Ap  |
| 275   | 10 | US-11-227-183A-17503  | Sequence 17503, A  |
| 1000  | 10 | US-11-266-748A-205192 | Sequence 205192, A |
| 2300  | 12 | US-60-762-056-37460   | Sequence 37460, A  |
| 2580  | 7  | US-10-276-817B-2668   | Sequence 2668, Ap  |
| 2622  | 7  | US-10-276-817B-2314   | Sequence 2314, Ap  |
| 1379  | 10 | US-11-266-748A-162166 | Sequence 162166, A |
| 1819  | 8  | US-11-174-307B-3253   | Sequence 3253, Ap  |
| 237   | 10 | US-11-227-183A-18998  | Sequence 18998, A  |
| 2300  | 12 | US-60-762-056-31257   | Sequence 31257, A  |
| 2300  | 12 | US-60-762-056-20206   | Sequence 20206, A  |
| 2300  | 12 | US-60-762-056-20207   | Sequence 20207, A  |
| 2501  | 1  | PCT-US04-20336-36     | Sequence 36, Appl  |
| 2501  | 10 | US-11-317-798-36      | Sequence 36, Appl  |
| 2778  | 7  | US-10-461-673-5700    | Sequence 5700, Ap  |
| 3286  | 12 | US-60-751-420-3381    | Sequence 3381, Ap  |
| 16842 | 7  | US-10-506-111-30      | Sequence 30, Appl  |
| 2300  | 12 | US-60-762-056-4634    | Sequence 4634, Ap  |
| 2300  | 12 | US-60-762-056-16509   | Sequence 16509, A  |
| 460   | 8  | US-11-353-150-65596   | Sequence 65596, A  |
| 576   | 10 | US-11-266-748A-90641  | Sequence 90641, A  |
| 576   | 10 | US-11-266-748A-143452 | Sequence 143452, A |
| 1031  | 10 | US-11-266-748A-98299  | Sequence 98299, A  |
| 1031  | 10 | US-11-266-748A-151110 | Sequence 151110, A |
| 2300  | 12 | US-60-762-056-20106   | Sequence 20106, A  |
| 3523  | 7  | US-10-567-867-1152    | Sequence 1152, Ap  |
| 3686  | 7  | US-10-567-867-1150    | Sequence 1150, Ap  |
| 11000 | 12 | US-60-740-736-57      | Sequence 57, Appl  |
| 838   | 10 | US-11-266-748A-370877 | Sequence 370877, A |
| 838   | 10 | US-11-266-748A-454256 | Sequence 454256, A |
| 4631  | 10 | US-11-266-748A-23775  | Sequence 23775, A  |
| 852   | 7  | US-10-526-468-1       | Sequence 1, Appli  |
| 1072  | 8  | US-11-056-355B-67001  | Sequence 67001, A  |
| 1632  | 7  | US-10-953-343-28425   | Sequence 28425, A  |
| 2300  | 12 | US-60-762-056-27646   | Sequence 27646, A  |
| 467   | 8  | US-11-360-355-52941   | Sequence 52941, A  |

79 77.5 21.1 975 7 US-10-533-232A-103 Sequence 103, App  
80 77.5 21.1 1239 7 US-10-540-898-285 Sequence 285, App  
81 77.5 21.1 2182 7 US-11-360-355-22269 Sequence 22269, A  
82 77.5 21.1 2300 12 US-60-762-056-16197 Sequence 16197, A  
83 77.5 21.1 21239 8 US-10-540-898-284 Sequence 284, App  
84 77.5 21.1 84428 8 US-11-330-363-1 Sequence 1, Appl  
85 77.5 21.1 84428 8 US-11-239-625A-1671 Sequence 1671, Ap  
86 77 20.9 291 12 US-60-762-056-23276 Sequence 23276, A  
87 76.5 20.8 2300 12 US-11-227-183A-28897 Sequence 28897, A  
88 76.5 20.8 1522 8 US-11-174-307B-1097 Sequence 1097, Ap  
89 76.5 20.8 1522 8 US-11-056-355B-10007 Sequence 10007, A  
90 76.5 20.8 70782 6 US-10-526-572-47 Sequence 47, Appl  
91 76.5 20.8 82868 6 US-10-526-572-1 Sequence 1, Appl  
92 76.5 20.8 82868 6 US-10-526-572-18 Sequence 18, Appl  
93 75.5 20.5 402 10 US-11-227-183A-16939 Sequence 16939, A  
94 75.5 20.5 413 8 US-11-353-150-44264 Sequence 44264, A  
95 75.5 20.5 421 8 US-11-353-150-64448 Sequence 64448, A  
96 75.5 20.5 1552 8 US-11-174-307B-5185 Sequence 5185, Ap  
97 75.5 20.5 2300 12 US-60-762-056-28190 Sequence 28190, A  
98 75.5 20.5 2300 12 US-60-762-056-29256 Sequence 29256, A  
99 75.5 20.5 2300 12 US-60-762-056-29257 Sequence 29257, A  
100 75.5 20.5 4763 7 US-10-529-348-184 Sequence 184, App  
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102 75.5 20.5 15203 10 US-11-214-063A-1619 Sequence 1619, Ap  
103 75 20.4 613 7 US-10-953-349-37623 Sequence 37623, A  
104 75 20.4 908 10 US-11-266-748A-184390 Sequence 184390, A  
105 75 20.4 908 10 US-11-266-748A-191895 Sequence 191895, A  
106 75 20.4 922 10 US-11-266-748A-184386 Sequence 184386, A  
107 75 20.4 977 7 US-10-461-673-3209 Sequence 3209, Ap  
108 75 20.4 1000 10 US-11-266-748A-406913 Sequence 406913, A  
109 75 20.4 1000 10 US-11-266-748A-477959 Sequence 477959, A  
110 75 20.4 1047 12 US-60-763-373-372 Sequence 372, App  
111 75 20.4 1047 12 US-60-781-308-180 Sequence 180, App  
112 75 20.4 1388 8 US-11-360-358-76095 Sequence 76095, A  
113 75 20.4 1534 8 US-11-056-355B-51703 Sequence 51703, A  
114 75 20.4 1854 8 US-11-056-355B-66119 Sequence 66119, A  
115 75 20.4 2300 12 US-60-762-056-20212 Sequence 20212, A  
116 75 20.4 2300 12 US-60-762-056-26111 Sequence 26111, A  
117 75 20.4 2312 1 PCT-US05-46084-1 Sequence 1, Appl  
118 75 20.4 2312 7 US-10-529-348-769 Sequence 769, App  
119 75 20.4 2312 8 US-11-342-366-1204 Sequence 1204, Ap  
120 75 20.4 2312 8 US-11-342-367-1204 Sequence 1204, Ap  
121 75 20.4 2312 10 US-11-313-200-1 Sequence 1, Appl  
122 75 20.4 2312 12 US-60-751-420-1585 Sequence 1585, Ap  
123 75 20.4 2473 10 US-11-266-748A-73797 Sequence 73797, A  
124 75 20.4 2473 10 US-11-266-748A-108013 Sequence 108013, A  
125 75 20.4 2473 10 US-11-266-748A-126608 Sequence 126608, A  
126 75 20.4 2956 8 US-11-360-355-12464 Sequence 12464, A  
127 75 20.4 3363 1 PCT-US05-45818-51 Sequence 51, Appl  
128 75 20.4 3778 10 US-11-266-748A-29168 Sequence 29168, A  
129 75 20.4 3889 10 US-11-266-748A-27035 Sequence 27035, A  
130 75 20.4 90573 1 PCT-US05-45818-151 Sequence 151, App  
131 74.5 20.2 426 8 US-11-329-388-18655 Sequence 18655, A  
132 74.5 20.2 1270 8 US-11-089-097-6 Sequence 6, Appl  
133 74.5 20.2 1316 7 US-10-240-851A-76 Sequence 76, Appl  
134 74.5 20.2 1356 8 US-11-089-097-7 Sequence 7, Appl  
135 74.5 20.2 1356 8 US-11-342-366-1804 Sequence 1804, Ap  
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137 74.5 20.2 1363 10 US-11-266-748A-186709 Sequence 186709, A  
138 74.5 20.2 1363 10 US-11-266-748A-241491 Sequence 241491, A  
139 74.5 20.2 1700 10 US-11-266-748A-81026 Sequence 81026, A  
140 74.5 20.2 1700 10 US-11-266-748A-133837 Sequence 133837, A  
141 74.5 20.2 1740 7 US-10-531-147-312 Sequence 312, App  
142 74.5 20.2 1740 7 US-10-531-147-2447 Sequence 2447, Ap  
143 74.5 20.2 1772 10 US-11-266-748A-56645 Sequence 56645, A  
144 74.5 20.2 1848 8 US-11-056-355B-20264 Sequence 20264, A  
145 74.5 20.2 1956 7 US-10-461-673-5468 Sequence 5468, Ap  
146 74.5 20.2 2300 12 US-60-762-056-16025 Sequence 16025, A  
147 74.5 20.2 2300 12 US-60-762-056-40627 Sequence 40627, A  
148 74.5 20.2 2300 12 US-60-762-056-43992 Sequence 43992, A  
149 74.5 20.2 2300 12 US-60-762-056-44619 Sequence 44619, A  
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RESULT 1  
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; Sequence 4757, Application US/11329388  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Fisher, Dane K.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 16517.357 - 38-21(15503)C/US  
; CURRENT APPLICATION NUMBER: US/11/329,388  
; CURRENT FILING DATE: 2006-01-11  
; PRIOR APPLICATION NUMBER: 09/553,094  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 18831  
; SEQ ID NO 4757  
; LENGTH: 414  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3061-001-Q1-K2-ES  
US-11-329-388-4757

Alignment Scores:  
Pred. No.: 5,01e-29 Length: 414  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-329-388-4757 (1-414)

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Db GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 288  
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaLa 40  
229 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 288  
Db GCGGACAGCTCAGCATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60  
Qy 41 AlaSerThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnGlnAla 60  
289 GCGGACAGCTCAGCATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 348  
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
349 CGCGCGCGTGGCAGG-----TTCCCGTCGTCGTCGTCGTCGTCGTCGTCGTC 384  
Db

RESULT 2  
US-11-329-388-11949  
; Sequence 11949, Application US/11329388  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Fisher, Dane K.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 16517.357 - 38-21(15503)C/US  
; CURRENT APPLICATION NUMBER: US/11/329,388  
; CURRENT FILING DATE: 2006-01-11  
; PRIOR APPLICATION NUMBER: 09/553,094  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 18831  
; SEQ ID NO 11949  
; LENGTH: 634  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3061-091-Q1-K6-G11  
US-11-329-388-11949

## Alignment Scores:

Pred. No.: 8.96e-29 Length: 634  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-329-388-11949 (1-634)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 150 ATGGCGGCTCTGGCCACGTCGCAGCTGTCGCAAGCGCGCGGCTGGGGCTCCCGGAC 209  
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 210 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 269  
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 270 GCGGACACGTCAGCATGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 329  
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 330 CGCGCGGGGGGAGG-----TTCCCGTCGCTCGTGTGTGC 365

## RESULT 3

US-11-329-388-1278

; Sequence 1278, Application US/11329388

; GENERAL INFORMATION:

; APPLICANT: Andersen, Scott E.

; APPLICANT: Fisher, Dane K.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; FILE REFERENCE: 16517.357 - 38-21(15503)C/US

; CURRENT APPLICATION NUMBER: US/11/329,388

; CURRENT FILING DATE: 2006-01-11

; PRIOR APPLICATION NUMBER: 09/553,094

; PRIOR FILING DATE: 2000-04-18

; NUMBER OF SEQ ID NOS: 18831

; SEQ ID NO 1278

; LENGTH: 418

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3061-052-Q1-K1-F7

US-11-329-388-1278

## Alignment Scores:

Pred. No.: 1.92e-28 Length: 418  
Score: 328.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 89.1% Indels: 2  
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-329-388-1278 (1-418)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 179 ATGGCGGCTCTGGCCACGTCGCAGCTGTCGCAAGCGCGCGGCTGGGGCTCCCGGAC 238  
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 239 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 298  
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 299 GCGGACACGTCAGCATGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 358  
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 359 CGCGCGGGTGGCAGG-----TTCCCGTCGCTCGTGTGTGC 394

## RESULT 4

US-11-227-183A-19435

; Sequence 19435, Application US/11227183A

; GENERAL INFORMATION:

; APPLICANT: Fisher, Dane K.

; APPLICANT: Lalgudi, Raghunath V.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; FILE REFERENCE: 16517.336 - 38-21(51230)C/US

; CURRENT APPLICATION NUMBER: US/11/227,183A

; CURRENT FILING DATE: 2005-09-16

; PRIOR APPLICATION NUMBER: US 09/619,643

; PRIOR FILING DATE: 2000-07-19

; NUMBER OF SEQ ID NOS: 32236

; SEQ ID NO 19435

; LENGTH: 339

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3151-045-Q1-K1-D7

US-11-227-183A-19435

## Alignment Scores:

Pred. No.: 2.45e-28 Length: 339  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-19435 (1-339)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 65 ATGGCGGCTCTGGCCACGTCGCAGCTGTCGCAAGCGCGGCTGGGGCTCCCGGAC 124  
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 125 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 184  
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 185 GCGGACACGTCAGCATGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 244  
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 245 CGCGCGGGGGGAGG-----TTCCCGTCGCTCGTGTGTGC 280

## RESULT 5

US-11-227-183A-19534

; Sequence 19534, Application US/11227183A

; GENERAL INFORMATION:

; APPLICANT: Fisher, Dane K.

; APPLICANT: Lalgudi, Raghunath V.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; FILE REFERENCE: 16517.336 - 38-21(51230)C/US

; CURRENT APPLICATION NUMBER: US/11/227,183A

; CURRENT FILING DATE: 2005-09-16

; PRIOR APPLICATION NUMBER: US 09/619,643

; PRIOR FILING DATE: 2000-07-19

; NUMBER OF SEQ ID NOS: 32236

; SEQ ID NO 19534

; LENGTH: 386

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3151-046-Q1-K1-F12

US-11-227-183A-19534

## Alignment Scores:

Pred. No.: 2.93e-28 Length: 386

Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-19534 (1-386)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 146 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTCGCAACGCCCGCGGCTGGCGCTCCGGAC 205  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 206 GGTCCACGTTCCGCGCGCGCGCGCGCAGGCGCTGAGGGGGCCCGGCGTCGCGGGCG 265  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60  
DB 266 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 325  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 326 CGCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 361

## RESULT 6

US-11-227-183A-18500  
; Sequence 18500, Application US/11227183A  
; GENERAL INFORMATION:  
; APPLICANT: Fisher, Dane K.  
; APPLICANT: Lalquidi, Raghunath V.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US  
; CURRENT FILING DATE: 2005-09-16  
; PRIOR APPLICATION NUMBER: US 09/619,643  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 18500  
; LENGTH: 415  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-029-Q1-K1-B4

US-11-227-183A-18500

Alignment Scores:  
Pred. No.: 3,238-28 Length: 415  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-18500 (1-415)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 146 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTCGCAACGCCCGCGGCTGGCGCTCCGGAC 205  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 206 GGTCCACGTTCCGCGCGCGCGCGCGCAGGCGCTGAGGGGGCCCGGCGTCGCGGGCG 265  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60  
DB 266 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 325  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 326 CGCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 361

## RESULT 7

US-11-353-150-45112  
; Sequence 45112, Application US/11353150  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Conner, Timothy W.  
; APPLICANT: Lalquidi, Raghunath V.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US  
; CURRENT FILING DATE: 2006-02-14  
; PRIOR APPLICATION NUMBER: 09/565,386  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/132,860  
; PRIOR FILING DATE: 1999-05-07  
; NUMBER OF SEQ ID NOS: 83523  
; SEQ ID NO 45112  
; LENGTH: 428  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3066-030-Q1-K1-A8

US-11-353-150-45112

Alignment Scores:  
Pred. No.: 3,378-28 Length: 428  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-353-150-45112 (1-428)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 187 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTCGCAACGCCCGCGGCTGGCGCTCCGGAC 246  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 247 GGTCCACGTTCCGCGCGCGCGCGCGCAGGCGCTGAGGGGGCCCGGCGTCGCGGGCG 306  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60  
DB 307 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 366  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 367 CGCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 402

## RESULT 8

US-11-227-183A-17085  
; Sequence 17085, Application US/11227183A  
; GENERAL INFORMATION:  
; APPLICANT: Fisher, Dane K.  
; APPLICANT: Lalquidi, Raghunath V.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US  
; CURRENT FILING DATE: 2005-09-16  
; PRIOR APPLICATION NUMBER: US 09/619,643  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 17085  
; LENGTH: 449  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-008-Q1-K1-G3

US-11-227-183A-17085

## Alignment Scores:

Pred. No.: 3,59e-28 Length: 449  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservatives: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-17085 (1-449)

Qy 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 177 ATGGCGGCTCTGGCCACGTCGACGTCGTGCACAGCCCGCCGCTGGGGCTACCGGAC 236  
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 237 GCCTCCACGTTCCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 236  
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 297 GCGGACACGCTCAGCATCGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 356  
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 357 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGTC 392

## RESULT 9

US-11-227-183A-20738  
; Sequence 20738, Application US/11227183A  
; GENERAL INFORMATION:  
; APPLICANT: Fisher, Dane K.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated with  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 16517.336 - 38-21 (51230)C/US  
; CURRENT APPLICATION NUMBER: US/11/227,183A  
; PRIOR FILING DATE: 2005-09-16  
; PRIOR APPLICATION NUMBER: US 09/619,643  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 20738  
; LENGTH: 561  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB151-022-Q1-K1-D3.R2  
US-11-227-183A-20738

Alignment Scores:  
Pred. No.: 4,87e-28 Length: 561  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservatives: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-20738 (1-561)

Qy 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 173 ATGGCGGCTCTGGCCACGTCGACGTCGTGCACAGCCCGCCGCTGGGGCTACCGGAC 232  
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 233 GCCTCCACGTTCCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 232  
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 293 GCGGACACGCTCAGCATCGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 352  
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 353 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGTC 388

RESULT 10  
US-11-298-234A-9  
; Sequence 9, Application US/11298234A  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fenggao  
; APPLICANT: Hauge, Brian M.  
; APPLICANT: Oggero, Christopher M  
; TITLE OF INVENTION: Methods for Ligation Independent Cloning of DNA  
; FILE REFERENCE: 53344  
; CURRENT APPLICATION NUMBER: US/11/298,234A  
; PRIOR FILING DATE: 2005-12-09  
; PRIOR APPLICATION NUMBER: 60634779  
; PRIOR FILING DATE: 2004-12-09  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 9  
; LENGTH: 1409  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-11-298-234A-9

Alignment Scores:  
Pred. No.: 1,71e-27 Length: 1409  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservatives: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-298-234A-9 (1-1409)

Qy 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 175 ATGGCGGCTCTGGCCACGTCGACGTCGTGCACAGCCCGCCGCTGGGGCTACCGGAC 234  
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 235 GCCTCCACGTTCCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 294  
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 295 GCGGACACGCTCAGCATCGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 354  
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 355 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGTC 390

## RESULT 11

US-11-330-822-50  
; Sequence 50, Application US/11330822  
; GENERAL INFORMATION:  
; APPLICANT: GUAN, HANPING  
; APPLICANT: KEELING, PETER L.  
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN  
; TITLE OF INVENTION: HOSTS  
; FILE REFERENCE: 15053-04  
; CURRENT APPLICATION NUMBER: US/11/330,822  
; CURRENT FILING DATE: 2006-01-11  
; PRIOR APPLICATION NUMBER: PCT/US98/06660  
; PRIOR FILING DATE: 1998-04-03  
; PRIOR APPLICATION NUMBER: 60/042,939  
; PRIOR FILING DATE: 1997-04-04  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 50  
; LENGTH: 1915  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1815)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1819)..(1914)

## US-11-330-822-50

Alignment Scores:  
Pred. No.: 4,41e-27 Length: 1915  
Score: 324.00 Matches: 70  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 88.0% Indels: 2  
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-330-822-50 (1-1915)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAasp 20  
|||||  
DB 1 ATGGCGGCTCTGGCCAGCTCGCAGCTCGTCGCAACGGCGCGCTGGCGCTCCCGGAC 60  
|||||  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
|||||  
DB 61 GCGTCACGTTCCGCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCGG 120  
|||||  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
|||||  
DB 121 GCGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
|||||  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValVal 73  
|||||  
DB 181 CGCGCGCGGGGCAAG-----TTCCCGTCGCTCGTGTG 213  
|||||

## RESULT 12

US-11-227-183A-19022  
; Sequence 19022, Application US/11227183A

; GENERAL INFORMATION:  
; APPLICANT: Fisher, Dane K.  
; APPLICANT: Lalgudi, Raghunath V.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US  
; CURRENT APPLICATION NUMBER: US/11/227,183A  
; CURRENT FILING DATE: 2005-09-16  
; PRIOR APPLICATION NUMBER: US 09/619,643  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 19022

; LENGTH: 408  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-040-Q1-K1-A8

US-11-227-183A-19022

Alignment Scores:  
Pred. No.: 7e-28 Length: 408  
Score: 323.00 Matches: 69  
Percent Similarity: 94.6% Conservative: 1  
Best Local Similarity: 93.2% Mismatches: 2  
Query Match: 87.8% Indels: 2  
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-19022 (1-408)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAasp 20  
|||||  
DB 174 ATGGCGGCTCTGGCCAGCTCGCAGCTCGTCGCAACGGCGCGCTGGCGCTCCCGGAC 233  
|||||  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
|||||  
DB 234 GCGTCACGTTCCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCGG 293  
|||||  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
|||||  
DB 294 GCGGACACCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 353  
|||||  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
|||||

## Db

354 CGCGCGGGGGCAAG-----TTCCCGTCGCTCGTGTGTGC 389

## RESULT 13

US-11-227-183A-19076  
; Sequence 19076, Application US/11227183A

; GENERAL INFORMATION:  
; APPLICANT: Fisher, Dane K.  
; APPLICANT: Lalgudi, Raghunath V.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US  
; CURRENT APPLICATION NUMBER: US/11/227,183A  
; CURRENT FILING DATE: 2005-09-16  
; PRIOR APPLICATION NUMBER: US 09/619,643  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 19076

; LENGTH: 420  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-040-Q1-K1-G5

US-11-227-183A-19076

Alignment Scores:  
Pred. No.: 7,28e-28 Length: 420  
Score: 323.00 Matches: 69  
Percent Similarity: 94.6% Conservative: 1  
Best Local Similarity: 93.2% Mismatches: 2  
Query Match: 87.8% Indels: 2  
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-19076 (1-420)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAasp 20  
|||||  
DB 177 ATGGCGGCTCTGGCCAGCTCGCAGCTCGTCGCAACGGCGCGCTGGCGCTCCCGGAC 236  
|||||  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
|||||  
DB 237 GCGTCACGTTCCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCGG 296  
|||||  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
|||||  
DB 297 GCGGACACCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 356  
|||||  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
|||||

357 CGCGCGGGGGCAAG-----TTCCCGTCGCTCGTGTGTGC 392

## RESULT 14

US-11-227-183A-19289  
; Sequence 19289, Application US/11227183A

; GENERAL INFORMATION:  
; APPLICANT: Fisher, Dane K.  
; APPLICANT: Lalgudi, Raghunath V.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US  
; CURRENT APPLICATION NUMBER: US/11/227,183A  
; CURRENT FILING DATE: 2005-09-16  
; PRIOR APPLICATION NUMBER: US 09/619,643  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 19289

; LENGTH: 408  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: unsure at all n locations

OTHER INFORMATION: Clone ID: LIB3151-043-Q1-K1-E10

US-11-227-183A-19289

|                        |          |                 |
|------------------------|----------|-----------------|
| Alignment Scores:      | 7.65e-27 | 408             |
| Pred. No.:             | 314.00   | Length:         |
| Score:                 | 91.9%    | Matches: 68     |
| Percent Similarity:    | 91.9%    | Conservative: 0 |
| Best Local Similarity: | 91.9%    | Mismatches: 4   |
| Query Match:           | 85.3%    | Indels: 2       |
| DB:                    | 10       | Gaps: 1         |

US-10-628-525A-36 (1-74) x US-11-227-183A-19289 (1-408)

|    |     |                                                               |     |
|----|-----|---------------------------------------------------------------|-----|
| QY | 1   | MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp  | 20  |
| DB | 163 | ATGGCGGCGCTCGGCCACGTCGCGAGCTCGTCGCAACGCCCGCGCTGGCGTCCCGGAC    | 222 |
| QY | 21  | AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaAhrGAlaSerAlaAla    | 40  |
| DB | 223 | GGTTCACAGTTCCGCGCGCGCCCGCGCAGGCGCTCGAGGGGGGCGCGGGCGTTCGGCGCGC | 282 |
| QY | 41  | AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnGlnAla  | 60  |
| DB | 283 | CGGGACACGCTCAGCATCGGACACAGCGCGCGCGCGGCCCCANGCACCCAGCAGCAGCG   | 342 |
| QY | 61  | ArgArgGlyGlyArgPheProPheProSerLeuValValCys                    | 74  |
| DB | 343 | CGCCGCGGGGGGCGAG-----TTCCCGTCGCTCGTCGTGTGC                    | 378 |

**RESULT 15**

US-11-227-183A-20077  
; Sequence 20077, Application US/11227183A

```

; GENERAL INFORMATION: Dane K.
; APPLICANT: Fisher, Dane K.
; APPLICANT: Laigudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 16517,336 - 38-21(51230)C/US
; CURRENT APPLICATION NUMBER: US/11/227,183A
; CURRENT FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: US 09/619,643
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 20077
; LENGTH: 386
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3151-057-01-K1-F6

```

|                        |          |                 |
|------------------------|----------|-----------------|
| Alignment Scores:      |          |                 |
| Pred. No.:             | 1.72e-25 | 386             |
| Score:                 | 302.00   | 66              |
| Percent Similarity:    | 91.8%    | Conservative: 1 |
| Best Local Similarity: | 90.4%    | Mismatches: 4   |
| Query Match:           | 82.1%    | Indels: 2       |
| DB:                    | 10       | Gaps: 1         |

US-10-628-525A-36 (1-74) x US-11-227-183A-20077 (1-386)

|    |     |                                                              |     |
|----|-----|--------------------------------------------------------------|-----|
| QY | 1   | MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp | 20  |
| DB | 173 | ATGGGGCTCTGGCCACGTCGACGTCGTGTCGAAGCCCGCGSCCTGGGCGTCCGGAC     | 232 |
| QY | 21  | AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaIa  | 40  |
| DB | 233 | GGGTCCAGCTTCGCGCGGGCGCGCATGGCTGAGGGGGCGCGGCGTGGCGCG          | 292 |
| QY | 41  | AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnGlnAla | 60  |
| DB | 293 | GGGACACGCTCAGCATGCGAACGAGCGCGCGCGCGCCAGGACACAGCAGCAAGCG      | 352 |

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValVal 73  
Db 353 CGCCGCGGGGGCAAG-----GTCCCGTCGTCGTCGTG 385

**RESULT 16**

```

US-11-353-150-45136
; GENERAL 45136, Application US/11353150
; SEQUENCE INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Andersen, Timothy W.
; APPLICANT: Conner, Timothy V.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 16517,365 - 38-21(115459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 45136
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3066-030-Q1
US-11-353-150-45136

```

|                        |          |               |
|------------------------|----------|---------------|
| Alignment Scores:      |          |               |
| Pred. No.:             | 1.28e-24 | Length:       |
| Score:                 | 295.00   | Matches:      |
| Percent Similarity:    | 87.8%    | Conservative: |
| Best Local Similarity: | 86.5%    | Mismatches:   |
| Query Match:           | 80.2%    | Indels:       |
| DB:                    | 8        | Gaps:         |
|                        |          | 431           |

US-10-628-525A-36 (1-74) X US-11-353-150-45136 (1-431)

|    |     |                                                              |     |
|----|-----|--------------------------------------------------------------|-----|
| Qy | 1   | MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp | 20  |
| Db | 202 | ATGGGGGCTCTGGCCACGCTCGCAGCTGTCGCAACGCCCGCGGCTCTCGGAC         | 261 |
| Qy | 21  | AlaSerThrPheArgArgGlyAlaAlaGlnClyLeuArgGlyAlaArgAlaSerAlaAla | 40  |
| Db | 262 | GGGTCCACGTTCCGCGGGCGCGCCCATGGCTGAGGGGGGCCCGGGGCTCCGGGCG      | 321 |
| Qy | 41  | AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla    | 60  |
| Db | 322 | GGGGACAGCTCAGATCGGACACAGCGCGCGCGGCCCATTCACCATCAACACGCG       | 381 |
| Qy | 61  | ArgArgGlyGlyArgPheProPheProSerLeuValValCys                   | 74  |
| Db | 382 | CGCCGCGGGGGGCAAG-----TTCCTTCGCTCTTCGTGTGC                    | 417 |

RESULT 17

```

US-11-227-183A-16655
SEQUENCE 16655, APPLICATION US/11227183A
GENERAL INFORMATION:
/ APPLICANT: FISHER, DANE K.
/ APPLICANT: LALGUDI, RAGHUNATH V.
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES
/ TITLE OF INVENTION: PLANTS
/ FILE REFERENCE: 16517.336 - 38-21(51230)
/ CURRENT APPLICATION NUMBER: US/11/227,183
/ CURRENT FILING DATE: 2005-09-16
/ PRIOR APPLICATION NUMBER: US 09/619,643
/ PRIOR FILING DATE: 2000-07-19
/ NUMBER OF SEQ ID NOS: 32236
/ SEQ ID NO 16655
/ LENGTH: 400
/ TYPE: DNA

```



; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-003-Q1-K1-B3  
US-11-227-183A-16655

## Alignment Scores:

Pred. No.: 7.45e-24 Length: 400  
Score: 288.00 Matches: 63  
Percent Similarity: 86.5% Conservative: 1  
Best Local Similarity: 85.1% Mismatches: 8  
Query Match: 78.3% Indels: 2  
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-16655 (1-400)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProasp 20  
Db 169 ATGGCGGCTCTGGCCACGTTCGACGTAGTCGCAACCGCCGCGGCTGGCGCTCCGGAC 228  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 229 GGGTCCACGTTCCGCGAGCGCCACGCGACGCGCTGAGGGGGCCCGGCGTCCGGCGCG 288  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60  
Db 289 GTGGACACGCTTAACATGCGGACCGAGCGCGCTGCGCCAGGACCAGCAGCAGCGCG 348  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 349 CCGCGTGGTGCAGG-----TTCCGTCGCTCGACGTGTGC 384

## RESULT 18

US-11-227-183A-18495  
; Sequence 18495, Application US/11227183A  
; GENERAL INFORMATION:

; APPLICANT: Fisher, Dane K.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 16517-336 - 38-21(51230)C/US  
; CURRENT FILING DATE: 2005-09-16  
; PRIOR APPLICATION NUMBER: US 09/619,643  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 18495  
; LENGTH: 388

; TYPE: DNA  
; ORGANISM: Zea mays

; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-029-Q1-K1-E1

US-11-227-183A-18495

## Alignment Scores:

Pred. No.: 1.59e-23 Length: 388  
Score: 285.00 Matches: 60  
Percent Similarity: 89.6% Conservative: 0  
Best Local Similarity: 89.6% Mismatches: 7  
Query Match: 77.4% Indels: 0  
DB: 10 Gaps: 0

US-10-628-525A-36 (1-74) x US-11-227-183A-18495 (1-388)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProasp 20  
Db 174 ATGGCGGCTCTGGCCACGTTCGACGTAGTCGCAACCGCCGCGGCTGGCGCTCCGGAC 233  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 234 GGGTCCACGTTCCGCGTGGCGCGGACGCGCTGAGGGGGCCCGGCGTCCGCTGGG 293  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60

Db 294 GCGGACACGCTCAGCATGCCGACGAGCGCGCGCGGCGCTTAGGCACCATCATCATGCG 353  
QY 61 ArgArgGlyGlyArgPhePro 67  
Db 354 CGCCGAGGAGGAGGAGGTTCGCG 374

## RESULT 19

US-11-329-388-8047  
; Sequence 8047, Application US/11329388  
; GENERAL INFORMATION:

; APPLICANT: Andersen, Scott E.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 16517-357 - 38-21(15503)C/US  
; CURRENT APPLICATION NUMBER: US/11/329,388  
; CURRENT FILING DATE: 2006-01-11  
; PRIOR APPLICATION NUMBER: 09/553,094  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 18831  
; SEQ ID NO 8047  
; LENGTH: 625

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)-(625)

; OTHER INFORMATION: unsure at all n locations

; OTHER INFORMATION: Clone ID: LIB3061-084-Q1-K6-E9

US-11-329-388-8047

## Alignment Scores:

Pred. No.: 1.95e-22 Length: 625  
Score: 278.00 Matches: 63  
Percent Similarity: 92.6% Conservative: 0  
Best Local Similarity: 92.6% Mismatches: 3  
Query Match: 75.5% Indels: 3  
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-329-388-8047 (1-625)

QY 7 SerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArg 26  
Db 5 TCGCAGCTCGTCGC-ACGCGCGCGCGCTGGCGCTCCCGCGCGCTCCAGCTTCGCGCGC 63  
QY 27 GlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAlaAspThrLeuSerMet 46  
Db 64 GCGCGCGCGCAGGGCTGAGGGGGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCG 123  
QY 47 ArgThrSerAlaArgAlaAlaProArgHisGlnGlnGlnAlaAlaArgGlyGlyArgPhe 66  
Db 124 CGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

QY 67 ProPheProSerLeuValValCys 74

Db 181 ---TTCCCGTCGCTCGTGTGTGC 201

## RESULT 20

US-11-329-388-8026  
; Sequence 8026, Application US/11329388  
; GENERAL INFORMATION:

; APPLICANT: Andersen, Scott E.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 16517-357 - 38-21(15503)C/US  
; CURRENT APPLICATION NUMBER: US/11/329,388  
; CURRENT FILING DATE: 2006-01-11  
; PRIOR APPLICATION NUMBER: 09/553,094  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 18831  
; SEQ ID NO 8026  
; LENGTH: 649

```
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(649)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3061-084-Q1-K6-C9
US-11-329-388-8026

Alignment Scores:
Pred. No.: 2,05e-22 Length: 649
Score: 278.00 Matches: 59
Percent Similarity: 93.7% Conservative: 0
Best Local Similarity: 93.7% Mismatches: 2
Query Match: 75.5% Indels: 2
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-329-388-8026 (1-649)
QY 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31
DB 22 ACGGCGCGCGCGCTCG 81
QY 32 LeuArgGlyAlaArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSerAlaArg 51
DB 82 CTGAGCG 141
QY 52 AlaAlaProArgHisGlnGlnGlnAlaAlaArgArgGlyValArgPheProPheSerLeu 71
DB 142 GCGGCG 195
QY 72 ValValCys 74
DB 196 GTGGTGTGC 204

RESULT 21
US-11-329-388-1754
; Sequence 1754, Application US/11329388
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 16517.357 - 38-21(15503)C/US
; CURRENT APPLICATION NUMBER: US/11/329,388
; PRIOR FILING DATE: 2006-01-11
; PRIOR APPLICATION NUMBER: 09/553,094
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 18831
; SEQ ID NO 1754
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3061-023-Q1-K1-E8
US-11-329-388-1754

Alignment Scores:
Pred. No.: 2,01e-22 Length: 432
Score: 276.00 Matches: 58
Percent Similarity: 95.1% Conservative: 0
Best Local Similarity: 95.1% Mismatches: 1
Query Match: 75.0% Indels: 2
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-329-388-1754 (1-432)
QY 14 AlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArg 33
DB 16 GCGGCG 75
QY 34 GlyAlaArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAla 53
```

```
Db 76 GGGGCCCCGGGTCTCGCGCGCGCGGACACGCTCAGCATGCGGACCGCGCGCGCGG 135
QY 54 ProArgHisGlnGlnGlnAlaArgArgGlyGlyArgPheProPheProSerLeuValVal 73
DB 136 CCCAGGACCAGCAGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 189
QY 74 Cys 74
DB 190 TGC 192

RESULT 22
US-11-227-183A-17758
; Sequence 17758, Application US/11227183A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US
; CURRENT APPLICATION NUMBER: US/11/227,183A
; PRIOR FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: US 09/619,643
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 17758
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3151-018-Q1-K1-G9
US-11-227-183A-17758

Alignment Scores:
Pred. No.: 1,63e-21 Length: 422
Score: 268.00 Matches: 59
Percent Similarity: 81.1% Conservative: 1
Best Local Similarity: 79.7% Mismatches: 12
Query Match: 72.8% Indels: 2
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-17758 (1-422)
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 188 ATGGGGCTTTGGCCACGTTGTCATCTCTCGCAACGCCCGTGGCTGCGTTCGGAC 247
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40
DB 248 GCGTTCACTTCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 307
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
DB 308 GCGGACACGCTCAGCATGCGGACCATCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB 368 CGCCAGGCG 403

RESULT 23
US-11-227-183A-19448
; Sequence 19448, Application US/11227183A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US
; CURRENT APPLICATION NUMBER: US/11/227,183A
; PRIOR FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: US 09/619,643
; PRIOR FILING DATE: 2000-07-19
```

/ NUMBER OF SEQ ID NOS: 32236  
/ SEQ ID NO 19448  
/ LENGTH: 354  
/ TYPE: DNA  
/ ORGANISM: Zea mays  
/ FEATURE:  
/ OTHER INFORMATION: unsure at all n locations  
/ FEATURE:  
/ OTHER INFORMATION: Clone ID: LIB3151-045-Q1-K1-F11  
US-11-227-183A-19448

Alignment Scores:  
Pred. No.: 2,18e-21 Length: 354  
Score: 266.00 Matches: 57  
Percent Similarity: 95.0% Conservative: 0  
Best Local Similarity: 95.0% Mismatches: 3  
Query Match: 72.3% Indels: 0  
DB: 10 Gaps: 0

US-10-628-525A-36 (1-74) x US-11-227-183A-19448 (1-354)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAap 20  
DB 173 ATGGCGGCTCTGGCCACGCTCGAGCTCGTGCACAGCCCGCGGCTGGCGCTCCGGAC 232  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 233 GGTCCACGTTCCGCGCGCGCGCGCGCAAGCCTGAGGGGGCGCGGCTCGCGGGCG 292  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60  
DB 293 GCGGACACGCTCAGCATGGGACCGAGCGCGCGCGCGCGCCCGCCANGCACCAGCAGCGCG 352

## RESULT 24

US-11-329-388-3077  
/ Sequence 3077, Application US/11329388  
/ GENERAL INFORMATION:  
/ APPLICANT: Andersen, Scott E.  
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
/ FILE REFERENCE: 16517.357 - 38-21(15503)C/US  
/ CURRENT APPLICATION NUMBER: US/11/329,388  
/ CURRENT FILING DATE: 2006-01-11  
/ PRIOR APPLICATION NUMBER: 09/553,094  
/ PRIOR FILING DATE: 2000-04-18  
/ NUMBER OF SEQ ID NOS: 18831  
/ SEQ ID NO 3077  
/ LENGTH: 363  
/ TYPE: DNA  
/ ORGANISM: Zea mays  
/ FEATURE:  
/ OTHER INFORMATION: Clone ID: LIB3061-033-Q1-K1-C5  
US-11-329-388-3077

Alignment Scores:  
Pred. No.: 5,01e-21 Length: 363  
Score: 263.00 Matches: 55  
Percent Similarity: 96.6% Conservative: 2  
Best Local Similarity: 93.2% Mismatches: 2  
Query Match: 71.5% Indels: 0  
DB: 8 Gaps: 0

US-10-628-525A-36 (1-74) x US-11-329-388-3077 (1-363)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAap 20  
DB 185 ATGGCGGCTCTGGCCACGCTCGAGCTCGTGCACAGCCCGCGGCTGGCGCTACCGAC 244  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 245 GGTCCACGTTCCGCGCGCGCGCGCGCGAGGCCCTGAGGGGGCGCGGCTCGTGGCGCGCG 304

QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGln 59  
DB 305 GCGGACACGCTCAGCATGGGACCGAGCTCGCGCGCTGGCCCGGACCGACGAGCG 361

## RESULT 25

US-11-227-183A-18014  
/ Sequence 18014, Application US/11227183A  
/ GENERAL INFORMATION:  
/ APPLICANT: Fisher, Dane K.  
/ APPLICANT: Lalgudi, Raghunath V.  
/ TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
/ FILE REFERENCE: 16517.336 - 38-21(51230)C/US  
/ CURRENT APPLICATION NUMBER: US/11/227,183A  
/ CURRENT FILING DATE: 2005-09-16  
/ PRIOR APPLICATION NUMBER: US 09/619,643  
/ PRIOR FILING DATE: 2000-07-19  
/ NUMBER OF SEQ ID NOS: 32236  
/ SEQ ID NO 18014  
/ LENGTH: 365  
/ TYPE: DNA  
/ ORGANISM: Zea mays  
/ FEATURE:  
/ OTHER INFORMATION: Clone ID: LIB3151-022-Q1-K1-D3  
US-11-227-183A-18014

Alignment Scores:  
Pred. No.: 5,05e-21 Length: 365  
Score: 263.00 Matches: 58  
Percent Similarity: 92.4% Conservative: 3  
Best Local Similarity: 78.4% Mismatches: 11  
Query Match: 71.5% Indels: 2  
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-18014 (1-365)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAap 20  
DB 126 ATGTGGGCTCTGTGCACATGTCAGATCTGTCAACGCCCGCGGCTGTGGTGGGAC 185  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 186 GCGTGATATTTCCGCGCGCGCGCGCGCGCGCTGTGGGGCGCGCGGCTGTGGCGCG 245  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
DB 246 GCGGACACACTCAGCATGGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 305  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 306 CGCCGCGGGGCGAGG-----TTCCCGTGGTGGTGGTGGTGGTGGTGGTGGTGG 341

## RESULT 26

US-11-227-183A-18823  
/ Sequence 18823, Application US/11227183A  
/ GENERAL INFORMATION:  
/ APPLICANT: Fisher, Dane K.  
/ APPLICANT: Lalgudi, Raghunath V.  
/ TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
/ FILE REFERENCE: 16517.336 - 38-21(51230)C/US  
/ CURRENT APPLICATION NUMBER: US/11/227,183A  
/ CURRENT FILING DATE: 2005-09-16  
/ PRIOR APPLICATION NUMBER: US 09/619,643  
/ PRIOR FILING DATE: 2000-07-19  
/ NUMBER OF SEQ ID NOS: 32236  
/ SEQ ID NO 18823  
/ LENGTH: 371  
/ TYPE: DNA  
/ ORGANISM: Zea mays  
/ FEATURE:  
/ OTHER INFORMATION: Clone ID: LIB3151-037-Q1-K1-D3  
US-11-227-183A-18823

```
Alignment Scores:
Pred. No.: 3,63e-16 Length: 371
Score: 221.00 Matches: 49
Percent Similarity: 80.0% Conservative: 3
Best Local Similarity: 75.4% Mismatches: 13
Query Match: 60.1% Indels: 0
DB: 10 Gaps: 0

US-10-628-525A-36 (1-74) x US-11-227-183A-18823 (1-371)
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 176 ATGGGGCTCTGGCCAGCTGCGAGCTGTCGCAACGCCCGCCGCGCTGGCGGCTCCCGGAC 235
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40
DB 236 GCGTCCACGTTCCG 295
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60
DB 296 GCGGCCACCCCTAAGATGCGGACACAGGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 355
QY 61 ArgArgGlyGlyArg 65
DB 356 CCCCGGGGGGCCAGG 370

RESULT 27
US-11-227-183A-32098
; Sequence 32098, Application US/11227183A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US
; CURRENT APPLICATION NUMBER: US/11/227,183A
; CURRENT FILING DATE: 2005-09-16
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 32098
; LENGTH: 338
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3182-014-P2-M1-P5
US-11-227-183A-32098
Alignment Scores:
Pred. No.: 2,05e-15 Length: 338
Score: 214.00 Matches: 46
Percent Similarity: 87.0% Conservative: 1
Best Local Similarity: 85.2% Mismatches: 7
Query Match: 58.2% Indels: 0
DB: 10 Gaps: 0

US-10-628-525A-36 (1-74) x US-11-227-183A-32098 (1-338)
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 175 ATGGCGGCTCTGGCCAGCTGCGAGCTGTCGCAACGCCCGCCGCGCTGGCGGCTCCCGGAC 234
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40
DB 235 GCGTCCACGTTCCG 294
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaPro 54
DB 295 GTGGACACGCTTAGCATGTGACCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 336

RESULT 28
US-11-227-183A-18999
```

```
; Sequence 18999, Application US/11227183A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalugudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US
; CURRENT APPLICATION NUMBER: US/11/227,183A
; CURRENT FILING DATE: 2005-09-16
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 18999
; LENGTH: 203
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3151-039-Q1-K1-G5
US-11-227-183A-18999
```

```
Alignment Scores:
Pred. No.: 5,04e-15 Length: 203
Score: 208.00 Matches: 45
Percent Similarity: 92.2% Conservative: 2
Best Local Similarity: 88.2% Mismatches: 4
Query Match: 56.5% Indels: 0
DB: 10 Gaps: 0
```

US-10-628-525A-36 (1-74) x US-11-227-183A-18999 (1-203)

```
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 50 ATGGCGGCTCTGGCCAGCTGCGAGCTGTCGCAACGCCCGCCGCGCTGGCGGCTCCCGGAC 109
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40
DB 110 GCGTCCACGTTCCG 169
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArg 51
DB 170 GCGGACCTCTCAGCATGCGGACCAACCGCGCGC 202
```

## RESULT 29

```
US-11-227-183A-20737
; Sequence 20737, Application US/11227183A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalugudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US
; CURRENT APPLICATION NUMBER: US/11/227,183A
; CURRENT FILING DATE: 2005-09-16
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 20737
; LENGTH: 519
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3151-022-Q1-K1-D3.R1
US-11-227-183A-20737
```

## Alignment Scores:

```
Pred. No.: 1,81e-14 Length: 519
Score: 208.00 Matches: 60
Percent Similarity: 82.7% Conservative: 2
Best Local Similarity: 80.0% Mismatches: 8
Query Match: 56.5% Indels: 7
DB: 10 Gaps: 3
```

US-10-628-525A-36 (1-74) x US-11-227-183A-20737 (1-519)

```
QY      1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db      168 ATGGCGGCTCTGGCCACGTCGACGCTCGTCGACAGCCC-GCCGGCCTGGGCGTCCCGGAC 226

QY      21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db      227 CGGTCCACGTTCCGCGCGCGCGGCA---GGGCTGAGGGGGCGGCGGCTCGGCGGG 283

QY      41 AlaAspThrLeuSerMetArgThrSerAlaAlaArg-AlaAlaProArgHisGlnGlnAl 60
Db      284 GCGGACACCTC-AGCATGCGGACCGCGCGCTCCGCC---AGGCACACGACGAGGC 339

QY      60 aArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db      340 GCGCGCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 376
```

## RESULT 30

```
US-11-227-183A-18231
; Sequence 18231, Application US/11227183A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Jagudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US
; CURRENT APPLICATION NUMBER: US/11/227,183A
; CURRENT FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: US 09/619,643
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 18231
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3151-025-Q1-K1-C12
US-11-227-183A-18231
```

## Alignment Scores:

|                        |          |               |     |
|------------------------|----------|---------------|-----|
| Pred. No.:             | 2,248-09 | Length:       | 360 |
| Score:                 | 162.00   | Matches:      | 41  |
| Percent Similarity:    | 69.4%    | Conservative: | 2   |
| Best Local Similarity: | 66.1%    | Mismatches:   | 18  |
| Query Match:           | 44.0%    | Indels:       | 1   |
| DB:                    | 10       | Gaps:         | 0   |

US-10-628-525A-36 (1-74) x US-11-227-183A-18231 (1-360)

```
QY      1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db      170 ATGGCGGCTCTGGCCACGTCACATCTCGACCGCATCGCCCATCGGCTGGGCGTCCAGAC 229

QY      21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db      230 GGGTTACATTTCCGACGAGCGCGCTGCAAGGACTGAGGTGGGCCCTATCATATGAGGTA 289

QY      41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAl 60
Db      290 CGCTGACACGCTCATTAATCGGACCGAGCATGCGCGCAGCACATACACCAACATCAGGC 349

QY      60 aArg 61
Db      350 ACGC 353
```

Search completed: April 2, 2006, 03:51:38  
Job time : 143.391 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame plus p2n model

Run on: April 1, 2006, 04:29:01 ; Search time 776.782 Seconds  
(without alignments)  
2853.949 Million cell updates/sec

Title: US-10-628-525a-37

Perfect score: 191

Sequence: 1 MATPSAVGACLLARXAMPAAVGDRAFRRLQRLVLR 39

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-Q=/abs/ABSSWEB spool/US10628525/runat\_31032006\_095113\_16622/app\_query.fasta\_1  
-DB=GenEmbl -OPMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150  
-DOCALLIGN=200 -THR\_SCORE=pcet -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=pcio -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs06h  
-USER=US10628525 @CGN\_1.1\_4375 @runat\_31032006\_095113\_16622 -NCPU=6 -ICPU=3  
-NO WMAP -NEG SCORES=0 -WAIT -DISPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*  
1: gb.ba.\*  
2: gb.in.\*  
3: gb.env.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pr.\*  
9: gb.ro.\*  
10: gb.sts.\*  
11: gb.sy.\*  
12: gb.un.\*  
13: gb.vi.\*  
14: gb.htg.\*  
15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 191   | 100.0       | 153    | 6  | AR106497    |
| 2          | 191   | 100.0       | 153    | 6  | BD071190    |
| 3          | 191   | 100.0       | 1415   | 6  | BD249565    |

|    |       |       |        |    |              |
|----|-------|-------|--------|----|--------------|
| 4  | 191   | 100.0 | 1415   | 6  | AR340013     |
| 5  | 191   | 100.0 | 2008   | 6  | BD249566     |
| 6  | 191   | 100.0 | 2008   | 6  | AR340014     |
| 7  | 191   | 100.0 | 2357   | 15 | AF036891     |
| 8  | 191   | 100.0 | 2383   | 6  | A93359       |
| 9  | 191   | 100.0 | 2383   | 6  | AR174874     |
| 10 | 191   | 100.0 | 2383   | 6  | AR411327     |
| 11 | 191   | 100.0 | 2491   | 6  | BD249559     |
| 12 | 191   | 100.0 | 2491   | 6  | AR340007     |
| 13 | 190   | 99.5  | 2992   | 6  | A63308       |
| 14 | 168   | 88.0  | 2990   | 6  | AR049919     |
| 15 | 139.5 | 73.0  | 2592   | 15 | AF168786     |
| 16 | 74.5  | 39.0  | 110000 | 14 | AP006500_07  |
| 17 | 74    | 38.7  | 53583  | 14 | AC013160     |
| 18 | 71.5  | 37.4  | 110000 | 15 | AP008212_269 |
| 19 | 71.5  | 37.4  | 165270 | 15 | AP004744     |
| 20 | 71    | 37.2  | 2182   | 2  | AY310711     |
| 21 | 71    | 37.2  | 19791  | 1  | SPFXBAD      |
| 22 | 71    | 37.2  | 110000 | 1  | BA000012_29  |
| 23 | 70.5  | 36.9  | 3741   | 1  | AB091437     |
| 24 | 70.5  | 36.9  | 25768  | 1  | AY327575     |
| 25 | 70    | 36.6  | 2115   | 2  | AY310707     |
| 26 | 70    | 36.6  | 2146   | 2  | AY310691     |
| 27 | 70    | 36.6  | 2171   | 2  | AY310683     |
| 28 | 70    | 36.6  | 2171   | 2  | AY310693     |
| 29 | 70    | 36.6  | 2175   | 2  | AY310678     |
| 30 | 70    | 36.6  | 2175   | 2  | AY310679     |
| 31 | 70    | 36.6  | 2175   | 2  | AY310682     |
| 32 | 70    | 36.6  | 2176   | 2  | AY310684     |
| 33 | 70    | 36.6  | 2176   | 2  | AY310686     |
| 34 | 70    | 36.6  | 2176   | 2  | AY310712     |
| 35 | 70    | 36.6  | 140953 | 14 | AC159112     |
| 36 | 69    | 36.1  | 2144   | 2  | AY310696     |
| 37 | 69    | 36.1  | 2175   | 2  | AY310677     |
| 38 | 69    | 36.1  | 2177   | 2  | AY310697     |
| 39 | 69    | 36.1  | 2178   | 2  | AY310673     |
| 40 | 69    | 36.1  | 2178   | 2  | AY310675     |
| 41 | 69    | 36.1  | 2178   | 2  | AY310687     |
| 42 | 69    | 36.1  | 2178   | 2  | AY310689     |
| 43 | 69    | 36.1  | 2178   | 2  | AY310714     |
| 44 | 69    | 36.1  | 2179   | 2  | AY310685     |
| 45 | 68.5  | 35.9  | 168278 | 9  | AC126246     |
| 46 | 68.5  | 35.9  | 187977 | 9  | AL672229     |
| 47 | 68.5  | 35.9  | 211386 | 9  | AC153418     |
| 48 | 68    | 35.6  | 2184   | 2  | AY310709     |
| 49 | 68    | 35.6  | 2185   | 2  | AY310713     |
| 50 | 68    | 35.6  | 2206   | 2  | AY310702     |
| 51 | 68    | 35.6  | 18270  | 1  | AF148496     |
| 52 | 68    | 35.6  | 62630  | 14 | AC101139     |
| 53 | 68    | 35.6  | 110000 | 1  | AB017282_02  |
| 54 | 68    | 35.6  | 110000 | 1  | AB017282_03  |
| 55 | 68    | 35.6  | 110000 | 15 | AP008210_099 |
| 56 | 68    | 35.6  | 120840 | 15 | OSJN00113    |
| 57 | 68    | 35.6  | 195700 | 14 | AC162574     |
| 58 | 68    | 35.6  | 210614 | 1  | AB088224     |
| 59 | 67.5  | 35.3  | 835    | 15 | AK105139     |
| 60 | 67.5  | 35.3  | 2000   | 6  | AX655130     |
| 61 | 67.5  | 35.3  | 9754   | 1  | AE012077     |
| 62 | 67.5  | 35.3  | 10873  | 1  | AE012494     |
| 63 | 67.5  | 35.3  | 67480  | 7  | AY129334     |
| 64 | 67.5  | 35.3  | 110000 | 1  | CR555306_20  |
| 65 | 67.5  | 35.3  | 110000 | 1  | AP006840_11  |
| 66 | 67.5  | 35.3  | 110000 | 1  | AP006840_20  |
| 67 | 67.5  | 35.3  | 110000 | 1  | CP000050_44  |
| 68 | 67.5  | 35.3  | 110000 | 1  | CP000050_45  |
| 69 | 67.5  | 35.3  | 110000 | 15 | AP008209_000 |
| 70 | 67.5  | 35.3  | 125217 | 15 | AC097627     |
| 71 | 67.5  | 35.3  | 134431 | 13 | AY386265     |
| 72 | 67.5  | 35.3  | 156933 | 15 | AC125411     |
| 73 | 67.5  | 35.3  | 274762 | 1  | EX664015     |
| 74 | 67    | 35.1  | 692    | 10 | EV640012     |
| 75 | 67    | 35.1  | 127392 | 8  | AC008570     |
| 76 | 67    | 35.1  | 154462 | 14 | AC145149     |

AR340013 Sequence  
BD249566 Modificat  
AR340014 Sequence  
AF036891 Zea mays  
A93359 Sequence 1  
AR174874 Sequence  
AR411327 Sequence  
BD249559 Modificat  
AR340007 Sequence  
AG3308 Sequence 1  
AR049919 Sequence  
AF168786 Sorghum b  
Continuation 18 of  
AC013160 Drosophila  
Continuation (270  
AP004744 Oryza sat  
AY310711 Saccomyce  
Y10438 Streptomyce  
Continuation (30 o  
AB091437 Burkholde  
AY327575 Delftia a  
AY310707 Episcaphu  
AY310691 Mycotretu  
AY310683 Lybas sp.  
AY310678 Mycotretu  
AY310679 Mycotretu  
AY310682 Mycotretu  
AY310684 Pselaphac  
AY310686 Pselaphac  
AY310712 Pselaphac  
AC159112 Pan trogl  
AY310696 Megalodac  
AY310677 Iphiclus  
AY310697 Megalodac  
AY310673 Iphiclus  
AY310675 Iphiclus  
AY310687 Iphiclus  
AY310689 Prepophar  
AY310714 Prepophar  
AY310685 Iphiclus  
AC126246 Mus muscu  
AL672229 Mouse DNA  
AC153418 Mus muscu  
AY310709 Aegithus  
AY310713 Nitridulin  
AY310702 Encaustes  
AF148496 Pseudomon  
AC101139 Mus muscu  
Continuation (3 of  
Continuation (4 of  
Continuation (100  
AL606991 Oryza sat  
AC162574 Bos tauru  
AB088224 Streptomy  
AK105139 Oryza sat  
AX655130 Sequence  
AE012077 Xanthomon  
AE012494 Xanthomon  
AY129334 Mycobacte  
Continuation (21 o  
Continuation (12 o  
Continuation (21 o  
Continuation (45 o  
Continuation (46 o  
AP008209 Oryza sat  
AC097627 Genomic s  
AY386265 Bovine pa  
AC125411 Genomic s  
EX664015 Serratia  
EV640012 S215P6132  
AC008570 Homo sapi  
AC145149 Homo sapi

|                                                                                                                                                                              |                                                               |                                                                                |               |        |              |                     |                                      |                 |      |        |   |          |                    |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------|--------------------------------------------------------------------------------|---------------|--------|--------------|---------------------|--------------------------------------|-----------------|------|--------|---|----------|--------------------|
| C 77                                                                                                                                                                         | 67                                                            | 35.1                                                                           | 162269        | 8      | AC0000097    | AC0000097 Homo sapi | C 150                                | 65              | 34.0 | 123057 | 8 | AL390236 | AL390236 Human DNA |
| C 78                                                                                                                                                                         | 67                                                            | 35.1                                                                           | 168239        | 8      | AC007663     | AC007663 Homo sapi  | ALIGNMENTS                           |                 |      |        |   |          |                    |
| C 79                                                                                                                                                                         | 67                                                            | 35.1                                                                           | 174840        | 8      | AC006549     | AC006549 Homo sapi  |                                      |                 |      |        |   |          |                    |
| C 80                                                                                                                                                                         | 67                                                            | 35.1                                                                           | 178195        | 14     | AC145134     | AC145134 Homo sapi  |                                      |                 |      |        |   |          |                    |
| C 81                                                                                                                                                                         | 67                                                            | 35.1                                                                           | 179269        | 8      | AC006547     | AC006547 Homo sapi  |                                      |                 |      |        |   |          |                    |
| C 82                                                                                                                                                                         | 67                                                            | 35.1                                                                           | 184929        | 8      | AC058790     | AC058790 Homo sapi  |                                      |                 |      |        |   |          |                    |
| C 83                                                                                                                                                                         | 67                                                            | 35.1                                                                           | 186842        | 14     | AC146283     | AC146283 Callithri  |                                      |                 |      |        |   |          |                    |
| C 84                                                                                                                                                                         | 67                                                            | 35.1                                                                           | 213050        | 1      | AL646067     | AL646067 Ralstonia  |                                      |                 |      |        |   |          |                    |
| C 85                                                                                                                                                                         | 66.5                                                          | 34.8                                                                           | 1254          | 15     | AK098879     | AK098879 Oryza sat  |                                      |                 |      |        |   |          |                    |
| C 86                                                                                                                                                                         | 66.5                                                          | 34.8                                                                           | 1254          | 15     | AK104639     | AK104639 Oryza sat  |                                      |                 |      |        |   |          |                    |
| C 87                                                                                                                                                                         | 66.5                                                          | 34.8                                                                           | 1284          | 15     | AK060054     | AK060054 Oryza sat  |                                      |                 |      |        |   |          |                    |
| C 88                                                                                                                                                                         | 66.5                                                          | 34.8                                                                           | 6297          | 6      | CS073980     | CS073980 Sequence   |                                      |                 |      |        |   |          |                    |
| C 89                                                                                                                                                                         | 66.5                                                          | 34.8                                                                           | 6297          | 6      | AX598629     | AX598629 Sequence   |                                      |                 |      |        |   |          |                    |
| C 90                                                                                                                                                                         | 66.5                                                          | 34.8                                                                           | 10603         | 1      | AE001997     | AE001997 Deinococc  |                                      |                 |      |        |   |          |                    |
| C 91                                                                                                                                                                         | 66.5                                                          | 34.8                                                                           | 50543         | 6      | CS073968     | CS073968 Sequence   |                                      |                 |      |        |   |          |                    |
| C 92                                                                                                                                                                         | 66.5                                                          | 34.8                                                                           | 50543         | 6      | AX598617     | AX598617 Sequence   |                                      |                 |      |        |   |          |                    |
| C 93                                                                                                                                                                         | 66.5                                                          | 34.8                                                                           | 110000        | 1      | CP000091_11  | CP000091_11         |                                      |                 |      |        |   |          |                    |
| C 94                                                                                                                                                                         | 66                                                            | 34.6                                                                           | 2492          | 8      | AY004252     | Continuation (12 o  |                                      |                 |      |        |   |          |                    |
| C 95                                                                                                                                                                         | 66                                                            | 34.6                                                                           | 4619          | 15     | AY766114     | AY766114 Homo sapi  |                                      |                 |      |        |   |          |                    |
| C 96                                                                                                                                                                         | 66                                                            | 34.6                                                                           | 110000        | 1      | AP006618_20  | Continuation (21 o  |                                      |                 |      |        |   |          |                    |
| C 97                                                                                                                                                                         | 66                                                            | 34.6                                                                           | 129920        | 14     | AC152993     | AC152993 Bos tauru  |                                      |                 |      |        |   |          |                    |
| C 98                                                                                                                                                                         | 66                                                            | 34.6                                                                           | 158264        | 14     | AC015497     | AC015497 Homo sapi  |                                      |                 |      |        |   |          |                    |
| C 99                                                                                                                                                                         | 66                                                            | 34.6                                                                           | 173463        | 8      | AL359092     | AL359092 Human DNA  |                                      |                 |      |        |   |          |                    |
| C 100                                                                                                                                                                        | 66                                                            | 34.6                                                                           | 181812        | 14     | AC153062     | AC153062 Bos tauru  |                                      |                 |      |        |   |          |                    |
| C 101                                                                                                                                                                        | 66                                                            | 34.6                                                                           | 235338        | 14     | AL357893     | AL357893 Homo sapi  |                                      |                 |      |        |   |          |                    |
| C 102                                                                                                                                                                        | 65.5                                                          | 34.3                                                                           | 365           | 6      | AR637836     | AR637836 Sequence   |                                      |                 |      |        |   |          |                    |
| C 103                                                                                                                                                                        | 65.5                                                          | 34.3                                                                           | 14152         | 1      | AE005085     | AE005085 Halobacte  |                                      |                 |      |        |   |          |                    |
| C 104                                                                                                                                                                        | 65.5                                                          | 34.3                                                                           | 22029         | 8      | HS419C1      | Z99754 Human DNA s  |                                      |                 |      |        |   |          |                    |
| C 105                                                                                                                                                                        | 65.5                                                          | 34.3                                                                           | 30098         | 14     | AC079026     | AC079026 Leishmani  |                                      |                 |      |        |   |          |                    |
| C 106                                                                                                                                                                        | 65.5                                                          | 34.3                                                                           | 53477         | 14     | AC130790     | AC130790 Pan trogl  |                                      |                 |      |        |   |          |                    |
| C 107                                                                                                                                                                        | 65.5                                                          | 34.3                                                                           | 110000        | 1      | BX571965_36  | Continuation (37 o  |                                      |                 |      |        |   |          |                    |
| C 108                                                                                                                                                                        | 65.5                                                          | 34.3                                                                           | 110000        | 14     | CT005260_3   | Continuation (4 of  |                                      |                 |      |        |   |          |                    |
| C 109                                                                                                                                                                        | 65.5                                                          | 34.3                                                                           | 110000        | 15     | AP008213_157 | Continuation (158   |                                      |                 |      |        |   |          |                    |
| C 110                                                                                                                                                                        | 65.5                                                          | 34.3                                                                           | 110000        | 15     | AP008213_158 | Continuation (159   |                                      |                 |      |        |   |          |                    |
| C 111                                                                                                                                                                        | 65.5                                                          | 34.3                                                                           | 133069        | 14     | AC026836     | AC026836 Homo sapi  |                                      |                 |      |        |   |          |                    |
| C 112                                                                                                                                                                        | 65.5                                                          | 34.3                                                                           | 179669        | 15     | AP005641     | AP005641 Oryza sat  |                                      |                 |      |        |   |          |                    |
| C 113                                                                                                                                                                        | 65.5                                                          | 34.3                                                                           | 187272        | 14     | AC069076     | AC069076 Homo sapi  |                                      |                 |      |        |   |          |                    |
| C 114                                                                                                                                                                        | 65.5                                                          | 34.3                                                                           | 227604        | 14     | AC163484     | AC163484 Mus muscu  |                                      |                 |      |        |   |          |                    |
| C 115                                                                                                                                                                        | 65.5                                                          | 34.3                                                                           | 260418        | 8      | AE006463     | AE006463 Homo sapi  |                                      |                 |      |        |   |          |                    |
| C 116                                                                                                                                                                        | 65.5                                                          | 34.3                                                                           | 308050        | 1      | SC0939124    | AL939124 Streptomy  |                                      |                 |      |        |   |          |                    |
| C 117                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 702           | 6      | AX061806     | AX061806 Sequence   |                                      |                 |      |        |   |          |                    |
| C 118                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1035          | 6      | AR016699     | AR016699 Sequence   |                                      |                 |      |        |   |          |                    |
| C 119                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1035          | 6      | AR029433     | AR029433 Sequence   |                                      |                 |      |        |   |          |                    |
| C 120                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1035          | 6      | AR083574     | AR083574 Sequence   |                                      |                 |      |        |   |          |                    |
| C 121                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1035          | 6      | AR153834     | AR153834 Sequence   |                                      |                 |      |        |   |          |                    |
| C 122                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1035          | 6      | BD056820     | BD056820 Enhance    |                                      |                 |      |        |   |          |                    |
| C 123                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1035          | 6      | BD057604     | BD057604 Insect co  |                                      |                 |      |        |   |          |                    |
| C 124                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1035          | 6      | BD075124     | BD075124 Hyperse    |                                      |                 |      |        |   |          |                    |
| C 125                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1035          | 6      | BD106651     | BD106651 Hyperse    |                                      |                 |      |        |   |          |                    |
| C 126                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1035          | 6      | BD243133     | BD243133 Hyperse    |                                      |                 |      |        |   |          |                    |
| C 127                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1035          | 6      | BD243671     | BD243671 Hyperse    |                                      |                 |      |        |   |          |                    |
| C 128                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1035          | 6      | AR345090     | AR345090 Sequence   |                                      |                 |      |        |   |          |                    |
| C 129                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1035          | 6      | AR403557     | AR403557 Sequence   |                                      |                 |      |        |   |          |                    |
| C 130                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1035          | 6      | AR640602     | AR640602 Sequence   |                                      |                 |      |        |   |          |                    |
| C 131                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1035          | 6      | AX287008     | AX287008 Sequence   |                                      |                 |      |        |   |          |                    |
| C 132                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1035          | 6      | AX343158     | AX343158 Sequence   |                                      |                 |      |        |   |          |                    |
| C 133                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1035          | 6      | AX370161     | AX370161 Sequence   |                                      |                 |      |        |   |          |                    |
| C 134                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1035          | 6      | AX536278     | AX536278 Sequence   |                                      |                 |      |        |   |          |                    |
| C 135                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 1573          | 15     | AK106157     | AK106157 Oryza sat  |                                      |                 |      |        |   |          |                    |
| C 136                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 2054          | 2      | AY310701     | AY310701 Iphi       |                                      |                 |      |        |   |          |                    |
| C 137                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 2182          | 2      | AY310681     | AY310681 Iphi       |                                      |                 |      |        |   |          |                    |
| C 138                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 2183          | 2      | AY310717     | AY310717 Iphi       |                                      |                 |      |        |   |          |                    |
| C 139                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 2184          | 2      | AY310688     | AY310688 Iphi       |                                      |                 |      |        |   |          |                    |
| C 140                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 2218          | 2      | AY310657     | AY310657 Toramus p  |                                      |                 |      |        |   |          |                    |
| C 141                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 11629         | 1      | AE012222     | AE012222 Xanthom    |                                      |                 |      |        |   |          |                    |
| C 142                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 23407         | 1      | RG0245811    | RG0245811           |                                      |                 |      |        |   |          |                    |
| C 143                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 110000        | 1      | BA000040_79  | BA000040_79         |                                      |                 |      |        |   |          |                    |
| C 144                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 110000        | 1      | CP000050_35  | Continuation (80 o  |                                      |                 |      |        |   |          |                    |
| C 145                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 110000        | 1      | CP000050_36  | Continuation (36 o  |                                      |                 |      |        |   |          |                    |
| C 146                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 110000        | 1      | CP000089_06  | Continuation (37 o  |                                      |                 |      |        |   |          |                    |
| C 147                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 110000        | 2      | CP000081_01  | Continuation (2 of  |                                      |                 |      |        |   |          |                    |
| C 148                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 110000        | 14     | BX252576_12  | Continuation (13 o  |                                      |                 |      |        |   |          |                    |
| C 149                                                                                                                                                                        | 65                                                            | 34.0                                                                           | 110000        | 15     | AP008207_020 | Continuation (21 o  |                                      |                 |      |        |   |          |                    |
| LOCUS                                                                                                                                                                        |                                                               |                                                                                |               |        |              |                     | 153 bp DNA linear PAT 14-FEB-2001    |                 |      |        |   |          |                    |
| DEFINITION                                                                                                                                                                   |                                                               |                                                                                |               |        |              |                     | Sequence 18 from patent US 6107060.  |                 |      |        |   |          |                    |
| ACCESSION                                                                                                                                                                    |                                                               |                                                                                |               |        |              |                     | AR106497                             |                 |      |        |   |          |                    |
| VERSION                                                                                                                                                                      |                                                               |                                                                                |               |        |              |                     | AR106497.1 GI:12821027               |                 |      |        |   |          |                    |
| KEYWORDS                                                                                                                                                                     |                                                               |                                                                                |               |        |              |                     | Unknown.                             |                 |      |        |   |          |                    |
| SOURCE                                                                                                                                                                       |                                                               |                                                                                |               |        |              |                     | Unknown.                             |                 |      |        |   |          |                    |
| ORGANISM                                                                                                                                                                     |                                                               |                                                                                |               |        |              |                     | Unclassified.                        |                 |      |        |   |          |                    |
| REFERENCE                                                                                                                                                                    |                                                               |                                                                                |               |        |              |                     | 1 (bases 1 to 153)                   |                 |      |        |   |          |                    |
| AUTHORS                                                                                                                                                                      |                                                               |                                                                                |               |        |              |                     | Keeling, P. and Guan, H.             |                 |      |        |   |          |                    |
| TITLE                                                                                                                                                                        |                                                               |                                                                                |               |        |              |                     | Starch encapsulation                 |                 |      |        |   |          |                    |
| JOURNAL                                                                                                                                                                      |                                                               |                                                                                |               |        |              |                     | Patent: US 6107060-A 18 22-AUG-2000; |                 |      |        |   |          |                    |
| FEATURES                                                                                                                                                                     |                                                               |                                                                                |               |        |              |                     | Location/Qualifiers                  |                 |      |        |   |          |                    |
| source                                                                                                                                                                       |                                                               |                                                                                |               |        |              |                     | 1..153                               |                 |      |        |   |          |                    |
| /organism="unknown"                                                                                                                                                          |                                                               |                                                                                |               |        |              |                     | /mol_type="unassigned DNA"           |                 |      |        |   |          |                    |
| ORIGIN                                                                                                                                                                       |                                                               |                                                                                |               |        |              |                     | Alignment Scores:                    |                 |      |        |   |          |                    |
| Pred. No.:                                                                                                                                                                   |                                                               |                                                                                |               |        |              |                     | 2,218-11 Length: 153                 |                 |      |        |   |          |                    |
| Score:                                                                                                                                                                       |                                                               |                                                                                |               |        |              |                     | 191.00 Matches: 38                   |                 |      |        |   |          |                    |
| Percent Similarity:                                                                                                                                                          |                                                               |                                                                                |               | 97.4%  |              |                     |                                      | Conservative: 0 |      |        |   |          |                    |
| Best Local Similarity:                                                                                                                                                       |                                                               |                                                                                |               | 97.4%  |              |                     |                                      | Mismatches: 1   |      |        |   |          |                    |
| Query Match:                                                                                                                                                                 |                                                               |                                                                                |               | 100.0% |              |                     |                                      | Indels: 0       |      |        |   |          |                    |
| DB:                                                                                                                                                                          |                                                               |                                                                                |               | 6      |              |                     |                                      | Gaps: 0         |      |        |   |          |                    |
| US-10-628-525A-37 (1-39) x AR106497 (1-153)                                                                                                                                  |                                                               |                                                                                |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| QY                                                                                                                                                                           | 1                                                             | MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpPro                      | 20            |        |              |                     |                                      |                 |      |        |   |          |                    |
| Db                                                                                                                                                                           | 1                                                             | ATGCGCAGCGCCCTCGCGCGTGGCGCGTCTCTCTCTCGCGCGCGCGCTGCGCG                          | 60            |        |              |                     |                                      |                 |      |        |   |          |                    |
| QY                                                                                                                                                                           | 21                                                            | AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg                      | 39            |        |              |                     |                                      |                 |      |        |   |          |                    |
| Db                                                                                                                                                                           | 61                                                            | GCCGCCGTGCGCAGCCGCGCGCGCGCGCGCGCTCAGCGCTGTGCGCGCGCGG                           | 117           |        |              |                     |                                      |                 |      |        |   |          |                    |
| RESULT 2                                                                                                                                                                     |                                                               |                                                                                |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| LOCUS                                                                                                                                                                        | BD071190                                                      | 153 bp DNA linear PAT 27-AUG-2002                                              |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| DEFINITION                                                                                                                                                                   | Plant like starches and the method of making them in hosts.   |                                                                                |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| ACCESSION                                                                                                                                                                    | BD071190                                                      |                                                                                |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| VERSION                                                                                                                                                                      | BD071190.1                                                    | GI:22616793                                                                    |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| KEYWORDS                                                                                                                                                                     | JP 2001519664-A/29.                                           |                                                                                |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| SOURCE                                                                                                                                                                       | Zea mays                                                      |                                                                                |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| ORGANISM                                                                                                                                                                     | Zea mays                                                      |                                                                                |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. |                                                               |                                                                                |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| REFERENCE                                                                                                                                                                    | 1 (bases 1 to 153)                                            |                                                                                |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| AUTHORS                                                                                                                                                                      | Guan, H. and Keeling, P. L.                                   |                                                                                |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| TITLE                                                                                                                                                                        | Plant like starches and the method of making them in hosts    |                                                                                |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| JOURNAL                                                                                                                                                                      | Patent: JP 2001519664-A 29 23-OCT-2001;                       |                                                                                |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| COMMENT                                                                                                                                                                      | OS                                                            | Zea mays                                                                       |               |        |              |                     |                                      |                 |      |        |   |          |                    |
|                                                                                                                                                                              | PN                                                            | JP 2001519664-A/29                                                             |               |        |              |                     |                                      |                 |      |        |   |          |                    |
|                                                                                                                                                                              | PD                                                            | 23-OCT-2001                                                                    |               |        |              |                     |                                      |                 |      |        |   |          |                    |
|                                                                                                                                                                              | PP                                                            | 03-APR-1998                                                                    | JP 1998542940 |        |              |                     |                                      |                 |      |        |   |          |                    |
|                                                                                                                                                                              | PR                                                            | 04-APR-1997                                                                    | US 60/042939  |        |              |                     |                                      |                 |      |        |   |          |                    |
|                                                                                                                                                                              | PI                                                            | HANFING GUAN, PETER L KEELING                                                  |               |        |              |                     |                                      |                 |      |        |   |          |                    |
|                                                                                                                                                                              | PC                                                            | AO1H5/00, C12N15/29, C12N15/31, C12N15/54, C12N15/70, C12N15/74, PC C12N15/80. |               |        |              |                     |                                      |                 |      |        |   |          |                    |
|                                                                                                                                                                              | PC                                                            | C12N15/81, C12N15/82, C12P19/04                                                |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| CC                                                                                                                                                                           | Plant like starches and the method of making them in hosts FH |                                                                                |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| Key                                                                                                                                                                          | Location/Qualifiers                                           |                                                                                |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| FT                                                                                                                                                                           | CDS                                                           | (1)..(153).                                                                    |               |        |              |                     |                                      |                 |      |        |   |          |                    |
| FEATURES                                                                                                                                                                     |                                                               |                                                                                |               |        |              |                     | Location/Qualifiers                  |                 |      |        |   |          |                    |



[illegible]

PI KAREN E BROGLIE, JONATHAN EDWARD LIGHTNER  
PC A01H5/00,A01H1/00,C08B3/00,C12N15/09,C12N15/00 CC  
Modification of starch biosynthesis enzyme  
gene expression for  
CC production  
CC of starch in grain crops  
FH Key Location/Qualifiers  
FT source 1..2008  
FT [/organism=Zea mays \(maize\)](#).  
FT

|                                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |               |                            |
|----------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------|----------------------------|
| Pred. No.:                                   | 2.6e-10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Length:       | 2357                       |
| Score:                                       | 191.00                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Matches:      | 38                         |
| Percent Similarity:                          | 97.4%                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Conservative: | 0                          |
| Best Local Similarity:                       | 97.4%                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Mismatches:   | 1                          |
| Query Match:                                 | 100.0%                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Indels:       | 0                          |
| DB:                                          | 15                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Gaps:         | 0                          |
| US-10-628-525A-37 (1-39) x AF036891 (1-2357) |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |               |                            |
| Qy                                           | 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg**AlaTrpPro 20                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |               |                            |
| Db                                           | 55 ATGCGAGCCCTCGGCGTGGCGCGCGCTCTCTCTCGCGCGGCGCTGGCGG 114                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |               |                            |
| Qy                                           | 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |               |                            |
| Db                                           | 115 GCCCGCGTGGCGAGCGGCGCGCGCGCGCGCTCCAGCGCGTGTGCGCGCGCGG 171                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |               |                            |
| RESULT 8                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |               |                            |
| LOCUS                                        | A93359                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 2383 bp       | DNA linear PAT 22-JAN-2000 |
| DEFINITION                                   | Sequence 1 from Patent WO9744472.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |               |                            |
| ACCESSION                                    | A93359                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |               |                            |
| VERSION                                      | A93359.1 GI:6741623                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |               |                            |
| KEYWORDS                                     | Zea mays                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |               |                            |
| SOURCE                                       | Zea mays                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |               |                            |
| ORGANISM                                     | Zea mays                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |               |                            |
| REFERENCE                                    | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |               |                            |
| AUTHORS                                      | 1 (bases 1 to 2383)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |               |                            |
| TITLE                                        | Kossmann, J. and Froberg, C.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |               |                            |
| JOURNAL                                      | NUCLEIC ACID MOLECULES CODING SOLUBLE MAIZE STARCH SYNTHASES Patent: WO 9744472-A 1 27-NOV-1997;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |               |                            |
| FEATURES                                     | KOSSMANN JENS (DB); FROBERG CLAUS (DB)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |               |                            |
| source                                       | Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |               |                            |
|                                              | 1..2383                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |               |                            |
|                                              | /organism="Zea mays"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |               |                            |
|                                              | /mol_type="unassigned DNA"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |               |                            |
|                                              | /db_xref="taxon:4577"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |               |                            |
|                                              | /tissue_type="ENDOSPERM"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |               |                            |
|                                              | <2..1951                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |               |                            |
|                                              | /function="STARCH SYNTHESIS"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |               |                            |
|                                              | /codon_start=1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |               |                            |
|                                              | /product="SOLUBLE STARCH SYNTHASE"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |               |                            |
|                                              | /protein_id="CAB69545.1"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |               |                            |
|                                              | /db_xref="GI:6741624"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |               |                            |
|                                              | /translation="ARGLLSLSWATPESAVGACLLILARAANPAVGDRAPRRLQVRVLRRCVAELSRGEPAPFPALLAPLVFGFLAPPAETGEBPALTPPPVFDAGLGLGVPEPTGAESIDNTVVVAEQDSIEIVVGEQAKAKVTQNI VFTVGASPYAKSGGLGVDSGTFVALLAAGRHVHVMVPRYLNGTSDKNANAFYTEKHIRIPCQGEHEVTFPHCYRSDVDVFDHPSVHRPCNLVGDGKFGDNQFRVTLACYACEAPLVLEGGVLYGONCMFVNDWHASLVPLLAAKRYPGVYKDSRSLVHNLAHQGVPEASTVPDLGLPFWYGALEWVPEWAKRHALDKEAVNFLKGAVVADTRIVTVSKGSWEVTTABGQQLGMELLSSRSVLVINGIDINDNPADKICPYHSDVLDLGGKAKCKALQKELGLPIRPDVLGIFIGRLDYGLDILQIPDLREDVQVFMVLSGDPLEBDMWRSTIRFKDKFRWGFGFVSPVSHRI TAGCD ILLMPSRFPCLGNQLYAMQGYVTPVPHATGTSIRDTVENFPPGCEGEGTGMAFAPLTITENMLATLTAISTYREHKSSWEGLMKRGMSIDFTWDHAAEQYEIQFQWAPIDRPPYM" |               |                            |
| CDS                                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |               |                            |
| ORIGIN                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |               |                            |
| Alignment Scores:                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |               |                            |
| Pred. No.:                                   | 2.62e-10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Length:       | 2383                       |
| Score:                                       | 191.00                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Matches:      | 38                         |
| Percent Similarity:                          | 97.4%                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Conservative: | 0                          |
| Best Local Similarity:                       | 97.4%                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Mismatches:   | 1                          |
| Query Match:                                 | 100.0%                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Indels:       | 0                          |
| DB:                                          | 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Gaps:         | 0                          |
| US-10-628-525A-37 (1-39) x A93359 (1-2383)   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |               |                            |
| Qy                                           | 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg**AlaTrpPro 20                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |               |                            |
| Db                                           | 29 ATGCGAGCCCTCGGCGTGGCGCGCGCGCTCTCTCTCGCGCGGCGCTGGCGG 88                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |               |                            |

US-10-628-525A-37 (1-39) x AR411327 (1-2383)

QY 1 MetaIaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20  
 Db ATGGCGACGCCCTCGCGCGTGGCGCGCGTGCCTCTCTCGCGCGCGCGCTGGCGG 88  
 QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
 Db GCGCGCGTGGCGACCGCGCGCGCGCGCGCGCTCCAGCGCGTGTCTGCGCGCGCGG 145

RESULT 11  
 BD249559  
 LOCUS 2491 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Modification of starch biosynthesis enzyme gene expression for  
 production of starch in grain crops.

ACCESSION BD249559  
 VERSION BD249559.1 GI:33059329  
 KEYWORDS JP 2002525029-A/5.  
 SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 2491)

AUTHORS Broglie, K.E. and Lightner, J.E.  
 TITLE Modification of starch biosynthesis enzyme gene expression for

JOURNAL Production of starch in grain crops  
 Patent: JP 2002525029-A 5 13-AUG-2002;

COMMENT E1 DU PONT DE NEMOURS AND CO  
 OS Zea mays (maize)  
 PN JP 2002525029-A/5  
 PD 13-AUG-2002  
 PP 26-JUL-1999 JP 2000562537  
 PR 28-JUL-1998 US 60/094436

PI KAREN E BROGLIE, JONATHAN EDWARD LIGHTNER  
 PC A01H5/00, A01H1/00, C08B33/00, C12N15/09, C12N15/00 CC  
 Modification of starch biosynthesis enzyme

gene expression for  
 CC production

CC of starch in grain crops  
 FH Key Location/Qualifiers

FT source 1..2491  
 FT /organism='Zea mays (maize)'.  
 FT Location/Qualifiers

FEATURES  
 source  
 1..2491  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4577"

ORIGIN

Alignment Scores:  
 Pred. No.: 2,73e-10 Length: 2491  
 Score: 191.00 Matches: 38  
 Percent Similarity: 97.4% Conservative: 0  
 Best Local Similarity: 97.4% Mismatches: 1  
 Query Match: 100.0% Indels: 0  
 DB: 6 Gaps: 0

US-10-628-525A-37 (1-39) x BD249559 (1-2491)

QY 1 MetaIaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20  
 Db ATGGCGACGCCCTCGCGCGTGGCGCGCGTGCCTCTCTCGCGCGCGCGCTGGCGG 204  
 QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
 Db GCGCGCGTGGCGACCGCGCGCGCGCGCGCGCTCCAGCGCGTGTCTGCGCGCGCGG 261

RESULT 12  
 AR340007  
 LOCUS 2491 bp DNA linear PAT 17-AUG-2003  
 DEFINITION Sequence 5 from patent US 6570008.  
 ACCESSION AR340007

VERSION AR340007.1 GI:33731301

KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2491)

AUTHORS Broglie, K.E. and Lightner, J.E.  
 TITLE Modification of starch biosynthetic enzyme gene expression to  
 produce starches in grain crops  
 JOURNAL Patent: US 6570008-A 5 27-MAY-2003;  
 E. I. du Pont de Nemours and Company; Wilmington, DE

FEATURES  
 source  
 1..2491  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
 Pred. No.: 2,73e-10 Length: 2491  
 Score: 191.00 Matches: 38  
 Percent Similarity: 97.4% Conservative: 0  
 Best Local Similarity: 97.4% Mismatches: 1  
 Query Match: 100.0% Indels: 0  
 DB: 6 Gaps: 0

US-10-628-525A-37 (1-39) x AR340007 (1-2491)

QY 1 MetaIaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20  
 Db ATGGCGACGCCCTCGCGCGTGGCGCGCGTGCCTCTCTCGCGCGCGCGCTGGCGG 204  
 QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
 Db GCCCGCGTGGCGACCGCGCGCGCGCGCGCTCCAGCGCGTGTCTGCGCGCGCGG 261

RESULT 13

A63308

LOCUS 2992 bp DNA linear PAT 12-MAR-1998

DEFINITION Sequence 1 from Patent WO9720936.

ACCESSION A63308

VERSION A63308.1 GI:3717138

KEYWORDS

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 unclassified sequences.

AUTHORS Keeling, P.L. and Knight, M.E.

TITLE MODIFICATION OF STARCH SYNTHESIS IN PLANTS

JOURNAL Patent: WO 9720936-A 1 12-JUN-1997;

COMMENT ZENECA LTD (GB)

FEATURES Other publication AU 1037197 19970627.

source

location/Qualifiers

1..2992  
 /organism="unidentified"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32644"  
 /clone="NUMBER 1"

ORIGIN

Alignment Scores:

Pred. No.: 4.08e-10 Length: 2992  
 Score: 190.00 Matches: 39  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 99.5% Indels: 0  
 DB: 6 Gaps: 0

US-10-628-525A-37 (1-39) x A63308 (1-2992)

QY 1 MetaIaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20  
 Db ATGGCGACGCCCTCGCGCGTGGCGCGCGTGCCTCTCTCGCGCGCGCGCTGGCGG 661

```
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
Db 662 GCCCGCTCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 718

RESULT 14
LOCUS AR049919 2990 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5824790.
ACCESSION AR049919
VERSION AR049919.1 GI:5971911
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2990)
AUTHORS Keeling,P.Lewis., Knight,M.E. and Guan,H.
TITLE Modification of starch synthesis in plants
JOURNAL Patent: US 5824790-A 1 20-OCT-1998;
FEATURES Location/Qualifiers
source 1..2990
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 7.24e-08 Length: 2990
Score: 168.00 Matches: 38
Percent Similarity: 97.4% Conservatives: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 88.0% Indels: 1
DB: 6 Gaps: 0

US-10-628-525A-37 (1-39) x AR049919 (1-2990)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpPro 20
Db 602 ATGGCGACGCCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660

QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
Db 661 GCCCGCTCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 717

RESULT 15
AF168786
LOCUS Sorghum bicolor (sorghum)
DEFINITION Sorghum bicolor soluble starch synthase mRNA, complete cds.
ACCESSION AF168786
VERSION AF168786.2 GI:12019655
KEYWORDS
SOURCE
ORGANISM Sorghum bicolor (sorghum)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 2592)
AUTHORS Hsieh,J.S., Chen,M.R. and Hsing,Y.I.C.
TITLE Molecular cloning of a Sorghum cDNA encoding the soluble starch
JOURNAL synthase SBSS
REFERENCE Unpublished
2 (bases 1 to 2592)
AUTHORS Hsieh,J.S., Chen,M.R. and Hsing,Y.I.C.
TITLE Direct Submission
JOURNAL Submitted (14-JUL-1999) Agronomy, National Taiwan University, No.
1, Sec. 4, Roosevelt Rd., Taipei 10617, Taiwan
3 (bases 1 to 2592)
AUTHORS Hsieh,J.S., Chen,M.R. and Hsing,Y.I.C.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2001) Agronomy, National Taiwan University, No.
1, Sec. 4, Roosevelt Rd., Taipei 10617, Taiwan
REMARK Sequence update by submitter
COMMENT On Jan 3, 2001 this sequence version replaced gi:5616514.
FEATURES Location/Qualifiers
source 1..2592
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/organism="Sorghum bicolor"
/mol_type="mRNA"
/strain="Kafir 5765-6-1-11-3"
/db_xref="taxon:4558"
59..1948
/codon_start=1
/product="soluble starch synthase"
/protein_id="AAD45815.2"
/db_xref="GI:12019656"
/translation="MATPSAVGAACLVARAAAGLGPGRGGDRARPRFORVRRR
CYAELREGPAPTEPLPALLAPLVPAPFLAPPSEPEGPASTPPPLPDAGLDGLG
QPEGIAEGSIDETVVVASQDSIEIVGKEQARAKVTQSIIVFTGEASPYAKSGGLGV
CGSLVALAAGHRVVMVPRYLNGTSDKNYANAFYTERHIRPCFGEHEVTFPHY
RDSVDVFDVHPSYRPNGLYGDKFGAGDNQPYTLCLCYAACAPLVLGLGYIYQQ
NCMFVNDWHASLVPVLLAAKYPYGVYKDSRSLIVHNLAHQGVBPASTYDGLGLPP
EMYGALWVPEWARHDLKGEAVNFKGAVTADRI VTVSGYKSWETVTTASGGQL
NELLSSKSLVINGIINDMNPATDKICPHYSVDLDSGAKCKSALQKBLGLPI
RPEVLLIGTIGRLDYKGLDLQLIIPHLMRDDVQFVLGSGDFELEDNRSTSDPK
DKFRGVGFSPVSHRITAGCDLILMPSRPEPCGLNQLYAMQYGTVPVVAHAGGLRDT
VENFNPPGNGEGGTGMAFAPLTTFENMFVDIANCFDIOGAQIFLGRAHEGHVKRLH
VGPCR"
```

## ORIGIN

```
Alignment Scores:
Pred. No.: 5.23e-05 Length: 2592
Score: 139.50 Matches: 31
Percent Similarity: 75.0% Conservatives: 2
Best Local Similarity: 70.5% Mismatches: 6
Query Match: 73.0% Indels: 5
DB: 15 Gaps: 1
```

US-10-628-525A-37 (1-39) x AF168786 (1-2592)

```
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***Ala----- 18
Db 59 ATGGCGACGCCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 118
```

```
QY 19 -----TrpProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgVal 35
Db 119 CTTGGGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 178
```

```
QY 36 LeuArgArgArg 39
Db 179 GTGCGCAGCGCG 190
```

```
RESULT 16
AP006500.07
WPCOMMENT
```

Sequence split into 13 fragments LOCUS AP006500 Accession AP006500

| Fragment Name | Begin   | End     |
|---------------|---------|---------|
| AP006500_00   | 1       | 110000  |
| AP006500_01   | 100001  | 210000  |
| AP006500_02   | 200001  | 310000  |
| AP006500_03   | 300001  | 410000  |
| AP006500_04   | 400001  | 510000  |
| AP006500_05   | 500001  | 610000  |
| AP006500_06   | 600001  | 710000  |
| AP006500_07   | 700001  | 810000  |
| AP006500_08   | 800001  | 910000  |
| AP006500_09   | 900001  | 1010000 |
| AP006500_10   | 1000001 | 1110000 |
| AP006500_11   | 1100001 | 1210000 |
| AP006500_12   | 1200001 | 1254097 |

Continuation (8 of 13) of AP006500 from base 700001 (AP006500 Cyanidioschyzon merolae str

```
Alignment Scores:
Pred. No.: 6.82e+03 Length: 110000
Score: 74.50 Matches: 19
Percent Similarity: 56.4% Conservatives: 3
Best Local Similarity: 48.7% Mismatches: 16
Query Match: 39.0% Indels: 1
DB: 14 Gaps: 1
```

US-10-628-525A-37 (1-39) x AP006500\_07 (1-110000)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20  
 Db 93954 ATGGCAACAAACAGTCCCTTGGCGGCTGCTGCTCTTGGGAGATTGTTTCGGA 94013  
 QY 21 AlaAlaValGlyAspArgAlaArg---ProArgArgLeuGlnArgValLeuArgArg 38  
 Db 94014 CAACGCAGCAGCATCGCGCGGCGCTCGNAGGCCATCAGTCGCAATTCGACGC 94070

RESULT 17

AC013160 53583 bp DNA linear HTG 03-NOV-1999  
 LOCUS Drosophila melanogaster, \*\*\* SEQUENCING IN PROGRESS \*\*\*.

DEFINITION AC013160  
 ACCESSION AC013160  
 VERSION AC013160.1 GI:6223171  
 HTG; HTGS\_PHASE2.  
 SOURCE Drosophila melanogaster (fruit fly)  
 ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 53583)  
 Adams,M. and Venter,J.C.  
 Direct Submission

TITLE Submitted (03-NOV-1999) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD, USA

COMMENT This sequence was identified as CDN:10213792 by the submitter.  
 For further information on this sequence you may e-mail to  
 fly@celera.com.

\* NOTE: This is a 'working draft' sequence.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.

FEATURES

source  
 1..53583  
 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7227"

ORIGIN

Alignment Scores:  
 Pred. No.: 4.01e+03 Length: 53583  
 Score: 74.00 Matches: 16  
 Percent Similarity: 56.8% Conservative: 5  
 Best Local Similarity: 43.2% Mismatches: 16  
 Query Match: 38.7% Indels: 0  
 DB: 14 Gaps: 0

US-10-628-525A-37 (1-39) x AC013160 (1-53583)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20  
 Db 37623 ATGGGCACCAAGCAGCTTGGGCAATAGTATTGACCGCATCGGGAAGCCATGGCG 37682

QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 37  
 Db 37683 GCTGTGGTCAGATAGGCTTAAGACGAGGATTTTAGTAGAATTCTTCGC 37733

RESULT 18  
 AP008212\_269/c

WPCOMMENT

Sequence split into 308 fragments LOCUS AP008212 Accession AP008212

| Fragment Name | Begin  | End    |
|---------------|--------|--------|
| AP008212_000  | 1      | 110000 |
| AP008212_001  | 100001 | 210000 |
| AP008212_002  | 200001 | 310000 |
| AP008212_003  | 300001 | 410000 |
| AP008212_004  | 400001 | 510000 |
| AP008212_005  | 500001 | 610000 |
| AP008212_006  | 600001 | 710000 |
| AP008212_007  | 700001 | 810000 |
| AP008212_008  | 800001 | 910000 |

|              |         |         |
|--------------|---------|---------|
| AP008212_009 | 900001  | 1010000 |
| AP008212_010 | 1000001 | 1110000 |
| AP008212_011 | 1100001 | 1210000 |
| AP008212_012 | 1200001 | 1310000 |
| AP008212_013 | 1300001 | 1410000 |
| AP008212_014 | 1400001 | 1510000 |
| AP008212_015 | 1500001 | 1610000 |
| AP008212_016 | 1600001 | 1710000 |
| AP008212_017 | 1700001 | 1810000 |
| AP008212_018 | 1800001 | 1910000 |
| AP008212_019 | 1900001 | 2010000 |
| AP008212_020 | 2000001 | 2110000 |
| AP008212_021 | 2100001 | 2210000 |
| AP008212_022 | 2200001 | 2310000 |
| AP008212_023 | 2300001 | 2410000 |
| AP008212_024 | 2400001 | 2510000 |
| AP008212_025 | 2500001 | 2610000 |
| AP008212_026 | 2600001 | 2710000 |
| AP008212_027 | 2700001 | 2810000 |
| AP008212_028 | 2800001 | 2910000 |
| AP008212_029 | 2900001 | 3010000 |
| AP008212_030 | 3000001 | 3110000 |
| AP008212_031 | 3100001 | 3210000 |
| AP008212_032 | 3200001 | 3310000 |
| AP008212_033 | 3300001 | 3410000 |
| AP008212_034 | 3400001 | 3510000 |
| AP008212_035 | 3500001 | 3610000 |
| AP008212_036 | 3600001 | 3710000 |
| AP008212_037 | 3700001 | 3810000 |
| AP008212_038 | 3800001 | 3910000 |
| AP008212_039 | 3900001 | 4010000 |
| AP008212_040 | 4000001 | 4110000 |
| AP008212_041 | 4100001 | 4210000 |
| AP008212_042 | 4200001 | 4310000 |
| AP008212_043 | 4300001 | 4410000 |
| AP008212_044 | 4400001 | 4510000 |
| AP008212_045 | 4500001 | 4610000 |
| AP008212_046 | 4600001 | 4710000 |
| AP008212_047 | 4700001 | 4810000 |
| AP008212_048 | 4800001 | 4910000 |
| AP008212_049 | 4900001 | 5010000 |
| AP008212_050 | 5000001 | 5110000 |
| AP008212_051 | 5100001 | 5210000 |
| AP008212_052 | 5200001 | 5310000 |
| AP008212_053 | 5300001 | 5410000 |
| AP008212_054 | 5400001 | 5510000 |
| AP008212_055 | 5500001 | 5610000 |
| AP008212_056 | 5600001 | 5710000 |
| AP008212_057 | 5700001 | 5810000 |
| AP008212_058 | 5800001 | 5910000 |
| AP008212_059 | 5900001 | 6010000 |
| AP008212_060 | 6000001 | 6110000 |
| AP008212_061 | 6100001 | 6210000 |
| AP008212_062 | 6200001 | 6310000 |
| AP008212_063 | 6300001 | 6410000 |
| AP008212_064 | 6400001 | 6510000 |
| AP008212_065 | 6500001 | 6610000 |
| AP008212_066 | 6600001 | 6710000 |
| AP008212_067 | 6700001 | 6810000 |
| AP008212_068 | 6800001 | 6910000 |
| AP008212_069 | 6900001 | 7010000 |
| AP008212_070 | 7000001 | 7110000 |
| AP008212_071 | 7100001 | 7210000 |
| AP008212_072 | 7200001 | 7310000 |
| AP008212_073 | 7300001 | 7410000 |
| AP008212_074 | 7400001 | 7510000 |
| AP008212_075 | 7500001 | 7610000 |
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| AP008212_077 | 7700001 | 7810000 |
| AP008212_078 | 7800001 | 7910000 |
| AP008212_079 | 7900001 | 8010000 |
| AP008212_080 | 8000001 | 8110000 |
| AP008212_081 | 8100001 | 8210000 |

AP008212\_082 8200001 8310000  
 AP008212\_083 8300001 8410000  
 AP008212\_084 8400001 8510000  
 AP008212\_085 8500001 8610000  
 AP008212\_086 8600001 8710000  
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AP008212\_155 15500001 15610000  
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 AP008212\_157 1570001 15810000  
 AP008212\_158 1580001 15910000  
 AP008212\_159 1590001 16010000  
 AP008212\_160 1600001 16110000  
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 AP008212\_165 1650001 16610000  
 AP008212\_166 1660001 16710000  
 AP008212\_167 1670001 16810000  
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 AP008212\_172 1720001 17310000  
 AP008212\_173 1730001 17410000  
 AP008212\_174 1740001 17510000  
 AP008212\_175 1750001 17610000  
 AP008212\_176 1760001 17710000  
 AP008212\_177 1770001 17810000  
 AP008212\_178 1780001 17910000  
 AP008212\_179 1790001 18010000  
 AP008212\_180 1800001 18110000  
 AP008212\_181 1810001 18210000  
 AP008212\_182 1820001 18310000  
 AP008212\_183 1830001 18410000  
 AP008212\_184 1840001 18510000  
 AP008212\_185 1850001 18610000  
 AP008212\_186 1860001 18710000  
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 AP008212\_190 1900001 19110000  
 AP008212\_191 1910001 19210000  
 AP008212\_192 1920001 19310000  
 AP008212\_193 1930001 19410000  
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 AP008212\_195 1950001 19610000  
 AP008212\_196 1960001 19710000

Alignment Scores:

Pred. No.: 1.38e+04 Length: 110000  
 Score: 71.50 Matches: 20  
 Percent Similarity: 60.0% Conservative: 1  
 Best Local Similarity: 57.1% Mismatches: 13  
 Query Match: 37.4% Indels: 1  
 DB: 15 Gaps: 1

US-10-628-525A-37 (1-39) x AP008212\_269 (1-110000)

Qy 5 SerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpProAlaAlaValGly 24  
 Db 48647 GCGCGGAGGCGCGCGCGCGGCTGAGATGGAGCGGAGCGGCTGGCAGCG---GGA 48591  
 Qy 25 AspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
 Db 48590 GGCAGAGCTCGCCCGCGCAGGTTGCGTCAGGTTGAGCGCGCG 48546

RESULT 19

AP004744/c  
 LOCUS AP004744 165270 bp DNA linear PLN 16-SEP-2004  
 DEFINITION Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6,  
 BAC clone: OSUNBB0065C04.  
 ACCESSION AP004744  
 VERSION AP004744.2 GI:47169781  
 KEYWORDS  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;



|                                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| REFERENCE<br>AUTHORS<br>TITLE            | Bhrhartoidaeae; Oryzaeae; Oryza.<br>1<br>Sasaki, T., Matsuoto, T. and Yamamoto, K.<br>Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC<br>clone:OSJNBb0065C04                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| JOURNAL<br>REFERENCE<br>AUTHORS<br>TITLE | Published Only in Database (2002)<br>2 (bases 1 to 165270)<br>Sasaki, T., Matsuoto, T. and Yamamoto, K.<br>Direct Submission<br>Submitted (13-FEB-2002) Takuji Sasaki, National Institute of<br>Agrobiological Sciences, Rice Genome Research Program; Kanondai<br>2-1-2, Tsukuba, Ibaraki 305-8602, Japan<br>(E-mail: tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,<br>Tel:81-298-38-7441, Fax:81-298-38-7468)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| COMMENT                                  | On May 13, 2004 this sequence version replaced gi:18656390.<br>Genes were predicted from the integrated results of the following:<br>GENSCAN (http://ccr-081.mit.edu/GENSCAN.html), FGENESH<br>(http://www.softberry.com/), GeneMark.hmm<br>(http://opal.biology.gatech.edu/GeneMark/), GlimmerM<br>(http://www.tigr.org/tcb/glimmer/glmr form.html), RiceHMM<br>(http://rgp.dna.affrc.go.jp/RiceHMM/), _SplicePredictor<br>(http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4<br>(http://globin.cse.psu.edu/html/docs/sim4.html), gap2<br>(http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The<br>genomic sequence was searched against NCBI NonRedundant Protein<br>database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA<br>sequence database at RGP or DDBJ. Protein homologies of the coding<br>regions were searched against NCBI NonRedundant Protein database<br>with BLASTP. ESTs represent the identified cDNA sequences using<br>BLASTN with the corresponding DDBJ accession no. and RGP clone ID.<br>Full-length cDNAs represent the identified cDNA sequences using<br>BLASTN with the corresponding DDBJ accession no.<br>A gene with identity or significant homology to a protein is<br>classified based on the protein name to indicate the homology level<br>such as same name, 'putative-' and '-like protein'. A gene without<br>significant homology to any protein but with full-length cDNA or<br>EST homology (covering almost the entire length of partial<br>sequence) is classified as an 'unknown' protein. A gene predicted<br>by two or more gene prediction programs is classified as a<br>'hypothetical' protein according to RGP standard. A gene<br>predicted by a single gene prediction program is also classified as<br>a probable 'hypothetical' protein and is included as a<br>miscellaneous feature of the sequence.<br>The orientation of the sequence is from M13rev to -21M13 of the BAC<br>clone. This sequence of OSJNBb0065C04 clone has an overlap with<br>OSJNBa0051002 (DDBJ: AP005769) clone at 5' end and with F0473H04<br>(DDBJ: AP003628) at 3' end. Detailed information on overlap and<br>assembly quality together with annotation of this entry is<br>available at <a href="http://rgp.dna.affrc.go.jp/GenomeSeq.html">http://rgp.dna.affrc.go.jp/GenomeSeq.html</a> .<br>Location/Qualifiers<br>1..165270<br>/organism="Oryza sativa (japonica cultivar-group)"<br>/mol_type="genomic DNA"<br>/cultivar="Nipponbare"<br>/db_xref="taxon:39947"<br>/chromosome="6"<br>/clone="OSJNBb0065C04"<br>complement(1420..2703)<br>/gene="OSJNBb0065C04.2"<br>complement(join(1420..1704,2159..2703))<br>/gene="OSJNBb0065C04.2"<br>/note="supported by full-length cDNA(s): AK099401"<br>/gene="OSJNBb0065C04.2"<br>/note="contains full-length cDNA(s): AK099401"<br>/codon_start=1<br>/product="unknown protein"<br>/protein_id="BAD45845.1"<br>/db_xref="GI:52075899"<br>/translation="MSASRRALSRAGFLRGGIGILAARCGYHRRRLPLTAEEV<br>EGGASAGAGSTSEEGSSSSARWEEAIDGAMARMEPEWAPRPGTSTYAPP<br>RPAAGALLLVSHAAARMGVPRLASDAEARVDAASRGFPCTTYFDGHFDEVE<br>RSDVTPAEDE"                                                                                                                                                                                                                                                                                                                                                  |
| FEATURES<br>source                       | 2920..4935<br>/gene="OSJNBb0065C04.3"<br>join(2920..3288,4750..4935)<br>/gene="OSJNBb0065C04.3"<br>/note="supported by full-length cDNA(s): AK068205"<br>3019..3264<br>/gene="OSJNBb0065C04.3"<br>/note="contains EST(s):<br>D23786(R0153),AU163854(E11214),C19915(E11214)<br>contains full-length cDNA(s): AK068205<br>similar to Arabidopsis thaliana chromosome 2, At3g15910"<br>/codon_start=1<br>/product="unknown protein"<br>/protein_id="BAD45846.1"<br>/db_xref="GI:52075900"<br>/translation="MSAIDEVEIDEMWNAELGATYPCPGDLFQITLADLRGBEI<br>ARCPSCSLFTVYNEEDFADAKEPHPKAPRPVAVA"<br>8368..8544,9074..9177,9657..10000)<br>/gene="OSJNBb0065C04.4-1"<br>complement(join(5413..5918,6337..6821,6942..8009,<br>8368..8544,9074..9177,9657..10000))<br>/gene="OSJNBb0065C04.4-1"<br>complement(join(5413..5918,6337..6821,6942..8009,<br>8368..8544,9074..9177,9657..10000))<br>/note="supported by full-length cDNA(s): AK066945"<br>complement(join(5527..5918,6337..8009,8368..8544,<br>9074..9177,9657..10015))<br>/gene="OSJNBb0065C04.4-2"<br>complement(join(5527..5918,6337..8009,8368..8544,<br>9074..9177,9657..10015))<br>/gene="OSJNBb0065C04.4-2"<br>complement(join(5527..5918,6337..8009,8368..8544,<br>9074..9177,9657..10015))<br>/note="supported by full-length cDNA(s): AK067348"<br>complement(join(5772..5918,6337..6821,6942..8009,<br>8368..8544,9074..9177,9657..9793))<br>/gene="OSJNBb0065C04.4-1"<br>/note="contains EST(s): AU063083(C52982)<br>contains full-length cDNA(s): AK066945"<br>/codon_start=1<br>/product="putative microtubule-associated protein"<br>/protein_id="BAD45847.1"<br>/db_xref="GI:52075901"<br>/translation="MPECPARERFSALRGARWRADLGVLPDCASVSTEEFRRAADSR<br>RRYANRRRLIDPLHSKDEENAPLAVENPLSQNPSTWQVFNAAELKMLNDLS<br>RLYPGLNFFQTTICQSMGLRILLVMSRLYRGYKQGHLLAPLLVYLHADVYFK<br>QVRELDLFDSDPDGQTFPDRILNRSRDTNTIRGSAKIRSLDLDSDTDLPLIN<br>DAYAGEGLGIIILSEKFEHDAYCMFESLMHGMNAGQVAITFYSLSPAPESSTG<br>LTPVREASAIYHLLASVDSPLSHLMELGVEPQYFALRWLRLVFGREFSLNLLFIW<br>DEIFSSPNHSYCAIDKNQSDYQKILCSHRGALILSMVSMMLHRSLLGSEHATSC<br>LVRLNFFGDTDLKSLIDKALQLPFALEANPLSSPLRKSPLNPNPTWEETKILQM<br>SEKRGSGSINRMKVRGLFRSSPNTEGNSVRTKDNFEDNSNSTENMITTNNVLEA<br>GOPEVHRSSVDVRDALGVACNLSDRSSTLSGCTEYDHTHDEPCASHDDKVVS<br>EPDPLVHNDKIDEVTIAAJOTCALVDYQSQQNKPCSVNGKSEVKYQONFAVHVGVR<br>KETELGSSSDVADKELLTGTLRLGESWENIEVDLLFQPNLHSTSLDKSEIVLGS<br>IEQAKAAALGLKKIKISELLRRI"<br>complement(join(5772..5918,6337..8009,8368..8544,<br>9074..9177,9657..9793))<br>/gene="OSJNBb0065C04.4-2"<br>/note="contains EST(s): AU063083(C52982)<br>contains full-length cDNA(s): AK067348"<br>/codon_start=1<br>/product="putative microtubule-associated protein"<br>/protein_id="BAD45848.1"<br>/db_xref="GI:52075902"<br>/translation="MPECPARERFSALRGARWRADLGVLPDCASVSTEEFRRAADSR<br>RRYANRRRLIDPLHSKDEENAPLAVENPLSQNPSTWQVFNAAELKMLNDLS<br>RLYPGLNFFQTTICQSMGLRILLVMSRLYRGYKQGHLLAPLLVYLHADVYFK<br>QVRELDLFDSDPDGQTFPDRILNRSRDTNTIRGSAKIRSLDLDSDTDLPLIN<br>DAYAGEGLGIIILSEKFEHDAYCMFESLMHGMNAGQVAITFYSLSPAPESSTG<br>LTPVREASAIYHLLASVDSPLSHLMELGVEPQYFALRWLRLVFGREFSLNLLFIW<br>DEIFSSPNHSYCAIDKNQSDYQKILCSHRGALILSMVSMMLHRSLLGSEHATSC<br>LVRLNFFGDTDLKSLIDKALQLPFALEANPLSSPLRKSPLNPNPTWEETKILQM<br>SEKRGSGSINRMKVRGLFRSSPNTEGNSVRTKDNFEDNSNSTENMITTNNVLEA<br>GOPEVHRSSVDVRDALGVACNLSDRSSTLSGCTEYDHTHDEPCASHDDKVVS<br>EPDPLVHNDKIDEVTIAAJOTCALVDYQSQQNKPCSVNGKSEVKYQONFAVHVGVR<br>KETELGSSSDVADKELLTGTLRLGESWENIEVDLLFQPNLHSTSLDKSEIVLGS<br>IEQAKAAALGLKKIKISELLRRI" |

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AICTCALVDYQQSQNKPCSVNGSKSVKYOQNFANVHVGRKETFELGSSSDVADKELL
GTRLLGSGSVNIEVIDLQPNLHSTSLDKSEIIVLGSIEQAKAALEGLKTISE
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gene      10516..10853
          /gene="OSJNBb0065C04.5"
mRNA     join(<10516..10686,10773..>10853)
          /gene="OSJNBb0065C04.5"
          /notes="start and end point are not identified"
CDS      join(10516..10686,10773..10853)
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          /notes="predicted by GeneMark.hmm etc."
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          /product="hypothetical protein"
          /protein_id="BAD45849.1"
          /db_xref="GI:52075903"
misc_feature join(11584..12408,15431..15460)
          /gene="OSJNBb0065C04.6"
          /notes="hypothetical ORF
          predicted by GlimmerM
          this category is not included in IRGSP standard"
          complement(15700..18959)
          /gene="OSJNBb0065C04.7"
          complement(join(<15700..15903,16106..16155,16306..16429,
          16536..16605,16698..16773,16946..17022,17232..17278,
          17349..17536,17669..17813,17898..18116,18274..18413,
          18551..>18959))
          /gene="OSJNBb0065C04.7"
          /notes="start and end point are not identified"
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          16536..16605,16698..16773,16946..17022,17232..17278,
          17349..17536,17669..17813,17898..18116,18274..18413,
          18551..18959))
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          /notes="contains full-length cDNA(s) : AK072287,AK102315"
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          /db_xref="GI:52075904"
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Alignment Scores:
Pred. No.:      2e+04      Length:      165270
Score:          71.50      Matches:      20
Percent Similarity: 60.0%      Conservative: 1
Best Local Similarity: 57.1%      Mismatches: 13
Query Match:      37.4%      Indels:      1
DB:              15        Gaps:        1

US-10-628-525A-37 (1-39) x AP004744 (1-165270)

QY      5 SerAlaValGlyAlaLaCysLeuLeuLeuAlaArg***AlaTrpProAlaValGly 24
      ::::|||||
DB      72408 GCGGCGGAGCGCGCGCGCGGCGGTGAGATGAGCGGCGGTGCGTGCAGCG---CGA 72352
      :|||||

QY      25 AspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 39
      :|||||
DB      72351 GGCAGAGCTGCGCCCGCGCAGGTTGCCGTGACAGTTGAGCGCGCG 72307
      :|||||

RESULT 20
AY310711/c      2182 bp      DNA      linear      INV 15-APR-2004
LOCUS
DEFINITION      Saccomorphus sp. JAR-2003 28S ribosomal RNA gene, partial sequence.
ACCESSION      AY310711
VERSION        AY310711.1      GI:37223334
KEYWORDS
SOURCE
ORGANISM      Saccomorphus sp. JAR-2003
              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Erotylidae; Saccomorphus.
1 (bases 1 to 2182)
Robertson,J.A., McHugh,J.V. and Whiting,M.P.
A molecular phylogenetic analysis of the Pleasing Fungus Beetles
(Coleoptera: Erotylidae): evolution of color patterns,
gregariousness and mycophagy
Syst. Entomol. 29 (2), 173-187 (2004)
2 (bases 1 to 2182)
Robertson,J.A., McHugh,J.V. and Whiting,M.P.
Direct Submission
Submitted (02-JUN-2003) Integrative Biology, Brigham Young
University, 401 WIDB, Provo, UT 84602, USA
Location/Qualifiers
source
1..2182
/organism="Saccomorphus sp. JAR-2003"
/mol_type="genomic DNA"
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<1..>2182
/product="28S ribosomal RNA"

ORIGIN
Alignment Scores:
Pred. No.:      454      Length:      2182
Score:          71.00      Matches:      17
Percent Similarity: 60.5%      Conservative: 6
Best Local Similarity: 44.7%      Mismatches: 9
Query Match:      37.2%      Indels:      6
DB:              2        Gaps:        1

US-10-628-525A-37 (1-39) x AY310711 (1-2182)

QY      2 AlaThrProSerAlaValGlyAlaLaCysLeuLeuLeuAlaArg***AlaTrpProAla 21
      :|:::|||||
DB      1672 GCAGGCCCTTCGCGCTCACCGCGGACCCCTCTACTGTCAGGCGCTTCATGGCGTCT 1613
      :|:::|||||

QY      22 AlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 39
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DB      1612 TCGGTA-----AGAAAGACAGACCGCACATGCCGCTGACCG 1577
      :|:::|||||

RESULT 21
SPFKBAD      19791 bp      DNA      linear      BCT 18-APR-2005
LOCUS
DEFINITION      Streptomyces sp. MA6548 fkbA gene and partial fkbD gene encoding
              FK506 polyketide synthase and cytochrome P-450-9-deoxo-FK506
              hydroxylase, respectively.
ACCESSION      Y10438
VERSION        Y10438.1      GI:1781343
KEYWORDS      acyl carrier protein; acyltransferase; beta-ketoacyl-ACP-synthase;
              beta-ketoreductase; cytochrome P-450-9-deoxo-FK506 hydroxylase;
              dehydratase; enoyl reductase; FK506 polyketide synthase; fkbA gene;
              fkbD gene.
SOURCE
ORGANISM      Streptomyces sp. MA6548
              Streptomyces sp. MA6548
              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
              Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE
1
Motamedi,H., Cai,S.J., Shafiee,A. and Elliston,K.O.
Structural organization of a multifunctional polyketide synthase
involved in the biosynthesis of the macrolide immunosuppressant
FK506
Eur. J. Biochem. 244 (1), 74-80 (1997)

JOURNAL      PUBLISHED      9063448
2 (bases 1 to 19791)
MOTAMEDI,H.
AUTHORS
Direct Submission
Submitted (08-JAN-1997) H. Motamedi, Merck Research Labs, P.O.Box
2000, Bldg. RY80X-225, Rayway, NJ 07065, USA
Location/Qualifiers
FEATURES
source
1..19791
/organism="Streptomyces sp. MA6548"
/mol_type="genomic DNA"

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VERSION          AB091437.1  GI:28971681
KEYWORDS         Burkholderia multivorans
SOURCE           Burkholderia multivorans
ORGANISM         Burkholderia multivorans
REFERENCE        1
AUTHORS          Komatsu,H., Imura,Y., Ohori,A., Nagata,Y. and Tauda,M.
TITLE            Distribution and Organization of Auxotrophic Genes on the
                  Multichromosomal Genome of Burkholderia multivorans ATCC 17616
JOURNAL          J. Bacteriol. 185 (11), 3333-3343 (2003)
PUBMED           12754231
AUTHORS          Komatsu,H.
TITLE            Direct Submission
JOURNAL          Submitted (10-SEP-2002) Harunobu Komatsu, Tohoku University,
                  Graduate School of Life Sciences, Katahira 2-1-1, Sendai, Miyagi
                  980-8577, Japan (E-mail:komatsu@ige.tohoku.ac.jp,
                  Tel:81-22-217-5743, Fax:81-22-217-5699)
FEATURES         Location/Qualifiers
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                     VLDCCGAGHASPAPVPHRVVAYDVLAAPLMATVDAARERLRLNVTQGPAPRLP
                     FDAATFDMVSRMSAAHHDVNAALAEVRVLKPGGRVIMIDIANDNHPLDLYLQAA
                     EYLDRSDVRYDRADEWLAMPFRDAGFEARVGRWRLLPIDFTWVRGS"
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                     DRNLIRFTFMSPAARTLIVDMETRARLRAERFADSIRHLTDAPTRALIDALTAGSDA
                     FAQYASQDVEREGLEFDFHPADGRLVYQQITLKPAREDLKLVLRD"
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                     /codon_start=1
                     /evidence=experimental
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                     SLAHNMLAAQKISADLAAIERGMAQIKGEIERGEFEWQDLDEVDHLNTEARLTAL
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                     FTHLQVAPQVTFGHLLAYVEMFSRDAERMDRCTRVNRLPLGMAALAGTSPYIDRHA
                     VAKSGPFGICANSIDAVSDRDFALTEFTAAALVMTHVSRFSEELVLMWSPRVGFIDI
                     ADREFTGSSIMPKNPDPVPELARKCTGRVNGHLMALLITLMKGQPLAYWKNQDEKEP
                     LFDVTVTADTVIRVAGITVKPFDAMRAALQGFSTADLADLYLVKRGPPRDAH
                     EAVAHAVKICDDRGLDLDLIDEMKRELPNVAQLIGDDVDFDLYLTLEGSVAARNHPGG
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CDS              3250..>3741
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ORIGIN
Alignment Scores:
Score: 830 Length: 3741
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Percent Similarity: 52.1% Conservative: 5
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                  dehydratase genes, complete cds; IS91-like insertion sequence,
                  complete sequence;
                  S-2,4-dichlorophenoxypropionate/alpha-ketoglutarate dioxygenase
                  (sdpa) gene, complete cds; IS91-like insertion sequence, and
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VERSION        AV327575.1 GI:32815753
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REFERENCE      1 (bases 1 to 25768)
AUTHORS        Schleinitz,K.M., Kleinstaub,S., Vallaeys,T. and Babel,W.
TITLE          Localization and Characterization of Two Novel Genes Encoding
                  Stereospecific Dioxygenases Catalyzing
                  2(2,4-Dichlorophenoxy)propionate Cleavage in Delftia acidovorans
                  MCI
JOURNAL         Appl. Environ. Microbiol. 70 (9), 5357-5365 (2004)
PUBMED         15345421
REFERENCE      2 (bases 1 to 25768)
AUTHORS        Schleinitz,K.M., Kleinstaub,S., Vallaeys,T. and Babel,W.
TITLE          Genetic background of enantiospecific 2,4-dichlorophenoxypropionate
                  cleavage in Delftia acidovorans MCI
JOURNAL         Unpublished
REFERENCE      3 (bases 1 to 25768)
AUTHORS        Schleinitz,K.M.
TITLE          Direct Submission
JOURNAL         Submitted (31-MAY-2002) Environmental Microbiology, Centre for

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Environmental Research, Permoserstrasse 15, Leipzig 04318, Germany  
4 (bases 1 to 25768)  
Schleinitz, K.M.  
Direct Submission  
Submitted (20-JUN-2003) Environmental Microbiology, UFZ Centre for  
Environmental Research, Permoserstrasse 15, Leipzig 04318, Germany  
Nucleotide sequence updated by submitter  
On or before Sep 8, 2004 this sequence version replaced  
gi:22087562, gi:22087559.

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Environmental Research, Permoserstrasse 15, Leipzig 04318, Germany  
4 (bases 1 to 25768)  
Schleinitz, K.M.  
Direct Submission  
Submitted (20-JUN-2003) Environmental Microbiology, UFZ Centre for  
Environmental Research, Permoserstrasse 15, Leipzig 04318, Germany  
Nucleotide sequence updated by submitter  
On or before Sep 8, 2004 this sequence version replaced  
gi:22087562, gi:22087559.

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/organism="Delftia acidovorans"  
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KEYWORDS
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  Lybas sp. 1-JAR-2003
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
  Erotylidae; Lybas.
REFERENCE
  1 (bases 1 to 2171)
  Robertson, J.A., McHugh, J.V. and Whiting, M.F.
  A molecular phylogenetic analysis of the Pleasing Fungus Beetles
  (Coleoptera: Erotylidae): evolution of color patterns,
  gregariousness and mycophagy
JOURNAL
  Syst. Entomol. 29 (2), 173-187 (2004)
REFERENCE
  2 (bases 1 to 2171)
  Robertson, J.A., McHugh, J.V. and Whiting, M.F.
  Direct Submission
AUTHORS
  Robertson, J.A., McHugh, J.V. and Whiting, M.F.
JOURNAL
  Submitted (02-JUN-2003) Integrative Biology, Brigham Young
  University, 401 WIDB, Provo, UT 84602, USA
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ACCESSION
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VERSION
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  Erotylidae; Mycotretus.
REFERENCE
  1 (bases 1 to 2171)
  Robertson, J.A., McHugh, J.V. and Whiting, M.F.
  A molecular phylogenetic analysis of the Pleasing Fungus Beetles
  (Coleoptera: Erotylidae): evolution of color patterns,
  gregariousness and mycophagy
JOURNAL
  Syst. Entomol. 29 (2), 173-187 (2004)
REFERENCE
  2 (bases 1 to 2171)
  Robertson, J.A., McHugh, J.V. and Whiting, M.F.
  Direct Submission
AUTHORS
  Robertson, J.A., McHugh, J.V. and Whiting, M.F.
JOURNAL
  Submitted (02-JUN-2003) Integrative Biology, Brigham Young
  University, 401 WIDB, Provo, UT 84602, USA
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US-10-628-525A-37 (1-39) x AY310693 (1-2171)
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  Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
  Erotylidae; Mycotretus.
REFERENCE
  1 (bases 1 to 2175)
  Robertson, J.A., McHugh, J.V. and Whiting, M.F.
  A molecular phylogenetic analysis of the Pleasing Fungus Beetles
  (Coleoptera: Erotylidae): evolution of color patterns,
  gregariousness and mycophagy
JOURNAL
  Syst. Entomol. 29 (2), 173-187 (2004)
REFERENCE
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  Robertson, J.A., McHugh, J.V. and Whiting, M.F.
  Direct Submission
AUTHORS
  Robertson, J.A., McHugh, J.V. and Whiting, M.F.
JOURNAL
  Submitted (02-JUN-2003) Integrative Biology, Brigham Young
  University, 401 WIDB, Provo, UT 84602, USA
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REFERENCE   1 (bases 1 to 2175)
            Robertson,J.A., McHugh,J.V. and Whiting,M.F.
            A molecular phylogenetic analysis of the Pleasing Fungus Beetles
            (Coleoptera: Erotylidae): evolution of color patterns,
            gregariousness and mycophagy
            Syst. Entomol. 29 (2), 173-187 (2004)
REFERENCE   2 (bases 1 to 2175)
            Robertson,J.A., McHugh,J.V. and Whiting,M.F.
            Direct Submission
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

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Ygapop 10.0 , Ygapext 0.5  
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Post-processing: Minimum Match 0%  
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Listing first 150 summaries

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2: Geneseqn1990s:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 5    | 191  | 100.0 | 2491   | 3  | Aaz50636  |
| 6    | 191  | 100.0 | 2991   | 8  | Abx09932  |
| 7    | 190  | 99.5  | 2992   | 2  | Aat67285  |
| 8    | 168  | 88.0  | 2990   | 2  | Aav66832  |
| 9    | 74   | 38.7  | 1531   | 11 | ACL26080  |
| C 10 | 71   | 37.2  | 1569   | 13 | AD860020  |
| C 11 | 69.5 | 36.4  | 1013   | 11 | ACN91862  |
| C 12 | 68   | 35.6  | 249    | 6  | ABQ90655  |
| C 13 | 68   | 35.6  | 507    | 6  | ABQ91048  |
| C 14 | 67.5 | 35.3  | 2000   | 8  | ADA71676  |
| C 15 | 67   | 35.1  | 778    | 6  | ABQ28522  |
| C 16 | 67   | 35.1  | 778    | 6  | ABQ28523  |
| C 17 | 67   | 35.1  | 1971   | 13 | AD082611  |
| C 18 | 66.5 | 34.8  | 957    | 11 | ADJ11765  |
| C 19 | 66.5 | 34.8  | 960    | 11 | ADJ11419  |
| C 20 | 66.5 | 34.8  | 1011   | 11 | ADJ11653  |
| C 21 | 66.5 | 34.8  | 1012   | 13 | ADT18986  |
| C 22 | 66.5 | 34.8  | 1284   | 14 | ABE67003  |
| C 23 | 66.5 | 34.8  | 6297   | 10 | AAD54236  |
| C 24 | 66.5 | 34.8  | 50543  | 10 | AAD54230  |
| C 25 | 66   | 34.6  | 1437   | 10 | ADF50282  |
| C 26 | 65.5 | 34.3  | 365    | 6  | AAD42748  |
| C 27 | 65.5 | 34.3  | 365    | 9  | ACA05145  |
| C 28 | 65.5 | 34.3  | 365    | 14 | ABE11213  |
| C 29 | 65.5 | 34.3  | 365    | 14 | ABE48334  |
| C 30 | 65.5 | 34.3  | 815    | 13 | ADX33610  |
| C 31 | 65   | 34.0  | 702    | 5  | ABL57895  |
| C 32 | 65   | 34.0  | 1035   | 2  | AAT49316  |
| C 33 | 65   | 34.0  | 1035   | 2  | AAV36430  |
| C 34 | 65   | 34.0  | 1035   | 2  | AAV39975  |
| C 35 | 65   | 34.0  | 1035   | 2  | AAV54609  |
| C 36 | 65   | 34.0  | 1035   | 2  | AAV83991  |
| C 37 | 65   | 34.0  | 1035   | 3  | AAAD00674 |
| C 38 | 65   | 34.0  | 1035   | 3  | AAA14944  |
| C 39 | 65   | 34.0  | 1035   | 4  | AAAD12808 |
| C 40 | 65   | 34.0  | 1035   | 6  | AAAL41136 |
| C 41 | 65   | 34.0  | 1035   | 6  | AAAD29128 |
| C 42 | 65   | 34.0  | 1035   | 6  | AAAD27021 |
| C 43 | 65   | 34.0  | 1035   | 6  | ABLS1714  |
| C 44 | 65   | 34.0  | 1035   | 13 | ADQ82191  |
| C 45 | 65   | 34.0  | 198849 | 14 | ADZ13007  |
| C 46 | 64.5 | 33.8  | 400    | 8  | ACC58118  |
| C 47 | 64.5 | 33.8  | 1973   | 8  | ACC58114  |
| C 48 | 64.5 | 33.8  | 2073   | 8  | ACC58112  |
| C 49 | 64.5 | 33.8  | 2502   | 14 | ACL68217  |
| C 50 | 64.5 | 33.8  | 3554   | 8  | ACC58113  |
| C 51 | 64.5 | 33.8  | 3854   | 8  | ACC58111  |
| C 52 | 64.5 | 33.8  | 3811   | 6  | AAAD28061 |
| C 53 | 64.5 | 33.8  | 24754  | 14 | ACL64767  |
| C 54 | 64.5 | 33.8  | 76994  | 12 | ADP64454  |
| C 55 | 64   | 33.5  | 36063  | 10 | ADB74391  |
| C 56 | 64   | 33.5  | 174155 | 14 | AEA07466  |
| C 57 | 63.5 | 33.2  | 2530   | 14 | AEA47619  |
| C 58 | 63.5 | 33.2  | 5710   | 4  | ABLI8813  |
| C 59 | 63.5 | 33.2  | 5922   | 4  | ABLI8812  |
| C 60 | 63.5 | 33.2  | 24379  | 2  | AAT93095  |
| C 61 | 63.5 | 33.2  | 24379  | 2  | AAV25925  |
| C 62 | 63.5 | 33.2  | 69300  | 6  | AAAD38804 |
| C 63 | 63   | 33.0  | 829    | 13 | ADX36796  |
| C 64 | 63   | 33.0  | 846    | 13 | ADU58501  |
| C 65 | 63   | 33.0  | 1338   | 13 | ADT43083  |
| C 66 | 63   | 33.0  | 2904   | 3  | AAAC76178 |
| C 67 | 63   | 33.0  | 8705   | 5  | ABA82624  |
| C 68 | 63   | 33.0  | 8705   | 8  | ACC45365  |
| C 69 | 63   | 33.0  | 8705   | 10 | ADB98065  |
| C 70 | 63   | 33.0  | 8705   | 10 | ADB82434  |
| C 71 | 63   | 33.0  | 8705   | 13 | ADR16928  |
| C 72 | 63   | 33.0  | 8705   | 13 | ADR47579  |
| C 73 | 63   | 33.0  | 8705   | 14 | ABE69308  |
| C 74 | 63   | 33.0  | 36305  | 6  | ABR32783  |
| C 75 | 63   | 33.0  | 156843 | 11 | ACN44786  |
| C 76 | 62.5 | 32.7  | 909    | 11 | ABD04642  |
| C 77 | 62.5 | 32.7  | 1197   | 14 | ACL70309  |

|   |     |      |      |       |    |          |                     |
|---|-----|------|------|-------|----|----------|---------------------|
| c | 78  | 62.5 | 32.7 | 1995  | 11 | ABD04718 | Abd04718 Pseudomon  |
|   | 79  | 62.5 | 32.7 | 4607  | 6  | ABK46540 | Abk46540 DNA encod  |
|   | 80  | 62.5 | 32.7 | 4801  | 10 | ADD78275 | Add78275 Human CGD  |
|   | 81  | 62.5 | 32.7 | 4884  | 9  | AAD57243 | Aad57243 Human CGD  |
|   | 82  | 62.5 | 32.7 | 4933  | 8  | ACD13338 | Acd13338 Human DNA  |
|   | 83  | 62.5 | 32.7 | 5079  | 9  | AAD57244 | Aad57244 Human CGD  |
|   | 84  | 62.5 | 32.7 | 5139  | 10 | ABV72514 | Abv72514 Nucleotid  |
|   | 85  | 62.5 | 32.7 | 5153  | 12 | ADO34015 | Ado34015 Human WBC  |
|   | 86  | 62.5 | 32.7 | 9501  | 4  | AAS59550 | Aas59550 Propionib  |
|   | 87  | 62.5 | 32.7 | 9501  | 8  | ACF64479 | Acf64479 Propionib  |
|   | 88  | 62.5 | 32.7 | 15271 | 14 | ACL64588 | ACL64588 M. xanthu  |
|   | 89  | 62   | 32.5 | 894   | 11 | ABD13132 | Abd13132 Pseudomon  |
|   | 90  | 62   | 32.5 | 894   | 11 | ABD12900 | Abd12900 Pseudomon  |
|   | 91  | 62   | 32.5 | 1035  | 13 | ADT42241 | Adt42241 Bacterial  |
|   | 92  | 62   | 32.5 | 1035  | 14 | ACL70343 | ACL70343 M. xanthu  |
|   | 93  | 62   | 32.5 | 1482  | 13 | ADT18764 | Adt18764 Plant CDN  |
|   | 94  | 62   | 32.5 | 1560  | 10 | ADC08230 | Adc08230 Rice DNA   |
|   | 95  | 62   | 32.5 | 1560  | 10 | ADC07849 | Adc07849 Rice DNA   |
|   | 96  | 62   | 32.5 | 2000  | 8  | ADA71962 | Ada71962 Rice gene  |
|   | 97  | 62   | 32.5 | 3112  | 4  | AAS06753 | Aas06753 Polynucle  |
|   | 98  | 62   | 32.5 | 3112  | 6  | AAD30563 | Aad30563 Human kin  |
|   | 99  | 62   | 32.5 | 3261  | 12 | ADH41718 | Adh41718 Novel hum  |
|   | 100 | 62   | 32.5 | 3694  | 2  | AAQ36930 | Aaq36930 Human KA-  |
|   | 101 | 62   | 32.5 | 4800  | 14 | ACL64099 | ACL64099 M. xanthu  |
|   | 102 | 62   | 32.5 | 16671 | 8  | ABQ76670 | Abq76670 Androgen   |
|   | 103 | 62   | 32.5 | 54000 | 8  | AAD52261 | Aad52261 Human int  |
|   | 104 | 62   | 32.5 | 54000 | 14 | ABE44785 | Aeb44785 Human int  |
|   | 105 | 62   | 32.5 | 79467 | 9  | ADA02717 | Ada02717 Mouse Nfa  |
|   | 106 | 62   | 32.5 | 79467 | 10 | ADB72455 | Adb72455 Mouse Nfa  |
|   | 107 | 62   | 32.5 | 79467 | 10 | ADE95965 | Ade95965 Mouse Nfa  |
|   | 108 | 61.5 | 32.2 | 1164  | 8  | ACA37786 | Aca37786 Prokaryot  |
|   | 109 | 61.5 | 32.2 | 1224  | 13 | ADX47573 | Adx47573 Plant ful  |
|   | 110 | 61.5 | 32.2 | 1255  | 8  | ABS58052 | Abs58052 Gene enco  |
|   | 111 | 61.5 | 32.2 | 1255  | 14 | ADW72705 | Adw72705 Rhodobact  |
|   | 112 | 61.5 | 32.2 | 1348  | 8  | ACC00853 | Acc00853 Oryza sat  |
|   | 113 | 61.5 | 32.2 | 1356  | 11 | ADA70921 | Ada70921 Rice gene  |
|   | 114 | 61.5 | 32.2 | 1356  | 11 | ACL26756 | ACL26756 Rice abio  |
|   | 115 | 61.5 | 32.2 | 2397  | 12 | ADM99263 | Adm99263 Environme  |
|   | 116 | 61.5 | 32.2 | 2742  | 8  | AAI61191 | Aai61191 Actinosyn  |
|   | 117 | 61.5 | 32.2 | 75839 | 11 | ACN43958 | Acn43958 Human gen  |
|   | 118 | 61.5 | 32.2 | 82746 | 8  | AAU61224 | Aau61224 Actinosyn  |
|   | 119 | 61   | 31.9 | 453   | 9  | ACH35388 | Ach35388 Human end  |
|   | 120 | 61   | 31.9 | 472   | 9  | ACH33745 | Ach33745 Human end  |
|   | 121 | 61   | 31.9 | 573   | 11 | ABD05682 | Abd05682 Pseudomon  |
|   | 122 | 61   | 31.9 | 609   | 12 | ADJ43098 | Adj43098 Plant CDN  |
|   | 123 | 61   | 31.9 | 1173  | 4  | ABJ29397 | Abj29397 Drosophil  |
|   | 124 | 61   | 31.9 | 1375  | 13 | ADX48635 | Adx48635 Plant ful  |
|   | 125 | 61   | 31.9 | 1785  | 4  | AAI20590 | Aai20590 Probe #10  |
|   | 126 | 61   | 31.9 | 1785  | 4  | ABA65633 | Abaa65633 Human foe |
|   | 127 | 61   | 31.9 | 1785  | 4  | AAI45799 | Aai45799 Probe #14  |
|   | 128 | 61   | 31.9 | 1785  | 4  | ABA47739 | Abaa47739 Human bre |
|   | 129 | 61   | 31.9 | 1785  | 4  | ABA32720 | Abaa32720 Probe #11 |
|   | 130 | 61   | 31.9 | 1785  | 4  | AAK39782 | Aak39782 Human bon  |
|   | 131 | 61   | 31.9 | 1785  | 4  | AAK14036 | Aak14036 Human bon  |
|   | 132 | 61   | 31.9 | 1785  | 4  | ABS39370 | Abs39370 Human liv  |
|   | 133 | 61   | 31.9 | 1785  | 5  | AAI06289 | Aai06289 Probe #62  |
|   | 134 | 61   | 31.9 | 1785  | 6  | ABS13877 | Abel13877 Human gen |
|   | 135 | 61   | 31.9 | 1967  | 13 | ADT18819 | Adt18819 Plant CDN  |
|   | 136 | 61   | 31.9 | 2133  | 8  | ACA37962 | Acta37962 Prokaryot |
|   | 137 | 61   | 31.9 | 2428  | 6  | ABK34868 | Abk34868 Human CDN  |
|   | 138 | 61   | 31.9 | 2673  | 6  | ABV72118 | Abv72118 Nucleotid  |
|   | 139 | 61   | 31.9 | 3356  | 4  | ABL29396 | Abi29396 Drosophil  |
|   | 140 | 61   | 31.9 | 3628  | 3  | AAZ88923 | Aaz88923 Human wml  |
|   | 141 | 61   | 31.9 | 3640  | 10 | ADP63183 | Adp63183 Human WPS  |
|   | 142 | 61   | 31.9 | 3640  | 13 | ADR25366 | Adr25366 Breast ca  |
|   | 143 | 61   | 31.9 | 3640  | 14 | ADZ67421 | Adz67421 Different  |
|   | 144 | 61   | 31.9 | 3673  | 3  | AAA08994 | Aaa08994 Human WPS  |
|   | 145 | 61   | 31.9 | 3686  | 3  | AAA08993 | Aaa08993 Human WPS  |
|   | 146 | 61   | 31.9 | 3688  | 3  | AAA09002 | Aaa09002 Human WPS  |
|   | 147 | 61   | 31.9 | 3688  | 3  | AAA08998 | Aaa08998 Human WPS  |
|   | 148 | 61   | 31.9 | 3688  | 3  | AAA09004 | Aaa09004 Human WPS  |
|   | 149 | 61   | 31.9 | 3688  | 3  | AAA08997 | Aaa08997 Human WPS  |
|   | 150 | 61   | 31.9 | 3688  | 3  | AAA09003 | Aaa09003 Human WPS  |

ALIGNMENTS

RESULT 1

AAV70963

ID AAV70963 standard; DNA; 153 BP.

XX

AC AAV70963;

XX

DT 23-AUG-1999 (first entry)

XX

DE DNA encoding transit peptide of maize starch soluble synthase I.

XX

KW Non-glycogen-like polysaccharide production; fermentation; starch synthesis enzyme; glycogen-synthase enzyme; glycogen synthesis; non-starch branching gene; amylopectin; amylose; plant-like starch; maize starch soluble synthase I; transit peptide; ss.

XX

OS Zea mays.

XX

PN WO9844780-A1.

XX

PD 15-OCT-1998.

XX

PF 03-APR-1998; 98WO-US006660.

XX

PR 04-APR-1997; 97US-0042939P.

XX

PA (EXSE-) EXSEED GENETICS LLC.

XX

PI Guan H, Keeling PL;

XX

DR WPI; 1998-568285/48.

XX

DR P-PSDB; AAW70897.

XX

PT Producing non-glycogen-like polysaccharides in bacteria, fungi or plants - transformed with genes for enzymes involved in starch or glycogen synthesis allows fermentative production of starches with engineered properties.

XX

PS Disclosure; Fig 55; 150pp; English.

XX

CC The specification describes a method for the production of non-glycogen-like polysaccharides in a host. The method comprises transforming a host, suitable for fermentation, with genes encoding starch- or glycogen-synthase enzymes, and fermenting the transformants. The specification also describes hosts transformed with a gene active in glycogen synthesis and at least one non-starch branching gene, involved in production of amylopectin or amylose in its original host. The method is used to produce plant-like starches by fermentation and new starches in plants. These starches are useful for all food and non-food applications of starch. The present sequence is used in the course of the invention

XX

SQ Sequence 153 BP; 10 A; 62 C; 64 G; 17 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

3.93e-15

191.00

97.4%

97.4%

100.0%

2

153

38

0

1

0

0

US-10-628-525A-37 (1-39) x AAV70963 (1-153)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20

DB 1 ATGGCGAGCGCTCGCGCGTGGCGCGCGGTCCTCTCTCGCGGGGCCCTGGCGG 60

QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39

DB 61 GCCGCGTGGCGAGCGCGCGCGCGCGCGGCTCCAGCGCGTGTGTCGCGCGCGG 117

```
RESULT 2
AAZ50642
ID AAZ50642 standard; cDNA; 1415 BP.
XX AC
XX AAZ50642;
XX DT
XX 23-MAY-2000 (first entry)
XX DE
XX Corn soluble starch synthase gene fragment inserted in pSS64-C5.
XX KW
XX Soluble starch synthase; starch fine structure; corn; transgenic plant;
XX amylose; amylopectin; amylose polymerisation;
XX non-granule bound starch synthase; non-GBSSI; altered starch; food;
XX paper; plastic; adhesive; ss.
XX OS
XX Zea mays.
XX PN
XX WO200006755-A2.
XX PD
XX 10-FEB-2000.
XX PF
XX 26-JUL-1999; 99WO-US016296.
XX PR
XX 28-JUL-1998; 98US-0094436P.
XX PA
XX (DUPO ) DU PONT DE NEMOURS & CO B I.
XX PI
XX Broglie KE, Lightner JE;
XX DR
XX WPI; 2000-195311/17.
XX PT
XX Producing transgenic cereal crops with altered starch structure useful
XX for preparing foodstuff, paper, plastic or adhesives, comprises
XX transforming crops with chimeric sense or antisense gene construct
XX encoding starch synthase.
XX PS
XX Claim 5; Page 52-53; 56pp; English.
XX CC
XX The present sequence is the corn soluble starch synthase (SSI) DNA
XX sequence comprising the SSI coding region of amino acids 1-494 inserted
XX into plasmid pSS64-C5. The chimeric gene containing the zein promoter
XX followed by the SSI gene fragment is used as a sense construct for
XX preparation of transgenic corn expressing altered starch structure. The
XX starch fine structure derived from a grain of the cereal crop can be
XX altered in the transformed cereal crop by changes in amylose to
XX amylopectin ratio, amylopectin fine structure, increased abundance of
XX very short amylopectin chains and in the degree of polymerisation of
XX amylose. These modifications can be created by controlling the expression
XX of non-GBSSI (non-granule bound starch synthase) in transgenic plants.
XX Altered starches are useful in foods, paper, plastics or adhesives
XX SQ
XX Sequence 1415 BP; 317 A; 335 C; 397 G; 366 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.92e-14 Length: 1415
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-628-525A-37 (1-39) x AAZ50642 (1-1415)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTPPro 20
DB 2 ATGGCGACGCCCTCGCGCGGCGCGCGCTCTCTCTCTCGCGCGCGCGCTCGCGCG 61
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
DB 62 GCCGCGTGGCGGACCGCGCGCGCGCGCTCCAGCGCGTGTGCGCGCGCGG 118

RESULT 3
AAZ50643
ID AAZ50643 standard; cDNA; 2008 BP.
XX AC
XX AAZ50643;
XX DT
XX 23-MAY-2000 (first entry)
XX DE
XX Corn soluble starch synthase gene fragment inserted in pSS65-C11.
XX KW
XX Soluble starch synthase; starch fine structure; corn; transgenic plant;
XX amylose; amylopectin; amylose polymerisation;
XX non-granule bound starch synthase; non-GBSSI; altered starch; food;
XX paper; plastic; adhesive; ss.
XX OS
XX Zea mays.
XX PN
XX WO200006755-A2.
XX PD
XX 10-FEB-2000.
XX PF
XX 26-JUL-1999; 99WO-US016296.
XX PR
XX 28-JUL-1998; 98US-0094436P.
XX PA
XX (DUPO ) DU PONT DE NEMOURS & CO B I.
XX PI
XX Broglie KE, Lightner JE;
XX DR
XX WPI; 2000-195311/17.
XX PT
XX Producing transgenic cereal crops with altered starch structure useful
XX for preparing foodstuff, paper, plastic or adhesives, comprises
XX transforming crops with chimeric sense or antisense gene construct
XX encoding starch synthase.
XX PS
XX Claim 5; Page 53; 56pp; English.
XX CC
XX The present sequence is the corn soluble starch synthase (SSI) DNA
XX sequence comprising the entire SSI coding region and a 3' UTR fragment
XX inserted into plasmid pSS65-C11. The chimeric gene containing the zein
XX promoter followed by the 3'UTR is used as a sense construct for
XX preparation of transgenic corn expressing altered starch structure. The
XX starch fine structure derived from a grain of the cereal crop can be
XX altered in the transformed cereal crop by changes in amylose to
XX amylopectin ratio, amylopectin fine structure, increased abundance of
XX very short amylopectin chains and in the degree of polymerisation of
XX amylose. These modifications can be created by controlling the expression
XX of non-GBSSI (non-granule bound starch synthase) in transgenic plants.
XX Altered starches are useful in foods, paper, plastics or adhesives
XX SQ
XX Sequence 2008 BP; 486 A; 463 C; 543 G; 516 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7.32e-14 Length: 2008
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-628-525A-37 (1-39) x AAZ50643 (1-2008)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTPPro 20
DB 2 ATGGCGACGCCCTCGCGCGGCGCGCGCTCTCTCTCTCGCGCGCGCGCTCGCGCG 61
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
DB 62 GCCGCGTGGCGGACCGCGCGCGCGCGCTCCAGCGCGTGTGCGCGCGCGG 118

RESULT 4
AAT95785
ID AAT95785 standard; cDNA to mRNA; 2383 BP.
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XX US5824790-A.
PN
XX
PD
XX
PD
XX
PF 15-DEC-1995; 95US-00572951.
XX
XX 21-JUN-1994; 94US-00263921.
PR
PR 29-NOV-1994; 94US-00346602.
XX
XX (ZENE ) ZENECA LTD.
PA
XX Guan H, Keeling PL, Knight ME;
PI
XX
XX WPI; 1998-582626/49.
DR
XX
XX Isolated nucleic acid molecule, used to produce transgenic plants -
PT comprises nucleotide sequence encoding polypeptide having soluble starch
PT synthase activity, where polypeptide is encoded by maize gene.
XX
XX Claim 1; Col 25-28; 29pp; English.
PS
XX The present sequence represents an isolated nucleic acid molecule which
CC has been isolated and comprises a nucleotide sequence encoding a
CC polypeptide having soluble starch synthase (SSS) activity, where the
CC polypeptide is encoded by a maize gene. The isolated nucleic acid
CC molecule can be used to produce transgenic plants with altered starch
CC production. The transgenic plants produced using the nucleic acid
CC molecule have an enhanced ability to produce structurally-altered starch
XX
SQ Sequence 2990 BP; 758 A; 655 C; 801 G; 776 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8e-11 Length: 2990
Score: 188.00 Matches: 38
Percent Similarity: 97.4% Conservativeness: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 88.0% Indels: 1
DB: 2 Gaps: 0

US-10-628-525A-37 (1-39) x AAV66832 (1-2990)
QY 1 MetaLThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpPro 20
Db 602 ATGGCGAGCCCTCGCGCGTGGCGCGCGTGCCTCTCTCGCGGCG-CCCTGGCGG 660
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
Db 661 GCCGCGTCTCGCGAGCCGCGCGCGCGCGCGAGGCTCCAGCGGTGTGTGCGCGCGG 717

RESULT 9
ACL26080
ID ACL26080 standard; cDNA; 1531 BP.
XX
AC ACL26080;
XX
DT 02-JUN-2005 (first entry)
XX
DE Rice abiotic stress responsive polynucleotide SEQ ID NO:36.
XX
KW ss; abiotic stress tolerance; transgenic plant; plant; cereal;
KW agriculture.
XX
OS Oryza sativa.
XX
XX WO2003008540-A2.
PN
XX
XX 30-JAN-2003.
PD
XX
XX 21-JUN-2002; 2002WO-US019668.
PF
XX
XX 22-JUN-2001; 2001US-0300112P.
PR
PR 24-AUG-2001; 2001US-0314662P.
XX
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PR 26-SEP-2001; 2001US-0325277P.
PR 21-NOV-2001; 2001US-0332132P.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA
XX
XX Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;
XX
XX WPI; 2003-248011/24.
DR
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
XX Claim 1; SEQ ID NO 36; 89pp; English.
PS
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
SQ Sequence 1531 BP; 181 A; 523 C; 543 G; 279 T; 0 U; 5 Other;

Alignment Scores:
Pred. No.: 15.4 Length: 1531
Score: 74.00 Matches: 15
Percent Similarity: 65.5% Conservativeness: 4
Best Local Similarity: 51.7% Mismatches: 10
Query Match: 38.7% Indels: 0
DB: 11 Gaps: 0

US-10-628-525A-37 (1-39) x ACL26080 (1-1531)
QY 3 ThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg**AlaTrpProAlaAla 22
Db 386 ACCGCGACGCGGTGAACGTGCGCATGTCTATCGTGGCGCATGCTCTCGGGTTCGGCG 445
QY 23 ValGlyAspArgAlaArgProArgArg 31
Db 446 TCGGGTTCAAGAACACGCGCGCGCGC 472

RESULT 10
ADS60020/c
ID ADS60020 standard; cDNA; 1569 BP.
XX
AC ADS60020;
XX
DT 02-DEC-2004 (first entry)
XX
XX Bacterial polynucleotide #12007.
DE
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.
XX
XX Bacteria.
OS
XX
XX US2003233675-A1.
PN
XX
```

PD 18-DEC-2003.  
 XX  
 PF 20-FEB-2003; 2003US-00369493.  
 XX  
 PR 21-FEB-2002; 2002US-0360039P.  
 XX  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 XX  
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
 XX WPI; 2004-061375/06.  
 DR  
 XX  
 PT New recombinant DNA construct comprising a promoter positioned to provide  
 PT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.  
 XX  
 XX Claim 1; SEQ ID NO 35694; 122pp; English.  
 PS  
 XX The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition. Improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polynucleotide used in  
 CC the scope of the invention. Note: The sequence data for this patent did  
 CC not form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 1569 BP; 290 A; 525 C; 474 G; 280 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 37.3 Length: 1569  
 Score: 71.00 Matches: 16  
 Percent Similarity: 56.8% Conservative: 5  
 Best Local Similarity: 43.2% Mismatches: 14  
 Query Match: 37.2% Indels: 2  
 DB: 13 Gaps: 1  
 US-10-628-525A-37 (1-39) x ADS60020 (1-1569)  
 QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaThrProAla 21  
 DB 134 AGCAGCCCTTCGGCGCGCAGCGCGTTCGGCATTCGGCGTCTTACCACGGGATGCGCGCA 75  
 QY 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 38  
 DB 74 GCC-----GACAGGCNAATCACCAGCGCCACTGCTCGCAGGTGATCAGGAGA 30  
 RESULT 11  
 ACN91862/c  
 ID ACN91862 standard; DNA; 1013 BP.  
 XX  
 AC ACN91862;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Breast cancer related marker, seq id 13012.  
 XX  
 KW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003099974-A1.  
 XX  
 PD 29-MAY-2003.  
 XX  
 PF 18-JUL-2002; 2002US-00198846.  
 XX  
 PR 18-JUL-2001; 2001US-0306220P.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Lillie J, Xu Y, Wang Y, Steinmann K;  
 XX WPI; 2003-787014/74.  
 DR  
 XX Novel isolated polypeptide associated with breast cancer, useful for  
 PT detecting presence of polypeptide in sample, as a marker for breast  
 PT cancer.  
 XX  
 PS Disclosure; SEQ ID NO 13012; 36pp; English.  
 XX  
 CC The invention relates to an isolated polypeptide (I) associated with a  
 CC breast cancer which is encoded by a nucleic acid molecule comprising a  
 CC nucleotide sequence (S1). Further disclosed is an antibody that binds to  
 CC the polypeptide of the invention. The activity of the polypeptide of the  
 CC invention may be described as cytostatic. The antibody is useful for  
 CC detecting the presence of (I) in a sample. Nucleic acid molecules of the  
 CC invention are useful in the detection of breast tumours. (I) is useful as  
 CC a marker for breast cancer and in breast cancer therapy. Sequences given  
 CC in records ACN78851-ACN9934 represent nucleic acid markers associated  
 CC with breast cancer. Note: The sequence listing does not form part of the  
 CC specification but may be obtained in electronic format from the USPTO web  
 CC site at seqdata.uspto.gov/sequence.html?DocID=20030099974  
 XX  
 SQ Sequence 1013 BP; 278 A; 285 C; 213 G; 208 T; 0 U; 29 Other;  
 Alignment Scores:  
 Pred. No.: 34.8 Length: 1013  
 Score: 69.50 Matches: 19  
 Percent Similarity: 58.5% Conservative: 5  
 Best Local Similarity: 46.3% Mismatches: 14  
 Query Match: 36.4% Indels: 3  
 DB: 11 Gaps: 1  
 US-10-628-525A-37 (1-39) x ACN91862 (1-1013)  
 QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg-----\*\*\* 17  
 DB 943 GTGCGCGCGCGCGCGTGTGTGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 884  
 QY 18 AlaThrProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 37  
 DB 883 TCTTGCCCGGGGCGCTGTGCTCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 824  
 QY 38 Arg 38  
 DB 823 CGC 821  
 RESULT 12  
 ABQ90655  
 ID ABQ90655 standard; DNA; 249 BP.  
 XX  
 AC ABQ90655;  
 XX  
 DT 01-OCT-2002 (first entry)  
 XX





PD 07-MAR-2002.  
XX  
PF 01-SEP-2001; 2001WO-EP010074.  
XX  
XX 01-SEP-2000; 2000DE-01043826.  
PR 05-SEP-2000; 2000DE-01044543.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K, Guetig D;  
XX WPI; 2002-371829/40.  
DR  
XX Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons  
PT from chemically treated DNA.  
XX  
PS Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX  
CC This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one member,  
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
CC degree of hybridisation to both classes is determined from the label on  
CC the amplicon. From the ratio of labels hybridised to the two classes of  
CC oligomers, the degree of methylation is calculated. The method is used:  
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
CC and of a wide range of diseases, e.g. cancer, disorders of the central  
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
CC particularly by detecting mutations or single nucleotide polymorphisms  
CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
CC investigating cell differentiation. The method allows the methylation  
CC status of many C residues to be determined simultaneously. ABQ13410-  
CC ABQ54121 represent genomic DNA sequences used to illustrate the method  
CC for determining the degree of cytosine methylation described in the  
CC disclosure of the invention  
XX  
SQ Sequence 778 BP; 210 A; 366 C; 114 G; 88 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: Length: 52.5 778  
Score: 67.00 Matches: 19  
Percent Similarity: 55.3% Conservative: 2  
Best Local Similarity: 50.0% Mismatches: 17  
Query Match: 35.1% Indels: 0  
DB: 6 Gaps:  
0  
  
US-10-628-525A-37 (1-39) x ABQ28523 (1-778)  
  
QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpProLa 21  
AD082611  
DB 469 GCGACACCGCGCGCCGACACACCGCGGTACAAACACACTCGCCCGGCTACCGCGCCGCA 528  
  
QY 22 AlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 39  
DB 529 CGCGCAGCGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 582  
  
RESULT 17  
AD082611  
ID AD082611 standard; cDNA; 1971 BP.  
XX  
AC AD082611;  
XX  
XX 21-APR-2005 (first entry)  
XX  
XX Plant full length insert polynucleotide seqid 1331.  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW Galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
XX protein content; gene; ss.  
OS Unidentified.  
XX  
XX US2004034888-A1.  
PN  
XX 19-FEB-2004.  
PD  
XX 28-APR-2003; 2003US-00425114.  
PF  
XX 06-MAY-1999; 99US-00304517.  
PR  
XX 05-NOV-2001; 2001US-00985678.  
XX  
XX (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
XX  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
DR  
XX New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
PS Claim 1; SEQ ID NO 1331; 15pp; English.  
XX  
CC The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
SQ Sequence 1971 BP; 370 A; 683 C; 591 G; 327 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: Length: 151 1971  
Score: 67.00 Matches: 22  
Percent Similarity: 51.1% Conservative: 1  
Best Local Similarity: 48.9% Mismatches: 10  
Query Match: 35.1% Indels: 12  
DB: 13 Gaps:  
2  
  
US-10-628-525A-37 (1-39) x AD082611 (1-1971)  
  
QY 6 AlaValGlyAlaAlaCysLeu-----LeuLeuAla 15  
DB 517 GCTGCAGCGCGTGTGCTGTCTTACCAGCTCTCCCTCGCGCGCTCGGCTCTCGGCTCGGCG 576  
  
QY 16 Arg\*\*\*AlaTrpProAlaAlaVal-----GlyAspArgAlaArgProArgLeuGln 33  
DB 577 CGCGCGCTGCCACCCACCGCTGTTCGGGCGAGAGGTCTCGAGTCTGCGCCCGCGCGCGCGCG 636

QY 34 ArgValLeuArgArg 38  
Db 637 CGGCATCGCGTGG 651  
RESULT 18  
ID ADJ11765/c  
XX ADJ11765 standard; DNA; 957 BP.  
AC ADJ11765;  
XX  
XX 20-MAY-2004 (first entry)  
DE Rice cDNA modulated by post-transcriptional gene silencing SeqID 401.  
XX  
XX rice; gene; ss; post-transcriptional gene silencing; PTGS; plant;  
KW trans-activation; cereal; plant-viral interaction.  
XX  
XX Oryza sp.  
XX  
XX US2003135888-A1.  
PN  
XX 17-JUL-2003.  
PD  
XX 26-SEP-2002; 2002US-00259165.  
PF  
XX 26-SEP-2001; 2001US-0325277P.  
PR 27-MAR-2002; 2002US-0368327P.  
PR 04-APR-2002; 2002US-0370620P.  
XX  
XX (ZHUT/) ZHU T.  
PA (WANG/) WANG X.  
PA (CHAN/) CHANG H.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (MOUG/) MOUGHAMER T.  
PA (PROV/) PROVART N.  
PA (RICK/) RICKES D.  
XX  
XX Zhu T, Wang X, Chang H, Briggs SP, Cooper B, Glazebrook J;  
PI Goff SA, Katagiri F, Kreps J, Moughamer T, Provart N, Ricke D;  
XX  
XX WPI; 2003-829655/77.  
DR P-PSDB; ADJ11766.  
XX  
XX New polynucleotide, useful for modulating gene expression within a cell  
PT by posttranscriptional gene silencing.  
XX  
XX Example 15; SEQ ID NO 401; 79pp; English.  
XX  
XX This invention relates to a novel method for identifying isolated  
CC polynucleotides that are modulated by post-transcriptional gene silencing  
CC (PTGS). Specifically, it refers to the regulation of gene expression in  
CC plants via PTGS and the trans-activation of homologous genes due to  
CC increased RNA degradation. The present invention describes clusters of  
CC polynucleotides from cereals, in particular rice, as well as homologues  
CC and the polypeptide sequences derived thereof, where gene expression is  
CC altered in response to PTGS. As such, the elucidation of gene silencing  
CC mechanisms can lead to more efficiently expressed transgenes, and can  
CC also improve the understanding of plant-viral interactions and targeting  
CC the suppression of specific plant genes. This polynucleotide sequence is  
CC a rice cDNA sequence where expression is modulated by gene silencing,  
CC given in an exemplification of the invention. NOTE: This sequence does  
CC not appear in the printed specification but has been obtained in  
CC electronic format from the US patent office at  
CC ftp.seqdata.uspto.gov/sequence.html?DocID=20030135888.  
XX  
XX Sequence 957 BP; 171 A; 295 C; 363 G; 128 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 76.5 Length: 957  
Score: 66.50 Matches: 17  
Percent Similarity: 50.0% Conservative: 1  
Best Local Similarity: 47.2% Mismatches: 13  
Query Match: 34.8% Indels: 5  
DB: 11 Gaps: 1  
US-10-628-525A-37 (1-39) x ADJ11765 (1-957)  
QY 3 ThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*AlaTTPProAlaAala 22  
Db 124 ACCGGACAGCTCTCCGGCTGCTGC-----GCCACTTGGCAGCGCCG 80  
QY 23 ValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 38  
Db 79 ACACCATCGCGCTGCTCCACGCCGAGCCACCGCCCTGAGAGG 32  
RESULT 19  
ADJ11419/c  
ID ADJ11419 standard; DNA; 960 BP.  
XX  
XX AC ADJ11419;  
XX  
XX DT 20-MAY-2004 (first entry)  
XX  
XX Rice DNA modulated by post-transcriptional gene silencing SeqID 55.  
DE  
XX rice; gene; ds; post-transcriptional gene silencing; PTGS; plant;  
KW trans-activation; cereal; plant-viral interaction.  
XX  
XX Oryza sp.  
XX  
XX US2003135888-A1.  
PD 17-JUL-2003.  
XX  
XX 26-SEP-2002; 2002US-00259165.  
XX  
XX 26-SEP-2001; 2001US-0325277P.  
PR 27-MAR-2002; 2002US-0368327P.  
PR 04-APR-2002; 2002US-0370620P.  
XX  
XX (ZHUT/) ZHU T.  
PA (WANG/) WANG X.  
PA (CHAN/) CHANG H.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (MOUG/) MOUGHAMER T.  
PA (PROV/) PROVART N.  
PA (RICK/) RICKES D.  
XX  
XX Zhu T, Wang X, Chang H, Briggs SP, Cooper B, Glazebrook J;  
PI Goff SA, Katagiri F, Kreps J, Moughamer T, Provart N, Ricke D;  
XX  
XX WPI; 2003-829655/77.  
DR P-PSDB; ADJ11420.  
XX  
XX New polynucleotide, useful for modulating gene expression within a cell  
PT by posttranscriptional gene silencing.  
XX  
XX Claim 1; SEQ ID NO 55; 79pp; English.  
XX  
XX This invention relates to a novel method for identifying isolated  
CC polynucleotides that are modulated by post-transcriptional gene silencing  
CC (PTGS). Specifically, it refers to the regulation of gene expression in  
CC plants via PTGS and the trans-activation of homologous genes due to  
CC increased RNA degradation. The present invention describes clusters of  
CC polynucleotides from cereals, in particular rice, as well as homologues





XX Kovalic DK;  
 XX WPI; 2004-757369/74.  
 XX New recombinant DNA constructs useful in the field of biochemistry and  
 XX genetics, and in particular for producing transgenic plants with improved  
 XX biological characteristics.  
 XX Claim 1; SEQ ID NO 4312; 14pp; English.  
 XX The invention relates a recombinant DNA construct comprising a  
 XX polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:  
 XX 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences  
 XX (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,  
 XX Arabidopsis, wheat and rape but the specification does not indicate which  
 XX producing a plant having an improved property. Also included is a method of  
 XX plant with a recombinant DNA construct comprising a promoter region  
 XX functional in a plant cell operably joined to a polynucleotide encoding a  
 XX polypeptide associated with the property, and growing the transformed  
 XX plant. The property is selected from improving plant cold tolerance, for  
 XX manipulating growth rate in plant cells by modification of the cell cycle  
 XX pathway, for improving plant drought tolerance, for providing increased  
 XX resistance to plant disease, for galactomannan production, for production  
 XX of plant growth regulators, for improving plant heat tolerance, for  
 XX improving plant tolerance to herbicides, for increasing the rate of  
 XX homologous recombination in plants, for lignin production, for improving  
 XX plant tolerance to extreme osmotic conditions, for improving plant  
 XX tolerance to pathogens or pests, for yield improvement by modification of  
 XX photosynthesis, for modifying seed oil yield and/or content, for  
 XX modifying seed protein yield and/or content, for yield improvement by  
 XX modification of carbohydrate, nitrogen or phosphorus use and/or uptake  
 XX and for yield improvement by providing improved plant growth and  
 XX development under at least one stress condition. The polynucleotide may  
 XX also encode a plant transcription factor. The methods and compositions of  
 XX the present invention are useful in the field of biochemistry and  
 XX genetics, in particular for producing transgenic plants with improved  
 XX biological characteristics such as increased yield, improved nitrogen  
 XX flow, increasing plant tolerance to cold or heat, improving plant  
 XX tolerance to extreme osmotic and drought conditions, and improving plant  
 XX tolerance to plant pests or pathogens. They can also be used in physical  
 XX arrays of molecules, plant breeding markers, computer-based storage and  
 XX analysis systems. The present sequence is one of the 5544 plant cDNA  
 XX sequences of the invention. Note: The sequence data for this patent did  
 XX not form part of the printed specification, but was obtained in  
 XX electronic format directly from USPTO at  
 XX seqdata.uspto.gov/sequence.html?DocID=20040216190.  
 XX  
 XX Sequence 1012 BP; 143 A; 340 C; 330 G; 199 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 81.5 Length: 1012  
 Score: 66.50 Matches: 19  
 Percent Similarity: 52.6% Conservative: 1  
 Best Local Similarity: 50.0% Mismatches: 17  
 Query Match: 34.8% Indels: 1  
 DB: 13 Gaps: 1  
 US-10-628-525A-37 (1-39) x ADT18986 (1-1012)  
 QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpProAla 21  
 DB 557 GCCGCGCCCTCGAGCGCTCTTGGGGGTGCGCGCGAGCGGCTCGACTCGAATCCAC 498  
 QY 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39  
 DB 497 GCAGCAGGCGACGCCG---CGCGCGCGCGGGGACGACGCGGACGCGCGGACGA 447  
 RESULT 22  
 ID AEB67003/C  
 ID AEB67003 standard; DNA; 1284 BP.  
 XX

AC AEB67003;  
 XX DT 22-SEP-2005 (first entry)  
 XX DE Rice genome derived DNA sequence, SEQ ID 2148.  
 XX KW transcription; gene regulation; transgenic plant; RNA interference;  
 XX transformation; antibody; ds.  
 XX OS Oryza sp.  
 XX PN JP2005185101-A.  
 XX PD 14-JUL-2005.  
 XX PF 11-DEC-2002; 2002JP-00383870.  
 XX PR 30-MAY-2002; 2002JP-00203269.  
 XX PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.  
 XX PA (SEIB-) SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU.  
 XX PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.  
 XX PA (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.  
 XX PI Kikuchi H, Hayashizaki Y, Otomo Y, Matsubara K, Murakami K;  
 PI Kishimoto N, Sato K, Nagata T, Kawakami N, Yazaki J, Ishikawa M;  
 PI Doi K, Kawai J;  
 XX WPI; 2005-566181/58.  
 XX Novel DNA encoding transcription factor, derived from rice plant, useful  
 XX for obtaining transcriptional-regulatory regions in plant and for  
 XX producing modified plant.  
 XX Claim 1; SEQ ID NO 2148; 2928pp; Japanese.  
 XX The invention relates to a novel DNA sequence encoding a transcription  
 XX factor derived from a plant. The invention further comprises antisense  
 XX RNA sequences, ribozyme activity RNA, RNAi sequences, a vector,  
 XX transformed plant cells, antibodies and proteins, all related to the  
 XX novel plant DNA sequences of the invention. The novel DNA is preferably  
 XX derived from a rice-genome database. The invention further provides a  
 XX method for determining the transcription regulatory regions of the rice  
 XX genome. The novel DNA is useful for controlling the expression of a gene  
 XX in a plant and for producing a modified plant with desired and different  
 XX characteristics. The plant DNA and method enables the acquisition of many  
 XX transcriptional-regulatory regions. This polynucleotide represents a DNA  
 XX sequence taken from a rice genome clone library for use in the invention.  
 XX Note: This sequence is not shown in the specification. It has been  
 XX retrieved from a sequence listing in electronic format from the Japanese  
 XX Patent Office. The invention claims DNA sequences of SEQ ID Nos 1 to  
 XX 28469 and encoded protein sequences of SEQ ID Nos 28470 to 56791.  
 XX However, the sequence listing only provided the DNA sequences of SEQ ID  
 XX Nos 1 to 3032.  
 XX  
 XX Sequence 1284 BP; 240 A; 375 C; 435 G; 234 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 107 Length: 1284  
 Score: 66.50 Matches: 17  
 Percent Similarity: 50.0% Conservative: 1  
 Best Local Similarity: 47.2% Mismatches: 13  
 Query Match: 34.8% Indels: 5  
 DB: 14 Gaps: 1  
 US-10-628-525A-37 (1-39) x AEB67003 (1-1284)  
 QY 3 ThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpProAla 22  
 DB 231 ACCCGACAGCTTCTCCGGCTGCTGC-----GCCACTTGGCCAGCGCG 187  
 QY 23 ValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 38

Db 186 ACACCATCGCGCTCGTCCACGCCGAGGCCACCGAGCCTGAGAGG 139

RESULT 23

AAD54236

ID AAD54236 standard; DNA; 6297 BP.

XX AAD54236;

DT 17-JUN-2003 (first entry)

DE Streptomyces amphibiae sp. nov. lactimidomycin ORF6 DNA.

KW Polyketide biosynthesis; dorrigin; DORR; lactimidomycin; LACT; gene;  
ds.

OS Streptomyces amphibiae sp. nov.

XX Key Location/Qualifiers

FT CDS 1..6297

FT /tag= a

FT /product= "LACT ORF6 protein"

XX WO200288176-A2.

XX 07-NOV-2002.

XX 26-APR-2002; 2002WO-CA000591.

XX 26-APR-2001; 2001US-0286346P.

XX (ECOP-) ECOPIA BIOSCIENCES INC.

PI Farnet CM, Zazopoulos E, Staffa A, Yang X;

XX WPI; 2003-201222/19.

DR P-PSDB; AAE35500.

XX Novel isolated or purified polypeptide involved in biosynthesis of  
PT polyketide dorrigin or polyketide lactimidomycin, useful for preparing  
PT dorrigin or lactimidomycin.

XX Claim 6; Page 301-304; 312pp; English.

XX The invention relates to novel proteins involved in the biosynthesis of  
CC polyketide dorrigin (DORR) or lactimidomycin (LACT) biosynthesis by  
CC microorganisms. Sequences of the invention allow direct manipulation of  
CC dorrigin, lactimidomycin and related chemical structures via chemical  
CC engineering of the enzymes involved in the biosynthesis of dorrigin and  
CC lactimidomycin. They are useful for introducing chemical handles into  
CC normally inert positions that permit subsequent chemical modifications  
CC and facilitate the development of polyketides. The genes and proteins of  
CC the invention can also be used to generate a focused library of analogues  
CC around a polyketide lead candidate to fine-tune the compound for optimal  
CC properties. They are useful for generating antibodies specific for the  
CC polyketide biosynthesis. The present sequence is S. amphibiae sp. nov.  
CC lactimidomycin ORF6 DNA

XX Sequence 6297 BP; 854 A; 2246 C; 2293 G; 904 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 650 Length: 6297  
Score: 66.50 Matches: 19  
Percent Similarity: 58.3% Conservative: 2  
Best Local Similarity: 52.8% Mismatches: 10  
Query Match: 34.8% Indels: 5  
DB: 10 Gaps: 2

US-10-628-525A-37 (1-39) x AAD54236 (1-6297)

Qy 4 ProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpProAlaVal 23

Db 2704 CCGAGCTGCCCGTGGCGGCTGTGGAGCTGGTCCGCGCGCTGGACCCACGCC--- 2760

Qy 24 GlyAspArgAla-----ArgProArgArgLeuGlnArgValLeu 36

Db 2761 ---GACCGTGGCGGCTGTGGAGCTGGTCCGCGCTGGACCGCTGCTG 2805

RESULT 24

AAD54230

ID AAD54230 standard; DNA; 50543 BP.

XX AAD54230;

DT 17-JUN-2003 (first entry)

DE Streptomyces amphibiae sp. nov. lactimidomycin DNA.

KW Polyketide biosynthesis; dorrigin; DORR; lactimidomycin; LACT; gene;  
ds.

OS Streptomyces amphibiae sp. nov.

XX Key Location/Qualifiers

FT CDS 1..1698

FT /tag= a

FT /product= "LACT ORF1 protein"

FT /note= "No start codon"

FT /partial

FT 1908..2162

FT /tag= b

FT /product= "LACT ORF2 protein"

FT 2166..4136

FT /tag= c

FT /product= "LACT ORF3 protein"

FT /note= "No start codon"

FT /partial

FT 4152..14462

FT /tag= d

FT /product= "LACT ORF4 protein"

FT 14549..39631

FT /tag= e

FT /product= "LACT ORF5 protein"

FT /note= "No start codon"

FT /partial

FT 39628..45924

FT /tag= f

FT /product= "LACT ORF6 protein"

FT 45926..48232

FT /tag= g

FT /product= "LACT ORF7 protein"

FT 48441..49697

FT /tag= h

FT /product= "LACT ORF8 protein"

FT complement(49800..40543)

FT /tag= i

FT /product= "LACT ORF9 protein"

PN WO200288176-A2.

PD 07-NOV-2002.

XX 26-APR-2002; 2002WO-CA000591.

XX 26-APR-2001; 2001US-0286346P.

XX (ECOP-) ECOPIA BIOSCIENCES INC.

PI Farnet CM, Zazopoulos E, Staffa A, Yang X;

XX WPI; 2003-201222/19.

DR P-PSDB; AAE35496; AAE35501; AAE35502; AAE35503; AAE34595; AAE34597;

DR AAE34598; AAE34599; AAE34500.

XX Novel isolated or purified polypeptide involved in biosynthesis of  
PT polyketide dorrigin or polyketide lactimidomycin, useful for preparing  
PT dorrigin or lactimidomycin.

**Claim 1;** Page 201-229; 312pp; English.

The invention relates to novel proteins involved in the biosynthesis of polyketide dorriginocin (DOKR) or lactimidomycin (LACT) biosynthesis by microorganisms. Sequences of the invention allow direct manipulation of dorriginocin, lactimidomycin and related chemical structures via chemical engineering of the enzymes involved in the biosynthesis of dorriginocin and lactimidomycin. They are useful for introducing chemical handles into normally inert positions that permit subsequent chemical modifications and facilitate the development of polyketides. The genes and proteins of the invention can also be used to generate a focused library of analogues around a polyketide lead candidate to fine-tune the compound for optimal properties. They are useful for generating antibodies specific for optimal polyketide biosynthesis. The present sequence is *S. amphibia*sporus CC lactimidomycin DNA  
XX  
SQ Sequence 50543 BP; 6619 A; 18841 C; 18399 G; 6684 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.:                6.92e+03                Length:                50543  
Score:                  66.50                 Matches:              19  
Percent Similarity:    58.3%              Conservative:        2  
Best Local Similarity: 52.8%              Mismatches:        10  
Query Match:           34.8%              Indels:             5  
DB:                     10                 Gaps:                2

US-10-628-525A-37 (1-39) x AAD54230 (1-50543)

QY                4 ProSerAlaValGlyAlalaCysLeuLeuAlaArg\*\*\*AlaTrpProAlaAlaVal 23  
Db                42331 CCAGCCCTGCCGGTGTCCGCCTGTCTGGAGCTGTTCGCGCGCTGGACCCACGCC--- 42387  
QY                24 GlyAspArgAla-----ArgProArgArgLeuGlnArgValLeu 36  
Db                42388 ---GACC GTGCCCCCAGCACCGCCCCGCTCGCGCTGCGCGAGTGCTG 42432

RESULT 25  
ADF50282  
ID    ADF50282 standard; DNA; 1437 BP.  
XX  
AC    ADF50282;  
XX  
DT    12-FEB-2004 (first entry)  
XX  
Human PFM9 genomic DNA, a PR/SET family member.  
human; PFM9; ds; gene; chromosome 9q33-34.1; SET;  
Su(Var)3-9, Enhancer-of-Zeste and Trithorax; cancer; PFM/SET;  
tumour suppressor; hyperproliferative disorder; scleroderma; arthritis;  
alcoholic liver cirrhosis; hypertrophic scarring; atherosclerosis;  
gene therapy; Duchenne's muscular dystrophy;  
insulin-dependent diabetes mellitus; Huntington's; Parkinson's;  
Alzheimer's disease; paralysis; cerebellar atrophy; cytostatic;  
neuroprotective; nootropic; antiarthritic; vulnary;  
antiatherosclerotic; antidiabetic; hepatotrophic; PFM; PR family member.  
Homo sapiens.  
XX  
Key Location/Qualifiers  
CDS    61..1164  
FT    /tag= a  
FT    /product= "PFM9 protein"  
XX  
US2003049623-A1.  
XX  
PD    13-MAR-2003.  
XX  
PR    18-JUL-2001; 200IUS-00910478.  
XX  
PR    18-JUL-2001; 200IUS-00910478.  
XX  
PA    (HUAN/) HUANG S.



```

Db      132 GCATCACCAAAATCTTCAGTTCTGCTGT-----GGGCGATATAGTTGGCCAAGT 82
Qy      22 AlaValGlyAspArgAlaAa-gProArgArgLeuGlnArg-----ValLeuArgArgArg 39
Db      81 GCAACAGGGGTGCTGCTCTCTCTCGTGAAGCAAGCGAGTGTCTGTGTCGTGTCAGAGA 22
RESULT 28
AEB11213/c
ID      AEB11213 standard; cDNA; 365 BP.
AC      AEB11213;
XX
XX
DT      25-AUG-2005 (first entry)
DE      Maize GGPP synthase coding sequence, SEQ ID 9.
XX
XX      Plant; transgenic plant; plant breeding;
KW      geranylgeranyl pyrophosphate synthase; gene; ss.
XX
XX      Zea mays.
XX
XX      Key Location/Qualifiers
FH      3. .116
CDS      /*tag= a
FT      /partial
FT      /product= "GGPP synthase"
FT      /note= "No start codon given"
XX
XX      US2005120407-A1.
XX
XX      02-JUN-2005.
XX
XX      10-JAN-2005; 2005US-00032643.
XX
XX      02-DEC-1998; 98US-0110592P.
XX      01-DEC-1999; 99US-00452238.
XX
XX      (CAHO/) CAHOON R E.
PA      (SHEN/) SHEN J B.
PA      (WILL/) WILLIAMS M E.
XX
XX      Cahoon RE, Shen JB, Williams ME;
XX
XX      WPI; 2005-504028/51.
DR      P-PSDB; AEB11214.
XX
XX      Novel polynucleotide encoding polypeptide having geranylgeranyl
PT      pyrophosphate synthase activity, useful for producing transgenic plant
PT      and useful as probes for genetically and physically mapping genes
PT      encoding above enzyme.
XX
XX      Disclosure; SEQ ID NO 9; 51pp; English.
XX
XX      The present invention relates to novel plant geranylgeranyl pyrophosphate
CC      (GGPP) synthases and their coding sequences. GGPP synthase is also known
CC      as geranylgeranyl-diphosphate synthase, farnesyl transferase and
CC      geranylgeranyl synthetase, and is a key enzyme in plant terpenoid
CC      biosynthesis. The GGPP synthase coding sequences are useful for
CC      transforming a cell, producing a transgenic plant, as probes for
CC      genetically and physically mapping the genes encoding GGPP synthase, and
CC      as markers for traits linked to genes encoding GGPP synthase, which is
CC      useful in plant breeding in order to develop lines with desired
CC      phenotypes, and also useful as restriction fragment length polymorphism
CC      markers. The present sequence is one such GGPP synthase coding sequence.
XX
XX      Sequence 365 BP; 136 A; 62 C; 72 G; 95 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 34 Length: 365
Score: 65.50 Matches: 16
Percent Similarity: 57.5% Conservative: 7
Best Local Similarity: 40.0% Mismatches: 12

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Query Match: 34.3% Indels: 5
DB: 14 Gaps: 2
US-10-628-525A-37 (1-39) x AEB11213 (1-365)
Qy      2 AlaThPrSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAla 21
Db      132 GCATCACCAAAATCTTCAGTTCTGCTGT-----GGGCGATATAGTTGGCCAAGT 82
Qy      22 AlaValGlyAspArgAlaAa-gProArgArgLeuGlnArg-----ValLeuArgArgArg 39
Db      81 GCAACAGGGGTGCTGCTCTCTCTCGTGAAGCAAGCGAGTGTCTGTGTCGTGTCAGAGA 22
RESULT 29
AEB48334/c
ID      AEB48334 standard; cDNA; 365 BP.
XX
XX      AC AEB48334;
XX
XX      DT 22-SEP-2005 (first entry)
DE      Corn GGPP synthase FIS cDNA clone, SEQ ID NO: 9.
XX
XX      Transgenic plant; feedstuff; geranylgeranyl pyrophosphate synthase;
KW      geranylgeranyl-diphosphate synthase; farnesyl transferase;
KW      geranylgeranyl synthase; gene; ss.
XX
XX      Zea mays.
XX
XX      Key Location/Qualifiers
FH      3. .116
CDS      /*tag= a
FT      /product= "Corn GGPP synthase"
FT      /partial
FT      /note= "No start codon"
XX
XX      US2005160489-A1.
XX
XX      21-JUL-2005.
XX
XX      10-JAN-2005; 2005US-00032490.
XX
XX      02-DEC-1998; 98US-0110592P.
XX      01-DEC-1999; 99US-00452238.
XX
XX      (CAHO/) CAHOON R E.
PA      (SHEN/) SHEN J B.
PA      (WILL/) WILLIAMS M E.
XX
XX      Cahoon RE, Shen JB, Williams ME;
XX
XX      WPI; 2005-512287/52.
DR      P-PSDB; AEB48335.
XX
XX      New polynucleotide encoding geranylgeranyl pyrophosphate synthase, useful
PT      in plant terpenoid biosynthesis and for producing plants with increased
PT      levels of defense-related substance and phytohormone gibberellin.
XX
XX      Disclosure; SEQ ID NO 9; 51pp; English.
XX
XX      The invention relates to geranylgeranyl pyrophosphate (GGPP) synthase and
CC      its corresponding nucleic acid sequence. GGPP synthase also known as
CC      geranylgeranyl-diphosphate synthase, farnesyl transferase and
CC      geranylgeranyl synthase is a key enzyme in plant terpenoid biosynthesis.
CC      The invention also relates to methods for producing transgenic plant. The
CC      polynucleotide, polypeptide and methods of the invention are useful in
CC      plant terpenoid biosynthesis and for producing transgenic plants with
CC      increased levels of defense-related substance and important phytohormone
CC      gibberellin and specifically, for manipulating corn gene resulting in
CC      increased xanthophyll content, which has value as coloring agent in
CC      poultry feed. The present sequence is the corn GGPP synthase FIS cDNA
CC      clone.
XX

```



GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 15:18:57 ; Search time 628.922 Seconds  
(without alignments)  
2901.306 Million cell updates/sec

Title: US-10-628-525A-37

Perfect score: 191

Sequence: 1 MATPSAVGACLLARXAWPAAVCDRAPRRLQVLRRR 39

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb.est2.\*  
3: gb.est3.\*  
4: gb.htc.\*  
5: gb.est4.\*  
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7: gb.est6.\*  
8: gb.est7.\*  
9: gb.gsa1.\*  
10: gb.gsa2.\*  
11: gb.gsa3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| CV767377 | FGAS06176   | 870  | 38.5 | 74   | 11 |
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| BG356255 | EMI_23_D0   | 213  | 37.7 | 72   | 13 |
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| BF413028 | UI-R-CA0-   | 359  | 36.6 | 69   | 17 |
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| CZ384877 | ZMMBF0160   | 861  | 35.1 | 67   | 49 |
| CC641737 | OGUHU52TH   | 943  | 35.1 | 67   | 50 |
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| BZ558918 | pac62_164   | 1056 | 35.1 | 67   | 53 |
| AY108563 | Zea mayas   | 1142 | 35.1 | 67   | 54 |
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| BP646053 | BP646053    | 394  | 34.8 | 66.5 | 56 |
| D39216   | RICR3052A_R | 394  | 34.8 | 66.5 | 57 |
| BY263738 | BY263738    | 406  | 34.8 | 66.5 | 58 |
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| CB644036 | OSUNEB05B   | 746  | 34.8 | 66.5 | 66 |
| CB658022 | OSUNEC13M   | 764  | 34.8 | 66.5 | 67 |
| CA245927 | SCBZFL508   | 777  | 34.8 | 66.5 | 68 |
| CB652416 | OSJNEC02E   | 782  | 34.8 | 66.5 | 69 |
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| AG075063 | pan.trog1   | 1193 | 34.8 | 66.5 | 71 |
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| CF650078 | 3530_1_81   | 292  | 34.6 | 66   | 75 |
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|                                             |      |      |      |    |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
|---------------------------------------------|------|------|------|----|-----------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| c 81                                        | 66   | 34.6 | 507  | 10 | CW305198  | CW305198 104 790 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| c 82                                        | 66   | 34.6 | 510  | 8  | DR960312  | ZM BFB007                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 83                                        | 66   | 34.6 | 519  | 8  | CA133214  | SCQRT103                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| c 84                                        | 66   | 34.6 | 558  | 10 | CG309123  | OGVLI93TV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 85                                        | 66   | 34.6 | 566  | 8  | DR787692  | ZM BFB000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
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| c 87                                        | 66   | 34.6 | 582  | 2  | BE453010  | 894067E09                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 88                                        | 66   | 34.6 | 608  | 8  | DN968009  | ISL1104 A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 89                                        | 66   | 34.6 | 656  | 3  | BM632122  | 170006875                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 90                                        | 66   | 34.6 | 660  | 3  | BM601482  | 170006870                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 91                                        | 66   | 34.6 | 672  | 8  | DR795443  | ZM BFB001                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 92                                        | 66   | 34.6 | 674  | 2  | BG537044  | 602565128                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 93                                        | 66   | 34.6 | 726  | 8  | DR959127  | ZM BFB006                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 94                                        | 66   | 34.6 | 728  | 7  | CV292538  | acof1-6mb                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 95                                        | 66   | 34.6 | 743  | 8  | DR971950  | ZM BFB009                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 96                                        | 66   | 34.6 | 756  | 8  | DR801698  | ZM BFB002                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 97                                        | 66   | 34.6 | 760  | 7  | CV2888775 | acof1-9mb                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 98                                        | 66   | 34.6 | 764  | 8  | DR956305  | ZM BFB005                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 99                                        | 66   | 34.6 | 764  | 8  | DR966798  | ZM BFB008                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 100                                       | 66   | 34.6 | 777  | 8  | DR808998  | ZM BFB003                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 101                                       | 66   | 34.6 | 782  | 8  | DR957683  | ZM BFB005                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 102                                       | 66   | 34.6 | 790  | 8  | DR955656  | ZM BFB004                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 103                                       | 66   | 34.6 | 794  | 8  | DR808964  | ZM BFB003                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 104                                       | 66   | 34.6 | 794  | 8  | DR971903  | ZM BFB009                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 105                                       | 66   | 34.6 | 800  | 8  | DR824554  | ZM BFB006                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 106                                       | 66   | 34.6 | 803  | 6  | CA196459  | SCBPAD108                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 107                                       | 66   | 34.6 | 812  | 8  | DR794748  | ZM BFB001                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 108                                       | 66   | 34.6 | 812  | 8  | DR967128  | ZM BFB008                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 109                                       | 66   | 34.6 | 836  | 8  | DR786564  | ZM BFB000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 110                                       | 66   | 34.6 | 838  | 7  | CN824488  | Os splbn                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| c 111                                       | 66   | 34.6 | 843  | 10 | CG448141  | OGTBL64TV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 112                                       | 66   | 34.6 | 864  | 10 | CG443798  | OGTCB08TV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 113                                       | 66   | 34.6 | 899  | 8  | DR811404  | ZM BFB003                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 114                                       | 66   | 34.6 | 901  | 10 | CG275369  | OG0FO57TV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 115                                       | 66   | 34.6 | 902  | 8  | DR792849  | ZM BFB001                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 116                                       | 66   | 34.6 | 913  | 9  | CC708012  | OGKAI06TV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 117                                       | 66   | 34.6 | 935  | 10 | CG453877  | OGTCJ13TV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 118                                       | 66   | 34.6 | 1362 | 8  | DN719924  | CNB130-HO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 119                                       | 65.5 | 34.3 | 396  | 10 | CG287894  | OGVCM38TH                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 120                                       | 65.5 | 34.3 | 414  | 6  | CF009940  | QBU24f06.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 121                                       | 65.5 | 34.3 | 492  | 2  | BG466276  | RESted51                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| c 122                                       | 65.5 | 34.3 | 508  | 6  | CF011566  | QBJ9f03.x                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 123                                       | 65.5 | 34.3 | 521  | 2  | BE318851  | FM1_1_A06                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 124                                       | 65.5 | 34.3 | 534  | 6  | CA827278  | 111401200                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 125                                       | 65.5 | 34.3 | 537  | 5  | BU097580  | 3524_1_51                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 126                                       | 65.5 | 34.3 | 545  | 5  | BU097545  | 3524_1_51                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 127                                       | 65.5 | 34.3 | 553  | 4  | AY104962  | Zea mays                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| c 128                                       | 65.5 | 34.3 | 612  | 6  | CA200830  | SCRFFL103                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 129                                       | 65.5 | 34.3 | 650  | 6  | CA232011  | SCQFPL303                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 130                                       | 65.5 | 34.3 | 686  | 7  | CV666203  | LCPE04EX0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 131                                       | 65.5 | 34.3 | 728  | 10 | CL852904  | OR CBA008                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 132                                       | 65.5 | 34.3 | 732  | 10 | CG300379  | OGWAC43TV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 133                                       | 65.5 | 34.3 | 764  | 10 | CG312447  | OGU8Q41TV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 134                                       | 65.5 | 34.3 | 773  | 9  | CC504797  | OGUEL95TV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 135                                       | 65.5 | 34.3 | 778  | 9  | BZ638711  | OGCBK38TC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 136                                       | 65.5 | 34.3 | 795  | 9  | CG334614  | OGIBJ26TH                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 137                                       | 65.5 | 34.3 | 888  | 10 | CG366938  | OG3DN20TV                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 138                                       | 65.5 | 34.3 | 911  | 7  | CO063370  | est_k_bre                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 139                                       | 65.5 | 34.3 | 931  | 10 | CG366925  | OG3DN20TH                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 140                                       | 65.5 | 34.3 | 1008 | 9  | BZ579745  | msh2_752.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 141                                       | 65.5 | 34.3 | 1101 | 10 | CW927367  | EDCBL42TF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 142                                       | 65.5 | 34.3 | 1691 | 10 | AG148945  | Pan trogl                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 143                                       | 65.5 | 34.3 | 2298 | 10 | CL973204  | OsIFCC042                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 144                                       | 65   | 34.0 | 302  | 10 | CR364303  | fsbb001f0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 145                                       | 65   | 34.0 | 500  | 8  | DR830762  | ZM BFB007                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 146                                       | 65   | 34.0 | 588  | 2  | BF728141  | 1000056F0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 147                                       | 65   | 34.0 | 628  | 10 | CW344244  | 104_846_1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 148                                       | 65   | 34.0 | 666  | 10 | CW243427  | 104_703_1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 149                                       | 65   | 34.0 | 865  | 8  | DR681309  | EST107142                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| c 150                                       | 65   | 34.0 | 905  | 6  | CA068668  | SCRUAD106                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| ALIGNMENTS                                  |      |      |      |    |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| RESULT 1                                    |      |      |      |    |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| CG356137                                    |      |      |      |    |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| LOCUS                                       |      |      |      |    |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| DEFINITION                                  |      |      |      |    |           | CG356137 605 bp DNA linear GSS 26-AUG-2003                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| ACCESSION                                   |      |      |      |    |           | OG3BC36TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0767E23,                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| VERSION                                     |      |      |      |    |           | genomic survey sequence.                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| KEYWORDS                                    |      |      |      |    |           | CG356137.1 GI:34273404                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| SOURCE                                      |      |      |      |    |           | GSS.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| ORGANISM                                    |      |      |      |    |           | Zea mays                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| REFERENCE                                   |      |      |      |    |           | 1 (bases 1 to 605)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| AUTHORS                                     |      |      |      |    |           | Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nuber,A., Robbins,D. and Lakey,N.                                                                                                                                                                                                                                                                                                                          |
| TITLE                                       |      |      |      |    |           | Consortium for Maize Genomics                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| JOURNAL                                     |      |      |      |    |           | Unpublished (2002)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| COMMENT                                     |      |      |      |    |           | Other_GSSs: OG3BC36TV<br>Contact: Cathy Whitelaw<br>TIGR<br>9712 Medical Center Drive, Rockville, MD 20850, USA<br>Tel: 301-838-5843<br>Fax: 301-838-0208<br>Email: whitelaw@igr.org<br>Seq primer: IR<br>Class: methylation filtered.<br>Location/Qualifiers<br>1..605<br>/organism="Zea mays"<br>/mol_type="genomic DNA"<br>/strain="B73"<br>/db_xref="taxon:4577"<br>/clone_lib="ZMMBMA0767E23"<br>/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library" |
| FEATURES                                    |      |      |      |    |           | source                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| ORIGIN                                      |      |      |      |    |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| Alignment Scores:                           |      |      |      |    |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| Pred. No.:                                  |      |      |      |    |           | 1.98e-13 Length: 605                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Score:                                      |      |      |      |    |           | 191.00 Matches: 38                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Percent Similarity:                         |      |      |      |    |           | 97.4% Conservative: 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| Best Local Similarity:                      |      |      |      |    |           | 97.4% Mismatches: 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| Query Match:                                |      |      |      |    |           | 100.0% Indels: 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| DB:                                         |      |      |      |    |           | 10 Gaps: 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| US-10-628-525A-37 (1-39) x CG356137 (1-605) |      |      |      |    |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| Qy                                          |      |      |      |    |           | 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaATpPro 20                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Db                                          |      |      |      |    |           | 323 ATGGCGACGCCCTCGCGCGTGGCGCGCGTCCCTCCCTCGCGCGCCCTGGCGG 382                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| Qy                                          |      |      |      |    |           | 21 AlaAlaValGlyAspArgAlaAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Db                                          |      |      |      |    |           | 383 GCCCGCGTGGCGACCCGCGCGCGCGCGCGCTCCAGCGCGTGTCTGCGCGCGCGG 439                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| RESULT 2                                    |      |      |      |    |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| CG663124                                    |      |      |      |    |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| LOCUS                                       |      |      |      |    |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| DEFINITION                                  |      |      |      |    |           | CG663124 606 bp DNA linear GSS 19-JUN-2003                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| ACCESSION                                   |      |      |      |    |           | OGUKA28TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0459E07,                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| VERSION                                     |      |      |      |    |           | genomic survey sequence.                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| KEYWORDS                                    |      |      |      |    |           | CG663124                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| SOURCE                                      |      |      |      |    |           | GSS.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| ORGANISM                                    |      |      |      |    |           | Zea mays                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| REFERENCE                                   |      |      |      |    |           | 1 (bases 1 to 606)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| AUTHORS                                     |      |      |      |    |           | Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nuber,A., Robbins,D. and Lakey,N.                                                                                                                                                                                                                                                                                                                          |
| TITLE                                       |      |      |      |    |           | Consortium for Maize Genomics                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| JOURNAL                                     |      |      |      |    |           | Unpublished (2002)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| COMMENT                                     |      |      |      |    |           | Other_GSSs: OG3BC36TV<br>Contact: Cathy Whitelaw<br>TIGR<br>9712 Medical Center Drive, Rockville, MD 20850, USA<br>Tel: 301-838-5843<br>Fax: 301-838-0208<br>Email: whitelaw@igr.org<br>Seq primer: IR<br>Class: methylation filtered.<br>Location/Qualifiers<br>1..605<br>/organism="Zea mays"<br>/mol_type="genomic DNA"<br>/strain="B73"<br>/db_xref="taxon:4577"<br>/clone_lib="ZMMBMA0767E23"<br>/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library" |

## AUTHORS

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
 Resnick, A., Frazer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
 Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.  
 Consortium for Maize Genomics  
 Unpublished (2002)  
 Contact: Cathy Whitelaw  
 TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208

Email: whitelaw@cigr.org

Seq primer: TR

Class: methylation filtered.

Location/Qualifiers

## FEATURES

source

1. .606  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBMA0459807"  
 /clone\_lib="ZM 0.7 1.5\_KB"  
 /notes="Vector: pBCKS-; Site 1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.98e-13 Length: 606  
 Score: 191.00 Matches: 38  
 Percent Similarity: 97.4% Conservative: 0  
 Best Local Similarity: 97.4% Mismatches: 1  
 Query Match: 100.0% Indels: 0  
 DB: 9 Gaps: 0

US-10-628-525A-37 (1-39) x CC663124 (1-606)

QY 1 MetAlaThrProSerAlaValGlyAlaAaCysLeuLeuLeuAlaArg\*\*\*AlaTtpPro 20  
 |||||  
 Db 467 ATGGCGAGCGCCTCGGCGGTGGGGCGCGGTGCTCTCTCGCGGGCGCGCTGGCCG 526  
 QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
 |||||  
 Db 527 GCCGCGGTGGCGACCGCGCGCGCGCGCGCTCCAGCGCTGCTGCGCGCGCGG 583

## RESULT 3

CG242761/c  
 LOCUS  
 DEFINITION CG242761 673 bp DNA linear GSS 22-AUG-2003  
 genomic survey sequence.

ACCESSION CG242761

VERSION CG242761.1 GI:34142647

KEYWORDS GSS.

SOURCE

## ORGANISM

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 673)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Frazer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: CG242761

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@cigr.org

Seq primer: TR

Class: methylation filtered.

Location/Qualifiers

## FEATURES

source

1. .673

/organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBMA074324"  
 /clone\_lib="ZM 0.7 1.5\_KB"  
 /notes="Vector: pBCKS-; Site 1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.21e-13 Length: 673  
 Score: 191.00 Matches: 38  
 Percent Similarity: 97.4% Conservative: 0  
 Best Local Similarity: 97.4% Mismatches: 1  
 Query Match: 100.0% Indels: 0  
 DB: 10 Gaps: 0

US-10-628-525A-37 (1-39) x CG242761 (1-673)

QY 1 MetAlaThrProSerAlaValGlyAlaAaCysLeuLeuLeuAlaArg\*\*\*AlaTtpPro 20  
 |||||

Db 624 ATGGCGAGCGCCTCGGCGGTGGGGCGCGGTGCTCTCTCGCGGGCGCGCTGGCCG 565

QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
 |||||

Db 564 GCCGCGGTGGCGACCGCGCGCGCGCGCTCCAGCGCTGCTGCGCGCGCGG 508

## RESULT 4

DR810603  
 LOCUS  
 DEFINITION ZM BFB003807.r ZM\_BFB Zea mays cDNA 5', mRNA linear EST 28-JUL-2005  
 ACCESSION DR810603  
 VERSION DR810603.1 GI:71429553  
 KEYWORDS EST.

SOURCE

Zea mays

Zea mays

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 707)

Kim, H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C.,

Rao, K., Haller, K., Wang, R., Soderlund, C., Walbot, V. and Yu, Y.

Maize Full-length cDNA Project

Unpublished (2005)

Contact: Yeisoo Yu

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The University of Arizona

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Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plate: 0038 row: G column: 07.

Location/Qualifiers

## FEATURES

source

1. .707

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/tissue\_type="mixed (silke, husks, ears, pollen, shoot

tips, leaf, root tips, whole seed, embryo)"

/dev\_stage="varies by tissue"

/lab\_host="DH10B T1 phage resistant"

/clone\_lib="ZM BFB"

/notes="Vector: PCMV-SPORT 6.1; Site 1: EcoRV; Site 2:

NotI; Maize Full length cDNA library (3530 library)

created by Invitrogen from multiple tissues; Organ: silks,

husks, ears, pollen, shoot tips, leaf, root tips, whole

seed, embryo. This is a Gateway compatible vector,

permitting clone movement to new vector backbones for

expression in diverse host cells using recombination

rather than restriction enzymes. poly(A)+ mRNA was

prepared by invitrogen, and equimolar amounts of RNA from

each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>).

ORIGIN

Alignment Scores:  
Pred. No.: 2,33e-13 Length: 707  
Score: 191.00 Matches: 38  
Percent Similarity: 97.4% Conservative: 0  
Best Local Similarity: 97.4% Mismatches: 1  
Query Match: 100.0% Indels: 0  
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x DR810603 (1-707)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20  
DB 181 ATGGCGACGCCCTCGCGCGTGGCGCGCGTGCCTCTCTCGCGCGCGCGCTGGCGG 240  
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
DB 241 GCCGCGTGGCGACCGCGCGCGCGCGCGCTCCAGCGGTGCTGCGCGCGG 297

RESULT 5

DR808291  
LOCUS ZM\_BFB0034P07.r ZM\_BFB Zea mays cDNA 5', mRNA linear EST 28-JUL-2005  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 719)  
Kim H., Collura, K., Wisotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wang, R., Soderlund, C., Walbot, V. and Yu, Y.  
Maize Full-length cDNA Project  
Unpublished (2005)  
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Plate: 0034 row: P column: 07.

FEATURES

source  
1..719  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultiivar="B73"  
/db\_xref="taxon:4577"  
/tissue\_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"  
/dev\_stage="varies by tissue"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="ZM\_BFB"

/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>).

ORIGIN

Alignment Scores:  
Pred. No.: 2,37e-13 Length: 719  
Score: 191.00 Matches: 38  
Percent Similarity: 97.4% Conservative: 0  
Best Local Similarity: 97.4% Mismatches: 1  
Query Match: 100.0% Indels: 0  
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x DR808291 (1-719)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20  
DB 99 ATGGCGACGCCCTCGCGCGTGGCGCGCGTGCCTCTCTCGCGCGCGCGCTGGCGG 158  
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
DB 159 GCCGCGTGGCGACCGCGCGCGCGCGCTCCAGCGGTGCTGCGCGCGG 215

RESULT 6

BG556880  
LOCUS EML\_39\_G08.b1\_A002 Embryo 1 (EML) Sorghum bicolor cDNA, mRNA linear EST 10-APR-2001  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.  
1 (bases 1 to 424)  
Reid, S.P., Cordonnier-Pratt, M.-M., Gingle, A. and Pratt, L.H.  
An EST database from Sorghum: developing embryos  
Unpublished (2000)  
Contact: Cordonnier-Pratt MM

REFERENCE

AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: JEN REV  
High quality sequence stop: 410  
POLYA=No.

FEATURES  
source  
1. .424  
Location/Qualifiers  
/organism="Sorghum bicolor"  
/mol\_type="mRNA"  
/db\_xref="taxon:4558"  
/clone\_lib="Embryo 1 (EM1)"  
/notes="Organ: Embryos germinated for 24 hr; Vector: pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."

## ORIGIN

Alignment Scores:  
Pred. No.: 9.44e-08 Length: 424  
Score: 143.50 Matches: 32  
Percent Similarity: 77.3% Conservatives: 2  
Best Local Similarity: 72.7% Mismatches: 5  
Query Match: 75.1% Indels: 5  
DB: 2 Gaps: 1

US-10-628-525A-37 (1-39) x BG556880 (1-424)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*Ala----- 18  
|||||  
Db 138 ATGGCGACGCCCTCGGCGGTGGCGCGTGGCTGCTCTAGCGGAGCGCGCGGG 197  
QY 19 -----TrpProAlaAlaValGlyAspArgAlaArgProArgLeuGlnArgVal 35  
|||||  
Db 198 CTTGGGCTTGGCGCGCGGCGGCGATCGGCGCGCGCGCGCTCCAGCGCGTG 257

QY 36 LeuArgArgArg 39  
:::  
Db 258 GTGCGAGGCGG 269

RESULT 7  
CA282588  
LOCUS  
DEFINITION  
SCCNR1001G11.g NR1 Saccharum officinarum cDNA clone SCCNR1001G11  
5' mRNA sequence.

ACCESSION  
CA282588  
VERSION  
CA282588.1 GI:36014712  
KEYWORDS  
EST.  
SOURCE  
Saccharum officinarum  
ORGANISM  
Saccharum officinarum

REFERENCE  
1 (bases 1 to 465)  
Vettore,A.L., da Silva,P.R., Kemper,E.L. and Arruda,P.  
The libraries that made SUCSEST  
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
Contact: Arruda P

AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Centro de Biologia Molecular e Engenhariaia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br  
Clone distribution: clone distribution information can be found  
through the Brazilian Clone Collection Center (BCCC) at  
http://www.bcccenter.fcav.unesp.br  
Plate: 001 row: G column: 11  
Seq primer: T7 Promoter Primer.

## FEATURES

source  
1. .465  
Location/Qualifiers  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"

/clone="SCCNR1001G11"  
/lab\_host="DH10B"  
/clone\_lib="NR1"

/notes="Organ: Pool of sugarcane tissues; Vector: pSport1;  
Site 1: SalI; Site 2: NotI; An unidirectional cDNA library  
generated from [pool of sugarcane tissues]. cDNA was  
prepared from polyA+ mRNA using SuperScript Plasmid  
System Kit (Invitrogen). The double-strand cDNAs were  
fractionated in a sepharose CL-2B 40cm-columns and  
fragments sizing between 0.8 and 1.5 Kb were  
directionally cloned into the vector. Details of each  
source of RNA and library construction can be obtained at  
http://sucsest.lad.ic.unicamp.br/public"

## ORIGIN

Alignment Scores:  
Pred. No.: 4.28e-07 Length: 465  
Score: 138.50 Matches: 31  
Percent Similarity: 82.1% Conservatives: 1  
Best Local Similarity: 79.5% Mismatches: 6  
Query Match: 72.5% Indels: 1  
DB: 6 Gaps: 1

US-10-628-525A-37 (1-39) x CA282588 (1-465)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20  
|||||  
Db 126 ATGGCGACGCCCTCGGCGGTGGCGCGTGGCTGCTCGCCCTCGCGGCGCGGCGCG 185

QY 21 AlaAlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 39  
|||||  
Db 186 GGCGCG---GGCGATCGGCGCGCGCGCTGCTCAGCGCGTGGTGCCTCGCGCGCG 239

RESULT 8  
CF850352  
LOCUS  
DEFINITION

CF850352 562 bp mRNA linear EST 30-OCT-2003  
psMA013009f USDA-IFAPs:Expression of Phytophthora sojae genes  
during infection and propagation\_sMA Phytophthora sojae cDNA clone  
sMA013009 5, mRNA sequence.

ACCESSION  
CF850352  
VERSION  
CF850352.1 GI:38066006  
KEYWORDS  
EST.  
SOURCE  
Phytophthora sojae  
ORGANISM  
Phytophthora sojae  
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;  
Phytophthora.

REFERENCE  
1 (bases 1 to 562)  
Tyler,B.  
Tyler,B. Not Published  
Unpublished (2003)  
Contact: Tyler B  
Tyler lab

VBI  
1880 Pratt Dr., Blacksburg, VA 24061, USA  
Tel: 540-231-7318  
Email: bmtylev@vt.edu  
PCR Primers  
FORWARD: BK reverse primer  
BACKWARD: BK reverse primer  
Plate: 013 row: O column: 09  
Seq primer: BK reverse primer  
High quality sequence stop: 562.  
Location/Qualifiers

## FEATURES

source  
1. .562  
/organism="Phytophthora sojae"  
/mol\_type="mRNA"  
/db\_xref="taxon:67593"  
/clone="sMA013009"  
/tissue\_type="mycelium"  
/cell\_line="P6497"  
/dev\_stage="mycelium"  
/lab\_host="synthetic medium"  
/clone\_lib="USDA-IFAPs:Expression of Phytophthora sojae"



QY 26 ArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
Db 233 CCGCGAGAGTCTCGCCCGCGCGGAGCTGCTCAGCGCGCG 192

RESULT 11  
CV767377/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CV767377  
FGAS061767 Triticum aestivum FGAS: Library 2 Gate 3 Triticum  
aestivum cDNA, mRNA sequence.

CV767377  
CV767377.1 GI:55611670  
EST.  
Triticum aestivum (bread wheat)  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 870)  
Allard, F., Crosby, W.L., Danyluk, J., Eudes, P., Frick, M., Gaudet, D.,  
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,  
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,  
Penniket, C., Roach, J.L. and Sarhan, F.  
Functional Genomics of Abiotic Stress in Wheat and Canola Crops  
Unpublished (2003)  
Contact: Wm L Crosby  
Bioinformatics  
University of Saskatchewan, Department of Computer Science  
1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
Saskatchewan, S7N 5A9, Canada  
Tel: 306 966 1769  
Fax: 306 966 2033  
Email: fgas\_est@cs.usask.ca

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

This sequence is the direct result of the Base calling software  
Phred (default parameters). It is the raw base calls. To aid in the  
identification of the high quality insert the software Lucy  
(default parameters) has been run on this sequence. Lucy identified  
the region [97..617].  
Plate: WEP050 row: H column: 22.  
Location/Qualifiers  
1. .870  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4565"  
/clone\_lib="Triticum aestivum FGAS: Library 2 Gate 3"  
/notes="Organ: Crown and leaf; Vector: pCMV.SPORT6; Aerial  
parts (crown and leaf) of wheat cultivar Norstar from  
control and long exposure times to low temperature. 4 mRNA  
populations were exposed before constructing the library;  
7 days non-acclimated plants and 1, 23, and 53 days  
cold-acclimated at 4C. Non-acclimated and cold-acclimated  
plants were grown in vermiculite This is the only library  
that was done according to the Invitrogen manual, and  
therefore, a percentage of clones will not have the 3  
prime end because of NotI digestion within the cDNA."

FEATURES  
source  
Location/Qualifiers  
1. .870  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4565"  
/clone\_lib="Triticum aestivum FGAS: Library 2 Gate 3"  
/notes="Organ: Crown and leaf; Vector: pCMV.SPORT6; Aerial  
parts (crown and leaf) of wheat cultivar Norstar from  
control and long exposure times to low temperature. 4 mRNA  
populations were exposed before constructing the library;  
7 days non-acclimated plants and 1, 23, and 53 days  
cold-acclimated at 4C. Non-acclimated and cold-acclimated  
plants were grown in vermiculite This is the only library  
that was done according to the Invitrogen manual, and  
therefore, a percentage of clones will not have the 3  
prime end because of NotI digestion within the cDNA."

ORIGIN  
Alignment Scores:  
Pred. No.: 70.3 Length: 870  
Score: 74.00 Matches: 16  
Percent Similarity: 55.9% Conservative: 3  
Best Local Similarity: 47.1% Mismatches: 15  
Query Match: 38.7% Indels: 0  
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x CV767377 (1-870)

QY 6 AlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpProAlaValGlyAsp 25  
Db 293 GCTGCTCGACTCCCTCGCGTGCAGCTGTCGCGTTCGCGCGCGGCA 234

QY 26 ArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
Db 233 CCGCGAGAGTCTCGCCCGCGCGGAGCTGCTCAGCGCGCG 192

RESULT 12  
CA971120  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CA971120  
IMAGR:6556939 5', mRNA sequence.  
CA971120.1 GI:27503471  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 861)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: NCI  
CDNA Library Preparation: Michael Brownstein Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM2724 row: C column: 19  
High quality sequence stop: 355.  
Location/Qualifiers  
1. .861  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6556939"  
/tissue\_type="mixed (pool of 40 RNAs)"  
/lab\_host="DH10B (T1-phage-resistant)"  
/clone\_lib="NIH MGC 126"  
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);  
Site 2: SfiI (ggccgctcgcc); Double-stranded cDNA was  
prepared from a pool of 40 cell line polyA+ RNAs (bladder  
- 2% blood - 33.4% brain - 5.6% breast - 12.5% colon -  
4% connective tissue - 1.4% eye - 1% intestine - 2.6%,  
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -  
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,  
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'  
adaptors were used in cloning as follows:  
5'-AGCAGTGTATACGACGAGTGCATAGCGCGG-3' and  
5'-ATCTAGAGCGGAGCGCGGACATG-TT(30)NN-3'. Full-length  
enriched library was constructed using the Clontech  
Creator SMART kit and size-selected to contain the 0.5-1  
kb size fraction (other fractions present in NIH MGC 127  
and NIH MGC 128). Library created in the laboratory of T.  
Udin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH\_MGC  
Library."

FEATURES  
source  
Location/Qualifiers  
1. .861  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6556939"  
/tissue\_type="mixed (pool of 40 RNAs)"  
/lab\_host="DH10B (T1-phage-resistant)"  
/clone\_lib="NIH MGC 126"  
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);  
Site 2: SfiI (ggccgctcgcc); Double-stranded cDNA was  
prepared from a pool of 40 cell line polyA+ RNAs (bladder  
- 2% blood - 33.4% brain - 5.6% breast - 12.5% colon -  
4% connective tissue - 1.4% eye - 1% intestine - 2.6%,  
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -  
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,  
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'  
adaptors were used in cloning as follows:  
5'-AGCAGTGTATACGACGAGTGCATAGCGCGG-3' and  
5'-ATCTAGAGCGGAGCGCGGACATG-TT(30)NN-3'. Full-length  
enriched library was constructed using the Clontech  
Creator SMART kit and size-selected to contain the 0.5-1  
kb size fraction (other fractions present in NIH MGC 127  
and NIH MGC 128). Library created in the laboratory of T.  
Udin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH\_MGC  
Library."

ORIGIN  
Alignment Scores:  
Pred. No.: 80.1 Length: 861  
Score: 73.50 Matches: 22  
Percent Similarity: 43.6% Conservative: 2  
Best Local Similarity: 40.0% Mismatches: 12  
Query Match: 38.5% Indels: 19  
DB: 6 Gaps: 2

US-10-628-525A-37 (1-39) x CA971120 (1-861)

QY 4 ProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpProAlaVal 23  
Db 673 CCGCTTGCCTAGGGGCTTTGTGCTCTCTCTCCCTCAGCGGAGCAAAACCCGCGCTGTC 732

QY 24 GlyAsp-----ArgAlaArgProArgLeu----- 32  
Db 24 GlyAsp-----ArgAlaArgProArgLeu----- 32





**AUTHORS**  
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,  
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,  
Wong, G. K. S., Deng, X. W. and Wang, J.

**TITLE**  
An analysis of transcriptional regulation of the rice genome and  
its comparison to Arabidopsis

**JOURNAL**  
COMMENT

Unpublished (2004)  
Contact: Chen Chen  
Department of Bioinformatic  
Beijing Institute of Genomics  
Chinese Academy of Sciences  
Tel: 86-10-80481559  
Fax: 86-10-80488676  
Email: chenchen@genomics.org.cn  
Rice genomic sequence.  
Class: exon-trapped.

**FEATURES**  
source

Location/Qualifiers  
1. .1011  
/organism="Oryza sativa  
/mol\_type="genomic DNA"  
/db\_xref="taxon:39946"  
/clone\_lib="Oryza sativa Exon Library"  
/note="Oryza sativa exon trapped genomic sequences"

**ORIGIN**

Alignment Scores:  
Pred. No.: 167 Length: 1011  
Score: 71.50 Matches: 17  
Percent Similarity: 52.8% Conservative: 2  
Best Local Similarity: 47.2% Mismatches: 12  
Query Match: 37.4% Indels: 5  
DB: 10 Gaps: 1

US-10-628-525A-37 (1-39) x CL971075 (1-1011)

**Qy** 3 ThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpProAlaAla 22  
|||||:::|||||  
**Db** 124 ACCGGACAGCTTCGGCTGCTGC-----GCCACTTGGCCAGCGCCG 80  
|||||:::|||||

**Qy** 23 ValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArg 38  
|||||:::|||||

**Db** 79 ACACCATCGCGCTGCTCCAGCGAGTCCAGCGCCCTGAGAGG 32  
|||||:::|||||

**RESULT 16**  
BG296816/c 1098 bp mRNA linear EST 21-FEB-2001  
**LOCUS** BG296816 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:4506481 5',  
**DEFINITION** mRNA sequence.

**ACCESSION** BG296816 GI:13059846

**VERSION** EST.

**KEYWORDS** Mus musculus (house mouse)

**SOURCE** Mus musculus

**ORGANISM** Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 1098)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strauberg, Ph.D.

Email: csapsb@mail.nih.gov

Tissue procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM10381 row: p column: 02

High quality sequence start: 2

High quality sequence stop: 625.

**FEATURES** Location/Qualifiers

1. .1098

source

/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4506481"  
/tissue\_type="retina"  
/lab\_host="DHI0B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_94"  
/notes="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 3.3 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

**ORIGIN**  
Alignment Scores:  
Pred. No.: 210 Length: 1098  
Score: 71.00 Matches: 14  
Percent Similarity: 60.0% Conservative: 4  
Best Local Similarity: 46.7% Mismatches: 12  
Query Match: 37.2% Indels: 0  
DB: 2 Gaps: 0

US-10-628-525A-37 (1-39) x BG296816 (1-1098)

**Qy** 7 ValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpProAlaAlaValGlyAspArg 26  
|||||:::|||||  
**Db** 568 GTTGTGCTCTTGTACTGTCTTCAGAGCCAGTGGCCAGGTCAGGTCAACCCAGG 509  
|||||:::|||||

**Qy** 27 AlaArgProArgLeuGlnArgValLeu 36  
|||||:::|||||

**Db** 508 CAGAGCCCTATGGAGCTGTGCTGCTGCTC 479  
|||||:::|||||

**RESULT 17**

BF413028

**LOCUS** BF413028

**DEFINITION** UI-R-CA0-bod-c-09-0-UI.s1 UI-R-CA0 Rattus norvegicus cDNA clone

**ACCESSION** BF413028.1 GI:11401057

**VERSION** EST.

**KEYWORDS** Rattus norvegicus (Norway rat)

**SOURCE** Rattus norvegicus

**ORGANISM** Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Rattus.

1 (bases 1 to 359)

Bonaldi, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

8889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Oligo-dT track not found, Not I site shown in beginning of sequence

is likely internal to the message. cDNA library preparation: M.B.

Soares Lab Clone distribution: clones will be available through

Research Genetics (www.resgen.com) The following repetitive

elements were found in this cDNA sequence: 226-289,

>GC rich#Low complexity

Seq primer: M13 Forward

POLYA=No.

**FEATURES** Location/Qualifiers

1. .359

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="UI-R-CA0-bod-c-09-0-UI"







```

Db      803 GGGCGGCGCTCACGT---CGGGGCACCGCGAACCCTCCGACGC 844
|||||  |||:||||| |||  :::||||| |||:|||||
RESULT 24
AW287063
LOCUS   AW287063
DEFINITION LG1_265_A07.b2_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA
sequence.
ACCESSION AW287063
VERSION   AW287063.2 GI:6858996
KEYWORDS  EST.
SOURCE    Sorghum bicolor (sorghum)
ORGANISM  Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 404)
Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C. and Pratt,L.H.
An EST database from Sorghum: light-grown seedlings
Unpublished (2000)
On Jan 6, 2000 this sequence version replaced gi:6676907.
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 348
POLYA=No.

FEATURES
source
1..404
Location/Qualifiers
/organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4558"
/clone_lib="Light Grown 1 (LG1)"
/notes="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2:
EcoRI; The library was made from poly-A RNA in the cloning
vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."

ORIGIN
Alignment Scores:
Pred. No.: 172 Length: 404
Score: 68.00 Matches: 18
Percent Similarity: 52.6% Conservat: 2
Best Local Similarity: 47.4% Mismatches: 14
Query Match: 35.6% Indels: 4
DB: 1 Gaps: 1

US-10-628-525A-37 (1-39) x AW287063 (1-404)

QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTPProAla 21
|||||  |||:||||| |||  :::||||| |||:|||||
Db 147 GCGCGCGCAACGTGCGCGCGCGCGCGCC-----GCTCTCGGTGGTGGCGGTAC 194
|||||  |||:||||| |||  :::||||| |||:|||||
QY 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
|||||  |||:||||| |||  :::||||| |||:|||||
Db 195 AGACGGGGCGCGAGAGCCGTCGTCGTCGCCAGCGCGCGCGCGAGG 248
|||||  |||:||||| |||  :::||||| |||:|||||

RESULT 25
CD236601
LOCUS   SSI_35_H03.g1_A012 Salt-stressed seedlings Sorghum bicolor cDNA
DEFINITION clone SSI_35_H03_A012 5', mRNA sequence.
ACCESSION CD236601
VERSION   CD236601.1 GI:30980066
KEYWORDS  EST.

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Sorghum bicolor (sorghum)
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 421)
Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S.,
Klein,R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Summer,E.J.,
Eastman,A. and Pratt,L.H.
An EST database from Sorghum: salt-stressed seedlings
Unpublished (2003)
Other_ESTs: SSI_35_H03.b1_A012
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug5 (CTTCTGCTCTAAAGCTGCG).
Location/Qualifiers
1..421
/organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4558"
/clone_lib="SSI_35_H03_A012"
/lab_host="DH10B-TI phage-resistant E. coli"
/clone_lib="Salt-stressed seedlings"
/notes="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The
library was prepared from polyA+ RNA from 9-day-old
seedlings grown in hydroponic culture. Seedlings were
transferred to a 150 mM NaCl solution and harvested at 3,
6, 12 and 24 hr following transfer. Roots and leaves were
pooled from all time points and RNA isolated.
Double-stranded cDNA was cloned unidirectionally into
different DraIII sites of the pME18S-FL3 vector (5-prime
DraIII site is CACTGTGTG, 3-prime DraIII site is
CACCATGTG)."

FEATURES
source
1..421
Location/Qualifiers
/organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4558"
/clone_lib="SSI_35_H03_A012"
/lab_host="DH10B-TI phage-resistant E. coli"
/clone_lib="Salt-stressed seedlings"
/notes="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The
library was prepared from polyA+ RNA from 9-day-old
seedlings grown in hydroponic culture. Seedlings were
transferred to a 150 mM NaCl solution and harvested at 3,
6, 12 and 24 hr following transfer. Roots and leaves were
pooled from all time points and RNA isolated.
Double-stranded cDNA was cloned unidirectionally into
different DraIII sites of the pME18S-FL3 vector (5-prime
DraIII site is CACTGTGTG, 3-prime DraIII site is
CACCATGTG)."

ORIGIN
Alignment Scores:
Pred. No.: 180 Length: 421
Score: 68.00 Matches: 18
Percent Similarity: 52.6% Conservat: 2
Best Local Similarity: 47.4% Mismatches: 14
Query Match: 35.6% Indels: 4
DB: 6 Gaps: 1

US-10-628-525A-37 (1-39) x CD236601 (1-421)

QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTPProAla 21
|||||  |||:||||| |||  :::||||| |||:|||||
Db 162 GCGCGCGCAACGTGCGCGCGCGCGCC-----GCTCTCGGTGGTGGCGGTAC 209
|||||  |||:||||| |||  :::||||| |||:|||||
QY 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
|||||  |||:||||| |||  :::||||| |||:|||||
Db 210 AGACGGGGCGCGAGAGCCGTCGTCGTCGCCAGCGCGCGCGAGG 263
|||||  |||:||||| |||  :::||||| |||:|||||

RESULT 26
CD461565
LOCUS   SAI_32_F10.g2_A002 Salicylic acid-treated seedlings Sorghum bicolor
DEFINITION cDNA clone SAI_32_F10_A002 5', mRNA sequence.
ACCESSION CD461565

```

CD461565.1 GI:31376662  
EST.  
Sorghum bicolor (sorghum)  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Salzman,R., Chua Tan,N., Gonzalez,M., Lane,S., Miller,V., Nanda,P., Olaseinde,O., Eastman,A. and Pratt,L.H.  
An EST database from Sorghum: salicylic acid-treated seedlings Unpublished (2003)  
Other ESTs: SAI 32 F10.b1 A002  
Contact: Cordonnier-Pratt,M.  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
Seq primer: Sug5 (CTTCTGCTCTAAAGTGGC) .  
Location/Qualifiers  
1. .440  
/organism="Sorghum bicolor"  
/mol\_type="mRNA"  
/cultivar="BTx623"  
/db\_xref="taxon:4558"  
/clone="SAI 32 F10 A002"  
/lab\_host="DH10B-Ti phage-resistant E. coli"  
/clone\_lib="Salicylic acid-treated seedlings"  
/note="Vector: pME18S-FL3; Site\_1: XhoI; Site\_2: XhoI; The library was prepared from polyA+ RNA from seedlings grown in hydroponic culture. At 8 days of age, medium was supplemented with 1 mM salicylic acid (SA). Roots and shoots were harvested after 27 and 72 hr and material from both time points was combined prior to RNA isolation. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN  
Alignment Scores:  
Pred. No.: 188 Length: 440  
Score: 68.00 Matches: 18  
Percent Similarity: 52.6% Conservative: 2  
Best Local Similarity: 47.4% Mismatches: 14  
Query Match: 35.6% Indels: 4  
DB: 6 Gaps: 1  
US-10-628-525A-37 (1-39) x CD461565 (1-440)

QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpProAla 21  
Db 151 GCGCGCCCAACGTGGCGCGCGCGCC-----GCCTTCGGTGGTGGCCGTAC 198  
QY 22 AlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 39  
Db 199 AGACGGGGCCGAGAGCGTCCCGTGTGTCTCCAGCGCGCGCGGAGG 252

RESULT 27  
CA612682/c  
LOCUS

CD461565.1 GI:31376662  
EST.  
Sorghum bicolor (sorghum)  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Salzman,R., Chua Tan,N., Gonzalez,M., Lane,S., Miller,V., Nanda,P., Olaseinde,O., Eastman,A. and Pratt,L.H.  
An EST database from Sorghum: salicylic acid-treated seedlings Unpublished (2003)  
Other ESTs: SAI 32 F10.b1 A002  
Contact: Cordonnier-Pratt,M.  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
Seq primer: Sug5 (CTTCTGCTCTAAAGTGGC) .  
Location/Qualifiers  
1. .440  
/organism="Sorghum bicolor"  
/mol\_type="mRNA"  
/cultivar="BTx623"  
/db\_xref="taxon:4558"  
/clone="SAI 32 F10 A002"  
/lab\_host="DH10B-Ti phage-resistant E. coli"  
/clone\_lib="Salicylic acid-treated seedlings"  
/note="Vector: pME18S-FL3; Site\_1: XhoI; Site\_2: XhoI; The library was prepared from polyA+ RNA from seedlings grown in hydroponic culture. At 8 days of age, medium was supplemented with 1 mM salicylic acid (SA). Roots and shoots were harvested after 27 and 72 hr and material from both time points was combined prior to RNA isolation. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN  
Alignment Scores:  
Pred. No.: 188 Length: 440  
Score: 68.00 Matches: 18  
Percent Similarity: 52.6% Conservative: 2  
Best Local Similarity: 47.4% Mismatches: 14  
Query Match: 35.6% Indels: 4  
DB: 6 Gaps: 1  
US-10-628-525A-37 (1-39) x CD461565 (1-440)

QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpProAla 21  
Db 151 GCGCGCCCAACGTGGCGCGCGCGCC-----GCCTTCGGTGGTGGCCGTAC 198  
QY 22 AlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 39  
Db 199 AGACGGGGCCGAGAGCGTCCCGTGTGTCTCCAGCGCGCGCGGAGG 252

RESULT 27  
CA612682/c  
LOCUS

CD461565.1 GI:31376662  
EST.  
Sorghum bicolor (sorghum)  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Salzman,R., Chua Tan,N., Gonzalez,M., Lane,S., Miller,V., Nanda,P., Olaseinde,O., Eastman,A. and Pratt,L.H.  
An EST database from Sorghum: salicylic acid-treated seedlings Unpublished (2003)  
Other ESTs: SAI 32 F10.b1 A002  
Contact: Cordonnier-Pratt,M.  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
Seq primer: Sug5 (CTTCTGCTCTAAAGTGGC) .  
Location/Qualifiers  
1. .440  
/organism="Sorghum bicolor"  
/mol\_type="mRNA"  
/cultivar="BTx623"  
/db\_xref="taxon:4558"  
/clone="SAI 32 F10 A002"  
/lab\_host="DH10B-Ti phage-resistant E. coli"  
/clone\_lib="Salicylic acid-treated seedlings"  
/note="Vector: pME18S-FL3; Site\_1: XhoI; Site\_2: XhoI; The library was prepared from polyA+ RNA from seedlings grown in hydroponic culture. At 8 days of age, medium was supplemented with 1 mM salicylic acid (SA). Roots and shoots were harvested after 27 and 72 hr and material from both time points was combined prior to RNA isolation. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN  
Alignment Scores:  
Pred. No.: 188 Length: 440  
Score: 68.00 Matches: 18  
Percent Similarity: 52.6% Conservative: 2  
Best Local Similarity: 47.4% Mismatches: 14  
Query Match: 35.6% Indels: 4  
DB: 6 Gaps: 1  
US-10-628-525A-37 (1-39) x CD461565 (1-440)

QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpProAla 21  
Db 151 GCGCGCCCAACGTGGCGCGCGCGCC-----GCCTTCGGTGGTGGCCGTAC 198  
QY 22 AlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 39  
Db 199 AGACGGGGCCGAGAGCGTCCCGTGTGTCTCCAGCGCGCGCGGAGG 252

RESULT 27  
CA612682/c  
LOCUS

CD461565.1 GI:31376662  
EST.  
Sorghum bicolor (sorghum)  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Salzman,R., Chua Tan,N., Gonzalez,M., Lane,S., Miller,V., Nanda,P., Olaseinde,O., Eastman,A. and Pratt,L.H.  
An EST database from Sorghum: salicylic acid-treated seedlings Unpublished (2003)  
Other ESTs: SAI 32 F10.b1 A002  
Contact: Cordonnier-Pratt,M.  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
Seq primer: Sug5 (CTTCTGCTCTAAAGTGGC) .  
Location/Qualifiers  
1. .440  
/organism="Sorghum bicolor"  
/mol\_type="mRNA"  
/cultivar="BTx623"  
/db\_xref="taxon:4558"  
/clone="SAI 32 F10 A002"  
/lab\_host="DH10B-Ti phage-resistant E. coli"  
/clone\_lib="Salicylic acid-treated seedlings"  
/note="Vector: pME18S-FL3; Site\_1: XhoI; Site\_2: XhoI; The library was prepared from polyA+ RNA from seedlings grown in hydroponic culture. At 8 days of age, medium was supplemented with 1 mM salicylic acid (SA). Roots and shoots were harvested after 27 and 72 hr and material from both time points was combined prior to RNA isolation. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN  
Alignment Scores:  
Pred. No.: 188 Length: 440  
Score: 68.00 Matches: 18  
Percent Similarity: 52.6% Conservative: 2  
Best Local Similarity: 47.4% Mismatches: 14  
Query Match: 35.6% Indels: 4  
DB: 6 Gaps: 1  
US-10-628-525A-37 (1-39) x CD461565 (1-440)

QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpProAla 21  
Db 151 GCGCGCCCAACGTGGCGCGCGCGCC-----GCCTTCGGTGGTGGCCGTAC 198  
QY 22 AlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 39  
Db 199 AGACGGGGCCGAGAGCGTCCCGTGTGTCTCCAGCGCGCGCGGAGG 252

RESULT 27  
CA612682/c  
LOCUS

CD461565.1 GI:31376662  
EST.  
Sorghum bicolor (sorghum)  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS





TITLE An EST database from Sorghum: Sorghum propinquum rhizomes  
JOURNAL Unpublished (2000)  
COMMENT Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
Seq primer: JEN REV  
High quality sequence stop: 433  
POLYA=No.

FEATURES Location/Qualifiers  
1..512  
source /organism="Sorghum propinquum"  
/mol\_type="mRNA"  
/db\_xref="taxon:132711"  
/clone\_lib="Rhizome2 (RHIZ2)"  
/note="Organ: Rhizomes; Vector: pBluescript II from Lambda  
Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made  
from poly-A RNA in the cloning vector lambda ZAP II.  
Clones to be sequenced were prepared by mass excision."

ORIGIN

| Alignment Scores:      |       |               |     |  |
|------------------------|-------|---------------|-----|--|
| Pred. No.:             | 221   | Length:       | 512 |  |
| Score:                 | 68.00 | Matches:      | 18  |  |
| Percent Similarity:    | 52.6% | Conservative: | 2   |  |
| Best Local Similarity: | 47.4% | Mismatches:   | 14  |  |
| Query Match:           | 35.6% | Indels:       | 4   |  |
| DB:                    | 2     | Gaps:         | 1   |  |

US-10-628-525A-37 (1-39) x BG560099 (1-512)

|    |    |                                                              |     |
|----|----|--------------------------------------------------------------|-----|
| QY | 2  | AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAla | 21  |
| Db | 15 | GC CGCGCCCAACGTGCGCGCGCGCGCC-----GCCTCTCGGTGGCGGTAC          | 62  |
| QY | 22 | AlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg       | 39  |
| Db | 63 | AGACGGGGCCGCAGAGCCGTCCTCCGTCGTCCACAGCGCGCGCGGAGG             | 116 |

Search completed: April 1, 2006, 19:23:29  
Job time : 630.922 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 31, 2006, 22:47:42 ; Search time 52.1578 Seconds  
(without alignments)  
1329.139 Million cell updates/sec

Title: US-10-628-525A-37

Perfect score: 191

Sequence: 1 MATPSAVGACLLAXWPAVGDPRRLQRLVRRR 39

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DBV=xlp  
-Q=/abes/ABSWEB spool/US10628525/runat\_31032006\_095123\_16858/app\_query.fasta\_1  
-DB=Issued Patents NA -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi  
-LIST=150 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=30  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abs02p -USER=US10628525 @CEN1 1 855 @runat\_31032006\_095123\_16858  
-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*  
7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
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| 2          | 191   | 100.0       | 1415   | 3  | US-09-345-214-11  |
| 3          | 191   | 100.0       | 1415   | 3  | US-09-743-980-11  |
| 4          | 191   | 100.0       | 2008   | 3  | US-09-345-214-12  |
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| 6          | 191   | 100.0       | 2383   | 3  | US-09-192-909-1   |
| 7          | 191   | 100.0       | 2383   | 3  | US-09-931-297-1   |
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|----|------|------|--------|---|----------------------|--------------------|
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| 11 | 66   | 34.6 | 1437   | 3 | US-10-200-012-7      | Sequence 7, Appli  |
| 12 | 65.5 | 34.3 | 365    | 3 | US-10-108-915-9      | Sequence 9, Appli  |
| 13 | 65   | 34.0 | 1035   | 2 | US-08-891-254-8      | Sequence 8, Appli  |
| 14 | 65   | 34.0 | 1035   | 2 | US-08-819-539-8      | Sequence 8, Appli  |
| 15 | 65   | 34.0 | 1035   | 2 | US-09-030-270A-8     | Sequence 8, Appli  |
| 16 | 65   | 34.0 | 1035   | 3 | US-08-984-207-8      | Sequence 8, Appli  |
| 17 | 65   | 34.0 | 1035   | 3 | US-09-013-587-8      | Sequence 8, Appli  |
| 18 | 65   | 34.0 | 1035   | 3 | US-09-086-118-28     | Sequence 8, Appli  |
| 19 | 65   | 34.0 | 1035   | 3 | US-09-431-614-16     | Sequence 16, Appli |
| 20 | 65   | 34.0 | 1035   | 3 | US-09-412-100-36     | Sequence 36, Appli |
| 21 | 65   | 34.0 | 1035   | 6 | PCT-US96-08813-8     | Sequence 8, Appli  |
| 22 | 64.5 | 33.8 | 2502   | 3 | US-09-902-540-4680   | Sequence 4680, Ap  |
| 23 | 64.5 | 33.8 | 24754  | 3 | US-09-902-540-1230   | Sequence 1230, Ap  |
| 24 | 64   | 33.5 | 36063  | 3 | US-08-311-731A-140   | Sequence 140, App  |
| 25 | 63   | 33.0 | 8705   | 3 | US-09-544-398B-10    | Sequence 10, Appli |
| 26 | 63   | 33.0 | 8705   | 3 | US-09-543-771B-10    | Sequence 10, Appli |
| 27 | 62.5 | 32.7 | 909    | 3 | US-09-252-991A-3246  | Sequence 3246, Ap  |
| 28 | 62.5 | 32.7 | 1197   | 3 | US-09-902-540-6772   | Sequence 6772, Ap  |
| 29 | 62.5 | 32.7 | 1995   | 3 | US-09-252-991A-3322  | Sequence 3322, Ap  |
| 30 | 62.5 | 32.7 | 15271  | 3 | US-09-902-540-1051   | Sequence 1051, Ap  |
| 31 | 62   | 32.5 | 894    | 3 | US-09-252-991A-11504 | Sequence 11504, A  |
| 32 | 62   | 32.5 | 894    | 3 | US-09-252-991A-11736 | Sequence 11736, A  |
| 33 | 62   | 32.5 | 1035   | 3 | US-09-902-540-6806   | Sequence 6806, Ap  |
| 34 | 62   | 32.5 | 3695   | 2 | US-08-091-569-1      | Sequence 1, Appli  |
| 35 | 62   | 32.5 | 3695   | 2 | US-08-203-676-1      | Sequence 1, Appli  |
| 36 | 62   | 32.5 | 3695   | 2 | US-08-822-238-1      | Sequence 1, Appli  |
| 37 | 62   | 32.5 | 4800   | 3 | US-09-902-540-562    | Sequence 562, App  |
| 38 | 62   | 32.5 | 38619  | 3 | US-09-949-002-669    | Sequence 669, App  |
| 39 | 62   | 32.5 | 38619  | 3 | US-09-949-002-833    | Sequence 833, App  |
| 40 | 62   | 32.5 | 54000  | 3 | US-09-843-377-11     | Sequence 11, Appl  |
| 41 | 61.5 | 32.2 | 57320  | 3 | US-09-949-016-13983  | Sequence 13983, A  |
| 42 | 61   | 31.9 | 573    | 3 | US-09-252-991A-4286  | Sequence 4286, Ap  |
| 43 | 61   | 31.9 | 6601   | 3 | US-09-356-952-10     | Sequence 10, Appl  |
| 44 | 61   | 31.9 | 245286 | 3 | US-09-949-016-15497  | Sequence 15497, A  |
| 45 | 60.5 | 31.7 | 927    | 3 | US-09-804-778A-1     | Sequence 1, Appli  |
| 46 | 60.5 | 31.7 | 17173  | 3 | US-09-902-540-1122   | Sequence 1122, Ap  |
| 47 | 60.5 | 31.7 | 112874 | 3 | US-09-949-016-13180  | Sequence 13180, A  |
| 48 | 60.5 | 31.7 | 536165 | 3 | US-09-214-808-1      | Sequence 1, Appli  |
| 49 | 60   | 31.4 | 624    | 3 | US-09-893-737-159    | Sequence 159, App  |
| 50 | 60   | 31.4 | 817    | 3 | US-09-508-824-13     | Sequence 13, Appl  |
| 51 | 60   | 31.4 | 833    | 3 | US-09-620-312D-440   | Sequence 440, App  |
| 52 | 60   | 31.4 | 1644   | 3 | US-09-902-540-371    | Sequence 371, App  |
| 53 | 60   | 31.4 | 1879   | 3 | US-09-614-748A-10    | Sequence 10, Appl  |
| 54 | 60   | 31.4 | 1886   | 2 | US-07-980-526-1      | Sequence 9, Appli  |
| 55 | 60   | 31.4 | 1975   | 3 | US-09-614-748A-9     | Sequence 9, Appli  |
| 56 | 60   | 31.4 | 2019   | 3 | US-09-614-748A-8     | Sequence 8, Appli  |
| 57 | 60   | 31.4 | 2113   | 3 | US-09-252-991A-5836  | Sequence 5836, Ap  |
| 58 | 60   | 31.4 | 2284   | 3 | US-09-193-792-1      | Sequence 7, Appli  |
| 59 | 60   | 31.4 | 2391   | 3 | US-09-252-991A-5812  | Sequence 5812, Ap  |
| 60 | 60   | 31.4 | 2744   | 3 | US-09-071-101-1      | Sequence 1, Appli  |
| 61 | 60   | 31.4 | 2744   | 3 | US-09-369-618-1      | Sequence 1, Appli  |
| 62 | 60   | 31.4 | 2744   | 3 | US-09-369-617-1      | Sequence 1, Appli  |
| 63 | 60   | 31.4 | 2748   | 3 | US-09-252-991A-13227 | Sequence 13227, A  |
| 64 | 60   | 31.4 | 2748   | 3 | US-08-494-907-1      | Sequence 1, Appli  |
| 65 | 59.5 | 31.2 | 342    | 3 | PCT-US96-10986-1     | Sequence 1, Appli  |
| 66 | 59.5 | 31.2 | 702    | 2 | US-08-313-181-1      | Sequence 2, Appli  |
| 67 | 59.5 | 31.2 | 792    | 2 | US-08-494-907-5      | Sequence 5, Appli  |
| 68 | 59.5 | 31.2 | 792    | 6 | PCT-US96-10986-5     | Sequence 5, Appli  |
| 69 | 59.5 | 31.2 | 1374   | 3 | US-09-252-991A-13227 | Sequence 13227, A  |
| 70 | 59.5 | 31.2 | 3680   | 2 | US-08-494-907-1      | Sequence 1, Appli  |
| 71 | 59.5 | 31.2 | 3680   | 6 | PCT-US96-10986-1     | Sequence 1, Appli  |
| 72 | 59.5 | 31.2 | 4086   | 2 | US-08-313-181-1      | Sequence 1, Appli  |
| 73 | 59.5 | 31.2 | 5076   | 2 | US-08-494-907-2      | Sequence 2, Appli  |
| 74 | 59.5 | 31.2 | 5076   | 6 | PCT-US96-10986-2     | Sequence 2, Appli  |
| 75 | 59.5 | 31.2 | 6170   | 2 | US-08-494-907-4      | Sequence 4, Appli  |
| 76 | 59.5 | 31.2 | 6170   | 6 | PCT-US96-10986-4     | Sequence 4, Appli  |
| 77 | 59.5 | 31.2 | 6387   | 2 | US-08-494-907-3      | Sequence 3, Appli  |
| 78 | 59.5 | 31.2 | 6387   | 6 | PCT-US96-10986-3     | Sequence 3, Appli  |
| 79 | 59.5 | 31.2 | 7198   | 3 | US-08-994-035C-4     | Sequence 4, Appli  |
| 80 | 59.5 | 31.2 | 7198   | 3 | US-09-395-861-4      | Sequence 4, Appli  |
| 81 | 59.5 | 31.2 | 26140  | 3 | US-09-949-016-14254  | Sequence 14254, A  |
| 82 | 59.5 | 31.2 | 26140  | 3 | US-09-949-016-14255  | Sequence 14255, A  |





Db 2 ATGGCGACGCGCTCGGCGCGCGCTGCTCTCTCTCGCGCGCGCGCGCGCG 61

Qy 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39

Db 62 GCCGCGCTCGGCGACCGGCGCGCGCGCGCTCCAGCGCTGCTGCGCGCGCG 118

RESULT 6

US-09-192-909-1

/ Sequence 1, Application US/09192909

/ Patent No. 6307124

/ GENERAL INFORMATION:

/ APPLICANT: Jens Kossmann

/ APPLICANT: Claus Froberg

/ TITLE OF INVENTION: Nucleic acid molecules encoding soluble

/ TITLE OF INVENTION: starch synthases from maize

/ NUMBER OF SEQUENCES: 3

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: James F. Haley, Jr., c/o FISH & NEAVE

/ STREET: 1251 Avenue of the Americas

/ CITY: New York

/ STATE: New York

/ COUNTRY: USA

/ ZIP: 10020

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

/ CURRENT APPLICATION NUMBER: US/09192,909

/ FILING DATE:

/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: PCT/EP97/02527

/ FILING DATE: 16-MAY-1997

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: DE 196 19 918.2

/ FILING DATE: 17-MAY-1996

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Haley, Jr., James F.

/ REGISTRATION NUMBER: 27,794

/ REFERENCE/DOCKET NUMBER: GFB-9

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 212-596-9000

/ TELEFAX: 212-96-9090

/ INFORMATION FOR SEQ ID NO: 1:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 2383 base pairs

/ TYPE: nucleotide

/ STRANDEDNESS: double

/ TOPOLOGY: linear

/ MOLECULE TYPE: cDNA to mRNA

/ HYPOTHETICAL: NO

/ ANTI-SENSE: NO

/ ORIGINAL SOURCE:

/ ORGANISM: Zea mays

/ TISSUE TYPE: endosperm

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: 2..1950

/ OTHER INFORMATION: /function= "starch synthesis"

/ OTHER INFORMATION: /product= "soluble starch synthase"

US-09-192-909-1

Alignment Scores:

Pred. No.: 3.38e-14 Length: 2383

Score: 191.00 Matches: 38

Percent Similarity: 97.4% Conservative: 0

Best Local Similarity: 97.4% Mismatches: 1

Query Match: 100.0% Indels: 0

DB: 3 Gaps: 0

US-10-628-525A-37 (1-39) x US-09-192-909-1 (1-2383)

Qy 1 MetaAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTTPPro 20

Db 29 ATGGGAGCGCCCTCGGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCGCGCGCGCGCGCG 88

Qy 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39

Db 89 GCCGCGCTCGGCGACCGGCGCGCGCGCGCTCCAGCGCTGCTGCGCGCGCGCG 145

RESULT 7

US-09-931-297-1

/ Sequence 1, Application US/09931297

/ Patent No. 6635804

/ GENERAL INFORMATION:

/ APPLICANT: Jens Kossmann

/ APPLICANT: Claus Froberg

/ TITLE OF INVENTION: Nucleic acid molecules encoding soluble

/ TITLE OF INVENTION: starch synthases from maize

/ NUMBER OF SEQUENCES: 3

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: James F. Haley, Jr., c/o FISH & NEAVE

/ STREET: 1251 Avenue of the Americas

/ CITY: New York

/ STATE: New York

/ COUNTRY: USA

/ ZIP: 10020

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/931,297

/ FILING DATE: 16-Aug-2001

/ CLASSIFICATION: <Unknown>

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: 09/192,909

/ FILING DATE: <Unknown>

/ APPLICATION NUMBER: DE 196 19 918.2

/ FILING DATE: 17-MAY-1996

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Haley, Jr., James F.

/ REGISTRATION NUMBER: 27,794

/ REFERENCE/DOCKET NUMBER: GFB-9

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 212-596-9000

/ TELEFAX: 212-96-9090

/ INFORMATION FOR SEQ ID NO: 1:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 2383 base pairs

/ TYPE: nucleotide

/ STRANDEDNESS: double

/ TOPOLOGY: linear

/ MOLECULE TYPE: cDNA to mRNA

/ HYPOTHETICAL: NO

/ ANTI-SENSE: NO

/ ORIGINAL SOURCE:

/ ORGANISM: Zea mays

/ TISSUE TYPE: endosperm

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: 2..1950

/ OTHER INFORMATION: /function= "starch synthesis"

/ OTHER INFORMATION: /product= "soluble starch synthase"

/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-931-297-1

Alignment Scores:

Pred. No.: 3.38e-14 Length: 2383

Score: 191.00 Matches: 38

Percent Similarity: 97.4% Conservative: 0

Best Local Similarity: 97.4% Mismatches: 1

Query Match: 100.0% Indels: 0



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Score: 168.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 88.0% Indels: 1
DB: 2 Gaps: 0

US-10-628-525A-37 (1-39) x US-08-572-951-1 (1-2990)

QY 1 MetaAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg**AlaTrpProLa 20
Db 602 ARGGGACCCCTCGGCGCGTGGCGCGCGGTGCTCTCTCGCGCGGC-GCCTGGCGG 660
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
Db 661 GCGGCGGTGGGACCGCGCGCGCGCGGAGGCTCCAGCGGTGCTGCGCGCGG 717

RESULT 11
US-10-200-012-7
; Sequence 7, Application US/10200012
; Patent No. 6955905
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: PR/SET- Domain Containing Nucleic Acids,
; FILE OF INVENTION: Polypeptides, Antibodies and Methods of Use
; FILE REFERENCE: P-LJ 5301
; CURRENT APPLICATION NUMBER: US/10/200,012
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US 09/910,478
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1437
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)...(1161)
US-10-200-012-7

Alignment Scores:
Pred. No.: 42.1 Length: 1437
Score: 66.00 Matches: 19
Percent Similarity: 55.3% Conservative: 2
Best Local Similarity: 50.0% Mismatches: 17
Query Match: 34.6% Indels: 0
DB: 3 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-200-012-7 (1-1437)

QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg**AlaTrpProLa 21
Db 1023 GCGGACCGCA 1082
QY 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
Db 1083 CCGGACCGC 1136

RESULT 12
US-10-108-915-9/c
; Sequence 9, Application US/10108915
; Patent No. 6855868
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Shen, Jennie
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: Geranylgeranyl Pyrophosphate Synthases
; FILE REFERENCE: BB1286 US NA
; CURRENT APPLICATION NUMBER: US/10/108,915
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 09/452,238
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/110,592
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; PRIOR FILING DATE: EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Zea mays
US-10-108-915-9

Alignment Scores:
Pred. No.: 10.7 Length: 365
Score: 65.50 Matches: 16
Percent Similarity: 57.5% Conservative: 7
Best Local Similarity: 40.0% Mismatches: 12
Query Match: 34.3% Indels: 5
DB: 3 Gaps: 2

US-10-628-525A-37 (1-39) x US-10-108-915-9 (1-365)

QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg**AlaTrpProLa 21
Db 132 GCATCACCAACAATCTTCAGTTCTGCTGT-----GGCGATATAGTTGGCCAGT 82
QY 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArg-----ValLeuArgArg 39
Db 81 GCAACAGGGGTGCTGCCTTCTCTGTCGACCAAGGAGCTGCTCTGTGCTCAGAGA 22

RESULT 13
US-08-891-254-8
; Sequence 8, Application US/08891254
; Patent No. 5776889
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Beer, Steven V.
; TITLE OF INVENTION: Hypersensitive Response
; TITLE OF INVENTION: Induced Resistance In Plants
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,254
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/475,775
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 14603/10050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1035 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-891-254-8

Alignment Scores:
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Pred. No.: 38.9 Length: 1035  
Score: 65.00 Matches: 17  
Percent Similarity: 67.9% Conservative: 2  
Best Local Similarity: 60.7% Mismatches: 6  
Query Match: 34.0% Indels: 3  
DB: 2 Gaps: 1

US-10-628-525A-37 (1-39) x US-08-891-254-8 (1-1035)

QY 15 AlaArg\*\*\*AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgLe 32  
Db 464 GCCAGGGCGCCTGGCGGAAGCGCTGCAGGAGATCGAGCAGATCCTCGCCCGAGCTCGGCG 523  
QY 32 uGlnArgValLeuArgArgArg 39  
Db 524 GCGGCGGTGCTGGCGCGCGCGG 545

## RESULT 14

US-08-819-539-8  
; Sequence 8, Application US/08819539  
; Patent No. 5859324  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Zhong-Min  
; APPLICANT: Beer, Steven V.  
; TITLE OF INVENTION: Hypersensitive Response  
; TITLE OF INVENTION: Induced Resistance In Plants  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
; STREET: Clinton Square, P.O. Box 1051  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 14603

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/819,539  
; FILING DATE: 17-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/475,775

; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldman, Michael L.  
; REGISTRATION NUMBER: 30,727  
; REFERENCE/DOCKET NUMBER: 14603/10050  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 263-1304  
; TELEFAX: (716) 263-1600  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1035 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-819-539-8

Alignment Scores:  
Pred. No.: 38.9 Length: 1035  
Score: 65.00 Matches: 17  
Percent Similarity: 67.9% Conservative: 2  
Best Local Similarity: 60.7% Mismatches: 6  
Query Match: 34.0% Indels: 3  
DB: 2 Gaps: 1

US-10-628-525A-37 (1-39) x US-08-819-539-8 (1-1035)

QY 15 AlaArg\*\*\*AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgLe 32

Db 464 GCCAGGGCGCCTGGCGGAAGCGCTGCAGGAGATCGAGCAGATCCTCGCCCGAGCTCGGCG 523  
QY 32 uGlnArgValLeuArgArgArg 39  
Db 524 GCGGCGGTGCTGGCGCGCGCGG 545

## RESULT 15

US-09-030-270A-8  
; Sequence 8, Application US/09030270A  
; Patent No. 5977060  
; GENERAL INFORMATION:  
; APPLICANT: Zitter, Thomas A.  
; APPLICANT: Wei, Zhong-Min  
; TITLE OF INVENTION: INSECT CONTROL WITH A  
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
; STREET: P.O. Box 1051, Clinton Square  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 14603

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,270A  
; FILING DATE:  
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/039,226  
; FILING DATE: 28-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldman, Michael L.  
; REGISTRATION NUMBER: 30,727  
; REFERENCE/DOCKET NUMBER: 19603/1521  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 263-1304  
; TELEFAX: (716) 263-1600  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1035 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-09-030-270A-8

Alignment Scores:  
Pred. No.: 38.9 Length: 1035  
Score: 65.00 Matches: 17  
Percent Similarity: 67.9% Conservative: 2  
Best Local Similarity: 60.7% Mismatches: 6  
Query Match: 34.0% Indels: 3  
DB: 2 Gaps: 1

US-10-628-525A-37 (1-39) x US-09-030-270A-8 (1-1035)

QY 15 AlaArg\*\*\*AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgLe 32  
Db 464 GCCAGGGCGCCTGGCGGAAGCGCTGCAGGAGATCGAGCAGATCCTCGCCCGAGCTCGGCG 523  
QY 32 uGlnArgValLeuArgArgArg 39  
Db 524 GCGGCGGTGCTGGCGCGCGCGG 545

## RESULT 16

US-08-984-207-8  
; Sequence 8, Application US/08984207

Patent No. 6235974  
GENERAL INFORMATION:  
APPLICANT: Qiu, Dewen  
APPLICANT: Wei, Zhong-Min  
APPLICANT: Beer, Steven V.  
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED  
TITLE OF INVENTION: RESISTANCE IN PLANTS BY SEED TREATMENT  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: P.O. Box 1051, Clinton Square  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/984,207  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/033,230  
FILING DATE: 05-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/1201  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1035 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

US-08-984-207-8  
Alignment Scores:  
Pred. No.: 38.9 Length: 1035  
Score: 65.00 Matches: 17  
Percent Similarity: 67.9% Conservative: 2  
Best Local Similarity: 60.7% Mismatches: 6  
Query Match: 34.0% Indels: 3  
DB: 3 Gaps: 1

US-10-628-525A-37 (1-39) x US-08-984-207-8 (1-1035)

QY 15 AlaArg\*\*AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgIe 32  
Db 464 GCGAGGGCGCTGCGCGAAGCGCTGCAGAGATCGAGCAGATCTCGCCAGCTCGGG 523  
QY 32 uGlnArgValLeuArgArgArg 39  
Db 524 GCGGCGGTGCTGCGCGCGCGG 545

RESULT 17

US-09-013-587-8  
Sequence 8, Application US/09013587  
Patent No. 6277814  
GENERAL INFORMATION:  
APPLICANT: Qiu, Dewen  
APPLICANT: Wei, Zhong-Min  
APPLICANT: Beer, Steven V.  
TITLE OF INVENTION: ENHANCEMENT OF GROWTH IN PLANTS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP

STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/013,587  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/036,048  
FILING DATE: 27-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/1501  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1035 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

US-09-013-587-8

Alignment Scores:  
Pred. No.: 38.9 Length: 1035  
Score: 65.00 Matches: 17  
Percent Similarity: 67.9% Conservative: 2  
Best Local Similarity: 60.7% Mismatches: 6  
Query Match: 34.0% Indels: 3  
DB: 3 Gaps: 1

US-10-628-525A-37 (1-39) x US-09-013-587-8 (1-1035)

QY 15 AlaArg\*\*AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgIe 32  
Db 464 GCGAGGGCGCTGCGCGAAGCGCTGCAGAGATCGAGCAGATCTCGCCAGCTCGGG 523  
QY 32 uGlnArgValLeuArgArgArg 39  
Db 524 GCGGCGGTGCTGCGCGCGCGG 545

RESULT 18

US-09-086-118-28  
Sequence 28, Application US/09086118  
Patent No. 6583107  
GENERAL INFORMATION:

APPLICANT: Laby, Ronald J.  
APPLICANT: Beer, Steven V.  
APPLICANT: Wei, Zhong-Min  
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR  
TITLE OF INVENTION: FRAGMENTS ELICITING A HYPERSENSITIVE RESPONSE AND USES  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,118
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,109
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1035 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-086-118-28

Alignment Scores:
Pred. No.: 38.9 Length: 1035
Score: 65.00 Matches: 17
Percent Similarity: 67.9% Conservative: 2
Best Local Similarity: 60.7% Mismatches: 6
Query Match: 34.0% Indels: 3
DB: Gaps: 1

US-10-628-525A-37 (1-39) x US-09-086-118-28 (1-1035)
QY 15 AlaArg**AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgle 32
Db 464 GCCAGGGCGGCTGCGCGAAGCGCTGCAGGAGATCGAGCAGATCTCTGCCCGCAGCTCGGG 523
QY 32 uGlnArgValLeuArgArgArg 39
Db 524 GCGGCGGTGCTGCGCGCGCGG 545

RESULT 19
US-09-431-614-16
; Sequence 16, Application US/09431614
; Patent No. 6624139
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
; TITLE OF INVENTION: RESISTANCE
; FILE REFERENCE: 21829/41 (BEC-003)
; CURRENT APPLICATION NUMBER: US/09/431,614
; CURRENT FILING DATE: 1999-11-02
; EARLIER APPLICATION NUMBER: 60/107,243
; EARLIER FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Pseudomonas solanacearum
US-09-431-614-16

Alignment Scores:
Pred. No.: 38.9 Length: 1035
Score: 65.00 Matches: 17
Percent Similarity: 67.9% Conservative: 2
Best Local Similarity: 60.7% Mismatches: 6
Query Match: 34.0% Indels: 3
DB: Gaps: 1

US-10-628-525A-37 (1-39) x US-09-086-118-28 (1-1035)
QY 15 AlaArg**AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgle 32
Db 464 GCCAGGGCGGCTGCGCGAAGCGCTGCAGGAGATCGAGCAGATCTCTGCCCGCAGCTCGGG 523
QY 32 uGlnArgValLeuArgArgArg 39
Db 524 GCGGCGGTGCTGCGCGCGCGG 545

RESULT 19
US-09-431-614-16
; Sequence 16, Application US/09431614
; Patent No. 6624139
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
; TITLE OF INVENTION: RESISTANCE
; FILE REFERENCE: 21829/41 (BEC-003)
; CURRENT APPLICATION NUMBER: US/09/431,614
; CURRENT FILING DATE: 1999-11-02
; EARLIER APPLICATION NUMBER: 60/107,243
; EARLIER FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Pseudomonas solanacearum
US-09-431-614-16

Alignment Scores:
Pred. No.: 38.9 Length: 1035
Score: 65.00 Matches: 17
Percent Similarity: 67.9% Conservative: 2
Best Local Similarity: 60.7% Mismatches: 6
Query Match: 34.0% Indels: 3
DB: Gaps: 1

US-10-628-525A-37 (1-39) x US-09-086-118-28 (1-1035)
QY 15 AlaArg**AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgle 32
Db 464 GCCAGGGCGGCTGCGCGAAGCGCTGCAGGAGATCGAGCAGATCTCTGCCCGCAGCTCGGG 523
QY 32 uGlnArgValLeuArgArgArg 39
Db 524 GCGGCGGTGCTGCGCGCGCGG 545

RESULT 21
PCT-US96-08819-8
; Sequence 8, Application PC/TUS9608819
; GENERAL INFORMATION:
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED
; TITLE OF INVENTION: RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/08819

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US-10-628-525A-37 (1-39) x US-09-431-614-16 (1-1035)
QY 15 AlaArg**AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgle 32
Db 464 GCCAGGGCGGCTGCGCGAAGCGCTGCAGGAGATCGAGCAGATCTCTGCCCGCAGCTCGGG 523
QY 32 uGlnArgValLeuArgArgArg 39
Db 524 GCGGCGGTGCTGCGCGCGCGG 545

RESULT 20
US-09-412-100-36
; Sequence 36, Application US/09412100
; Patent No. 6858707
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Fan, Hao
; APPLICANT: Niggemeyer, Jennifer L.
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR FRAGMENTS WHICH ARE
; TITLE OF INVENTION: ACTIVE BUT DO NOT ELICIT A HYPERSENSITIVE RESPONSE
; FILE REFERENCE: 21829/31 (BEC-002)
; CURRENT APPLICATION NUMBER: US/09/412,100
; CURRENT FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/103,050
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Pseudomonas solanacearum
US-09-412-100-36

Alignment Scores:
Pred. No.: 38.9 Length: 1035
Score: 65.00 Matches: 17
Percent Similarity: 67.9% Conservative: 2
Best Local Similarity: 60.7% Mismatches: 6
Query Match: 34.0% Indels: 3
DB: Gaps: 1

US-10-628-525A-37 (1-39) x US-09-412-100-36 (1-1035)
QY 15 AlaArg**AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgle 32
Db 464 GCCAGGGCGGCTGCGCGAAGCGCTGCAGGAGATCGAGCAGATCTCTGCCCGCAGCTCGGG 523
QY 32 uGlnArgValLeuArgArgArg 39
Db 524 GCGGCGGTGCTGCGCGCGCGG 545

RESULT 21
PCT-US96-08819-8
; Sequence 8, Application PC/TUS9608819
; GENERAL INFORMATION:
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED
; TITLE OF INVENTION: RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/08819

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; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36063 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium leprae
; US-08-311-731A-140

Alignment Scores:
Pred. No.: 2,6e+03 Length: 36063
Score: 64.00 Matches: 12
Percent Similarity: 63.2% Conservative: 0
Best Local Similarity: 63.2% Mismatches: 7
Query Match: 33.5% Indels: 0
DB: Gaps: 0

US-10-628-525A-37 (1-39) x US-08-311-731A-140 (1-36063)

QY 7 valGlyAlaAaCysLeuLeuLeuAlaAaG***AlaTTPProAlaAlaValGlyAaP 25
Db 13474 GTCGGTCAAGATGTTGGCTTCTGTAAGCCGAGCATGGCTCGGTGTGTGTGAC 13418

RESULT 25
US-09-544-398B-10
; Sequence 10, Application US/09544398B
; Patent No. 6770461
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US 09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 8705
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-544-398B-10

Alignment Scores:
Pred. No.: 719 Length: 8705
Score: 63.00 Matches: 14
Percent Similarity: 58.1% Conservative: 4
Best Local Similarity: 45.2% Mismatches: 11
Query Match: 33.0% Indels: 2
DB: Gaps: 1

US-10-628-525A-37 (1-39) x US-09-544-398B-10 (1-8705)

QY 8 GlyAlaAaCysLeuLeuLeuAlaAaG***AlaTTPProAlaAlaValGlyAaPArgAla 27
Db 13474 GTCGGTCAAGATGTTGGCTTCTGTAAGCCGAGCATGGCTCGGTGTGTGTGAC 13418

RESULT 26
US-09-543-771B-10
; Sequence 10, Application US/09543771B
; Patent No. 6780609
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-014
; CURRENT APPLICATION NUMBER: US 09/543,771B
; CURRENT FILING DATE: 2000-04-05
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 8705
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-543-771B-10

Alignment Scores:
Pred. No.: 719 Length: 8705
Score: 63.00 Matches: 14
Percent Similarity: 58.1% Conservative: 4
Best Local Similarity: 45.2% Mismatches: 11
Query Match: 33.0% Indels: 2
DB: Gaps: 1

US-10-628-525A-37 (1-39) x US-09-543-771B-10 (1-8705)

QY 8 GlyAlaAaCysLeuLeuLeuAlaAaG***AlaTTPProAlaAlaValGlyAaPArgAla 27
Db 7584 GGTGATGTGTGTGCTGTAGCCCGAGCTACTTGGAGGCTGAGGTGGAGATCACTT 7643

RESULT 27
US-09-252-991A-3246
; Sequence 3246, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US 09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3246
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3246
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Db 7584 GGTGATGTGTGTGCTGTAGCCCGAGCTACTTGGAGGCTGAGGTGGAGATCACTT 7643

QY 28 ArgProArg-----ArgLeuGlnArgValLeu 36
Db 7644 GAGCCCGAGGAGTGGAGGCTGCAGCGAGTCATG 7676

RESULT 26
US-09-543-771B-10
; Sequence 10, Application US/09543771B
; Patent No. 6780609
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-014
; CURRENT APPLICATION NUMBER: US 09/543,771B
; CURRENT FILING DATE: 2000-04-05
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 8705
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-543-771B-10

Alignment Scores:
Pred. No.: 719 Length: 8705
Score: 63.00 Matches: 14
Percent Similarity: 58.1% Conservative: 4
Best Local Similarity: 45.2% Mismatches: 11
Query Match: 33.0% Indels: 2
DB: Gaps: 1

US-10-628-525A-37 (1-39) x US-09-543-771B-10 (1-8705)

QY 8 GlyAlaAaCysLeuLeuLeuAlaAaG***AlaTTPProAlaAlaValGlyAaPArgAla 27
Db 7584 GGTGATGTGTGTGCTGTAGCCCGAGCTACTTGGAGGCTGAGGTGGAGATCACTT 7643

RESULT 27
US-09-252-991A-3246
; Sequence 3246, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US 09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3246
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3246
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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 2, 2006, 00:58:46 ; Search time 184.256 Seconds

(without alignments)

1750.313 Million cell updates/sec

Title: US-10-628-525A-37

Perfect score: 191

Sequence: 1 MATPSAVGACILLARXANPAVGDPRRLQVLR 39

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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-DB=Published Applications NA Main -QPMF=fastap -SUFFIX=p2n.rnpbm  
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1  
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=150 -DOCALLIGN=200 -THR\_SCORE=pct  
-THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFM=ptc -NORM=ext  
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-YGAPOF=10 -YGAPEXT=0.5 -DELOF=6 -DELEXT=7

Database : Published Applications NA Main:

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description                           |
|------------|-------|---------------|--------|----|---------------------------------------|
| 1          | 191   | 100.0         | 153    | 6  | US-10-336-753-58 Sequence 58, Appl    |
| 2          | 191   | 100.0         | 153    | 8  | US-10-628-525-18 Sequence 18, Appl    |
| 3          | 191   | 100.0         | 2383   | 3  | US-09-931-297-1 Sequence 1, Appl      |
| 4          | 191   | 100.0         | 2991   | 7  | US-10-109-048-1142 Sequence 1142, Ap  |
| 5          | 191   | 100.0         | 3123   | 8  | US-10-425-115-54073 Sequence 54073, A |
| 6          | 143.5 | 75.1          | 2670   | 7  | US-10-767-701-13043 Sequence 13043, A |
| 7          | 73    | 38.2          | 879    | 7  | US-10-767-701-12709 Sequence 12709, A |

Sequence 6595, Ap  
Sequence 35694, A  
Sequence 13012, A  
Sequence 12477, A  
Sequence 774283,  
Sequence 837284,  
Sequence 15113, A  
Sequence 15114, A  
Sequence 15113, A  
Sequence 15114, A  
Sequence 1331, Ap  
Sequence 401, App  
Sequence 505, Appl  
Sequence 289, App  
Sequence 4312, App  
Sequence 37, Appl  
Sequence 25, Appl  
Sequence 7, Appl  
Sequence 9, Appl  
Sequence 9, Appl  
Sequence 16430, A  
Sequence 134772, A  
Sequence 9638, Ap  
Sequence 28, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Sequence 16, Appl  
Sequence 8, Appl  
Sequence 8, Appl  
Sequence 8, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Sequence 1808, Ap  
Sequence 152464, A  
Sequence 48437, A  
Sequence 90364, A  
Sequence 2, Appl  
Sequence 25460, A  
Sequence 25459, A  
Sequence 6, Appl  
Sequence 1, Appl  
Sequence 174495, A  
Sequence 273237, A  
Sequence 4676, Ap  
Sequence 19616, A  
Sequence 34175, A  
Sequence 41521, A  
Sequence 44185, A  
Sequence 6773, Ap  
Sequence 10, Appl  
Sequence 10, Appl  
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Sequence 10, Appl  
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Sequence 10, Appl  
Sequence 1408, Ap  
Sequence 1, Appl  
Sequence 18308, A  
Sequence 73402, A  
Sequence 19904, A  
Sequence 81665, A  
Sequence 102, App  
Sequence 14, Appl  
Sequence 49263, A  
Sequence 51392, A





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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/941.445
; FILING DATE: 30-SEP-1997
; APPLICATION NUMBER: US 60/026.855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: Not Relevant
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..153
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-628-525-18
Alignment Scores:
Pred. No.: 2.5e-19 Length: 153
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0
US-10-628-525A-37 (1-39) x US-10-628-525-18 (1-153)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTPPro 20
Db 1 ATGGCGACGCCCTCGGCGCGTGGCGCGTGGCGCGTGGCGCGTGGCGCG 60
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
Db 61 GCCGCGCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 117
RESULT 3
US-09-931-297-1
; Sequence 1, Application US/09931297
; Publication No. US20020088023A1
; GENERAL INFORMATION:
; APPLICANT: Jens Kossmann
; Claus Froberg
; TITLE OF INVENTION: Nucleic acid molecules encoding soluble
; starch synthases from maize
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/931,297
; FILING DATE: 16-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/192,909
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 196 19 918.2
; FILING DATE: 17-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley, Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: GFB-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-96-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2383 base pairs
; TYPE: nucleotide
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; TISSUE TYPE: endosperm
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..1950
; OTHER INFORMATION: /function= "starch synthesis"
; /product= "soluble starch synthase"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-931-297-1
Alignment Scores:
Pred. No.: 4.03e-18 Length: 2383
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-628-525A-37 (1-39) x US-09-931-297-1 (1-2383)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTPPro 20
Db 29 ATGGCGACGCCCTCGGCGCGTGGCGCGTGGCGCGTGGCGCGTGGCGCG 88
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
Db 89 GCCGCGCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 145
RESULT 4
US-10-109-048-1142
; Sequence 1142, Application US/10109048
; Publication No. US20040107461A1
; GENERAL INFORMATION:
; APPLICANT: COMMURI, PADMA
; APPLICANT: KEELING, PETER L.
; APPLICANT: RAMIREZ, NONA
; APPLICANT: MCKEAN, ANGELA
; APPLICANT: GAO ZHONG
; APPLICANT: GUAN, HANPING
; TITLE OF INVENTION: GLUCAN CHAIN LENGTH DOMAINS
; FILE REFERENCE: 2461-76
; CURRENT APPLICATION NUMBER: US/10/109,048
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/279,720
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 1154
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1142
; LENGTH: 2991
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
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; NAME/KEY: modified_base
; LOCATION: (2709)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-109-048-1142

Alignment Scores:
Pred. No.: 5,08e-18 Length: 2991
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-109-048-1142 (1-2991)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpPro 20
Db 602 ATGGCGACGCCCTCGGCGCGTGGCGCGCGCTCTCTCTCGCGCGCGCGCTGGCGG 661
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
Db 662 GCCGCGCTCGGCGACCGCGGCGCGCGCGCGCTCCAGCGGTGCTGCGCGCGCGG 718

RESULT 5
US-10-425-115-54073/c
; Sequence 54073, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 54073
; LENGTH: 3123
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(3123)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: MPT4577_149315C.1
US-10-425-115-54073

Alignment Scores:
Pred. No.: 5.3e-18 Length: 3123
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-425-115-54073 (1-3123)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpPro 20
Db 2390 ATGGCGACGCCCTCGGCGCGTGGCGCGCGTCTCTCTCTCGCGCGCGCGCTGGCGG 2331
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
Db 2330 GCCGCGCTCGGCGACCGCGGCGCGCGCGCGCTCCAGCGGTGCTGCGCGCGCGG 2274

RESULT 6
US-10-767-701-13043
; Sequence 13043, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 12709
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS107500_1
US-10-767-701-12709

Alignment Scores:
Pred. No.: 0.473 Length: 879
Score: 73.00 Matches: 18
Percent Similarity: 43.4% Conservative: 5
Best Local Similarity: 34.0% Mismatches: 6
Query Match: 38.2% Indels: 24
DB: 7 Gaps: 2

US-10-628-525A-37 (1-39) x US-10-767-701-12709 (1-879)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpPro 17
Db 138 ATGGCGACGCCCTCGGCGCGTGGCGCGCGTCTCTCTCTCGCGCGCGCGCTGGCGG 197
QY 19 -----TrrProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgVal 35
Db 198 CTGCGCGTGGCGCGCGCGCGCGCGATCGCGCGCGCGCGCGCGCGCTCCAGCGCGGTG 257

RESULT 7
US-10-767-701-12709/c
; Sequence 12709, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 12709
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS107500_1
US-10-767-701-12709

Alignment Scores:
Pred. No.: 0.473 Length: 879
Score: 73.00 Matches: 18
Percent Similarity: 43.4% Conservative: 5
Best Local Similarity: 34.0% Mismatches: 6
Query Match: 38.2% Indels: 24
DB: 7 Gaps: 2

US-10-628-525A-37 (1-39) x US-10-767-701-12709 (1-879)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpPro 17
Db 138 ATGGCGACGCCCTCGGCGCGTGGCGCGCGTCTCTCTCTCGCGCGCGCGCTGGCGG 197
QY 19 -----TrrProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgVal 35
Db 198 CTGCGCGTGGCGCGCGCGCGCGCGATCGCGCGCGCGCGCGCGCGCTCCAGCGCGGTG 257
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Db 349 ATGGCCAGCCCTCCCAATCGGATCGGATGCTTCATGATGGGAGGGCGTAGGCGGCG 230
Qy 18 -----AlaTtp----- 19
Db 289 GAGTCTTCTGCTGTGGCAACGCGAGGACGCGGGGCGTGTGGATGCGCGGACGCGGCGG 230
Qy 20 -----ProAlaAlaValGlyAspArgAlaArgPro 29
Db 229 ATCCCTGCCCCCGCGCGGTGGGCGCGGCGCGCGCGCG 191
RESULT 8
US-10-425-115-6595
; Sequence 6595, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 6595
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_106006C.1
US-10-425-115-6595
Alignment Scores:
Pred. No.: 0.229 Length: 307
Score: 72.00 Matches: 14
Percent Similarity: 78.9% Conservative: 1
Best Local Similarity: 73.7% Mismatches: 4
Query Match: 37.7% Indels: 0
Gaps: 0
Db: 8
US-10-628-525A-37 (1-39) x US-10-425-115-6595 (1-307)
Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTtp 19
Db 211 TTGGTTACGCCCTCGTTTCGAGGGTGTGCTGCTCTCTCGCGGTACGCTCG 267
RESULT 9
US-10-369-493-35694/c
; Sequence 35694, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35694
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-369-493-35694
Alignment Scores:
Pred. No.: 1.68 Length: 1569
Score: 69.50 Matches: 19
Percent Similarity: 58.5% Conservative: 5
Best Local Similarity: 46.3% Mismatches: 14
Query Match: 36.4% Indels: 3
Gaps: 1
US-10-628-525A-37 (1-39) x US-10-369-493-35694 (1-1569)
Qy 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTtpProAla 21
Db 134 AGCAGCCCTCGCGCGCCAGCGGTCGCGATTCGGGCTCTTCACCGGATGCGCGCA 75
Qy 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 38
Db 74 GCC-----GACAGGCAATCACCGCCCACTGGTCGACGTCATCAGGAGA 30
RESULT 10
US-10-198-846-13012/c
; Sequence 13012, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; FILE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13012
; LENGTH: 1013
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 2, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997,
; LOCATION: 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007,
; LOCATION: 1008, 1009, 1010, 1011, 1012, 1013
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13012
Alignment Scores:
Pred. No.: 1.8 Length: 1013
Score: 69.50 Matches: 19
Percent Similarity: 58.5% Conservative: 5
Best Local Similarity: 46.3% Mismatches: 14
Query Match: 36.4% Indels: 3
Gaps: 1
US-10-628-525A-37 (1-39) x US-10-198-846-13012 (1-1013)
Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg----- 17
Db 943 GTGGCGCGGCGCGCGCGTGTGGGGGCGCGCGCTTTTGGGGGCGCGCGTGTGGTGGCGG 884
Qy 18 AlaTtpProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 37
Db 883 TCTTGGCGGCGCGCGCTGTGCTCTGCGCGCGCGCGCGCGGCTTGTAGGTTTGGGTCGCG 824
Qy 38 Arg 38
Db 823 CGC 821
RESULT 11
US-10-767-701-12477
; Sequence 12477, Application US/10767701
; Publication No. US20040172684A1
```

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/ GENERAL INFORMATION:
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
/ FILE REFERENCE: 38-21(53535)B
/ CURRENT APPLICATION NUMBER: US/10/767,701
/ NUMBER OF SEQ ID NOS: 2004-01-29
/ NUMBER OF SEQ ID NOS: 63128
/ SEQ ID NO 12477
/ LENGTH: 807
/ TYPE: DNA
/ ORGANISM: Sorghum bicolor
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(807)
/ OTHER INFORMATION: unsure at all n locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS12645_1
US-10-767-701-12477

Alignment Scores:
Pred. No.: 2.39 Length: 807
Score: 68.00 Matches: 18
Percent Similarity: 52.6% Conservative: 2
Best Local Similarity: 47.4% Mismatches: 14
Query Match: 35.6% Indels: 4
DB: 7 Gaps: 1

US-10-628-525A-37 (1-39) x US-10-767-701-12477 (1-807)

QY 2 AlaThrProSerAlaValGlyAlaAalaCysLeuLeuLeuAlaArg***AlaTrpProAla 21
Db 161 GCCGCGCCCAACGTGCGCGCGCGCGCC-----GCCCTCTCGGTGGTGGCGGTAC 208
QY 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
Db 209 AGACGGGGCGCGAGAGCGTCCCGTGTCTGCCAGCGCGCGCGGGAGG 262

RESULT 12
US-09-925-065A-774283/c
/ Sequence 774283, Application US/09925065A
/ Publication No. US20050228172A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 774283
/ LENGTH: 495
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-774283

Alignment Scores:
Pred. No.: 2.05 Length: 495
Score: 67.00 Matches: 18
Percent Similarity: 51.1% Conservative: 5
Best Local Similarity: 40.0% Mismatches: 14
Query Match: 35.1% Indels: 8
DB: 4 Gaps: 2

US-10-628-525A-37 (1-39) x US-09-925-065A-774283 (1-495)

QY 3 ThrProSerAlaValGlyAlaAalaCys-----LeuLeuLeuAla 15
Db 311 TCCCCACGTGCTGTGGCGGTGTCATGTCCCAAGGCTCCCAAGGGCCACCCTCACAGGC 252
QY 16 Arg***AlaTrpProAlaAalaVal---GlyAspArgAlaArgProArgArgLeuGlnArg 34
Db 251 AGAGTGTGTGGCCCGCAGGCCCTCAGTGGGAGCGTGGCGCGCGGAGGATCTGAGGTTTC 192

QY 35 ValLeuArgArgArg 39
Db 191 ACTGGGAGAGACGT 177

RESULT 14
US-10-363-345A-15113/c
/ Sequence 15113, Application US/10363345A
/ Publication No. US20040234960A1
```

```
Best Local Similarity: 40.0% Mismatches: 14
Query Match: 35.1% Indels: 8
DB: 4 Gaps: 2

US-10-628-525A-37 (1-39) x US-09-925-065A-774283 (1-495)

QY 3 ThrProSerAlaValGlyAlaAalaCys-----LeuLeuLeuAla 15
Db 311 TCCCCACGTGCTGTGGCGGTGTCATGTCCCAAGGCTCCCAAGGGCCACCCTCACAGGC 252
QY 16 Arg***AlaTrpProAlaAalaVal---GlyAspArgAlaArgProArgArgLeuGlnArg 34
Db 251 AGAGTGTGTGGCCCGCAGGCCCTCAGTGGGAGCGTGGCGCGCGGAGGATCTGAGGTTTC 192

QY 35 ValLeuArgArgArg 39
Db 191 ACTGGGAGAGACGT 177

RESULT 13
US-09-925-065A-837264/c
/ Sequence 837264, Application US/09925065A
/ Publication No. US20050228172A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 837264
/ LENGTH: 495
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-837264

Alignment Scores:
Pred. No.: 2.05 Length: 495
Score: 67.00 Matches: 18
Percent Similarity: 51.1% Conservative: 5
Best Local Similarity: 40.0% Mismatches: 14
Query Match: 35.1% Indels: 8
DB: 4 Gaps: 2

US-10-628-525A-37 (1-39) x US-09-925-065A-837264 (1-495)

QY 3 ThrProSerAlaValGlyAlaAalaCys-----LeuLeuLeuAla 15
Db 311 TCCCCACGTGCTGTGGCGGTGTCATGTCCCAAGGCTCCCAAGGGCCACCCTCACAGGC 252
QY 16 Arg***AlaTrpProAlaAalaVal---GlyAspArgAlaArgProArgArgLeuGlnArg 34
Db 251 AGAGTGTGTGGCCCGCAGGCCCTCAGTGGGAGCGTGGCGCGCGGAGGATCTGAGGTTTC 192

QY 35 ValLeuArgArgArg 39
Db 191 ACTGGGAGAGACGT 177

RESULT 14
US-10-363-345A-15113/c
/ Sequence 15113, Application US/10363345A
/ Publication No. US20040234960A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 15113
; LENGTH: 778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 15113
US-10-363-345A-15113

Alignment Scores:
Pred. No.: 3.24 Length: 778
Score: 67.00 Matches: 19
Percent Similarity: 55.3% Conservative: 2
Best Local Similarity: 50.0% Mismatches: 17
Query Match: 35.1% Indels: 0
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-363-345A-15113 (1-778)
QY 2 AlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 21
Db 310 GCGACACCGCCGCCACACCGCGCTACAAACACACTCGCCCGCGGTACCCCGCCGCA 251
QY 22 AlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 39
Db 250 CGCGCAGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 197

RESULT 15
US-10-363-345A-15114
; Sequence 15114, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 15114
; LENGTH: 778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 15114
US-10-363-345A-15114

Alignment Scores:
Pred. No.: 3.24 Length: 778
Score: 67.00 Matches: 19
Percent Similarity: 55.3% Conservative: 2
Best Local Similarity: 50.0% Mismatches: 17
Query Match: 35.1% Indels: 0
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-363-345A-15114 (1-778)
QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAla 21
Db 469 GCGACACCGCCGCCACACCGCGCTACAAACACACTCGCCCGCGGTACCCCGCCGCA 528

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QY 22 AlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 39
Db 529 CGCGCAGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 582

RESULT 16
US-10-363-483A-15113/c
; Sequence 15113, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 15113
; LENGTH: 778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 15113
US-10-363-483A-15113

Alignment Scores:
Pred. No.: 3.24 Length: 778
Score: 67.00 Matches: 19
Percent Similarity: 55.3% Conservative: 2
Best Local Similarity: 50.0% Mismatches: 17
Query Match: 35.1% Indels: 0
DB: 9 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-363-483A-15113 (1-778)
QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAla 21
Db 310 GCGACACCGCCGCCACACCGCGCTACAAACACACTCGCCCGCGGTACCCCGCCGCA 251
QY 22 AlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 39
Db 250 CGCGCAGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 197

RESULT 17
US-10-363-483A-15114
; Sequence 15114, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 15114
; LENGTH: 778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 15114
US-10-363-483A-15114

Alignment Scores:
Pred. No.: 3.24 Length: 778
Score: 67.00 Matches: 19
Percent Similarity: 55.3% Conservative: 2

```





```
; ORGANISM: Oryza sativa
US-10-259-165-55

Alignment Scores:
Pred. No.: 4.76 Length: 960
Score: 66.50 Matches: 17
Percent Similarity: 50.0% Conservative: 1
Best Local Similarity: 47.2% Mismatches: 13
Query Match: 34.8% Indels: 5
DB: 6 Gaps: 1

US-10-628-525A-37 (1-39) x US-10-259-165-55 (1-960)

Qy 3 ThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAlaAla 22
Db 124 ACCCGGACAGCTTCTCCGGCTGCTGC-----GCCACTTGCGCCAGCGCG 80

Qy 23 ValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 38
Db 79 ACACCATCGCGGCTCGTCCAGCCGAGGCCCGCCTGAGAAGG 32

RESULT 21
US-10-259-165-289/c
; Sequence 289, Application US/10259165
; Publication No. US20030135888A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, FumiYaki
; APPLICANT: Krepis, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR FILING DATE: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 289
; LENGTH: 1011
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-165-289

Alignment Scores:
Pred. No.: 5.02 Length: 1011
Score: 66.50 Matches: 17
Percent Similarity: 50.0% Conservative: 1
Best Local Similarity: 47.2% Mismatches: 13
Query Match: 34.8% Indels: 5
DB: 6 Gaps: 1

US-10-628-525A-37 (1-39) x US-10-259-165-289 (1-1011)

Qy 3 ThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAlaAla 22
Db 124 ACCCGGACAGCTTCTCCGGCTGCTGC-----GCCACTTGCGCCAGCGCG 80

Qy 23 ValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 38
Db 79 ACACCATCGCGGCTCGTCCAGCCGAGGCCCGCCTGAGAAGG 32
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## RESULT 22

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US-10-739-930-4312/c
; Sequence 4312, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: KOVALLIC, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 4312
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIAB-23APR03-CLUSTER19701_2
US-10-739-930-4312

Alignment Scores:
Pred. No.: 5.02 Length: 1012
Score: 66.50 Matches: 19
Percent Similarity: 52.6% Conservative: 1
Best Local Similarity: 50.0% Mismatches: 17
Query Match: 34.8% Indels: 1
DB: 8 Gaps: 1

US-10-628-525A-37 (1-39) x US-10-739-930-4312 (1-1012)

Qy 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAla 21
Db 557 GCGCGCCTCGAGCGCTCTTGGGGTGGCCCGCAGCGGCTCGCACTCGAACTCCACC 498

Qy 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
Db 497 GCAGCAGCGAGCGCGC---CGCGCGCGCGCGGAGCAGCAGCGGAGGAGA 447
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## RESULT 23

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US-10-132-134-37
; Sequence 37, Application US/10132134
; Publication No. US20030171562A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Yang, Xianshu
; APPLICANT: Staffa, Alfredo
; APPLICANT: Zazopoulos, Emmanuel
; TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES
; FILE REFERENCE: 3012-2US
; CURRENT APPLICATION NUMBER: US/10/132,134
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 6297
; TYPE: DNA
; ORGANISM: Streptomyces amphibiosporus
US-10-132-134-37

Alignment Scores:
Pred. No.: 32 Length: 6297
Score: 66.50 Matches: 19
Percent Similarity: 58.3% Conservative: 2
Best Local Similarity: 52.8% Mismatches: 10
Query Match: 34.8% Indels: 5
DB: 6 Gaps: 2

US-10-628-525A-37 (1-39) x US-10-132-134-37 (1-6297)

Qy 4 ProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAlaAlaVal 23
Db 2704 CCGAGCGCTCCCGGTCGCCCTGTCTGGAGCTGTCTCGCGCGCTGGACCCACGCC 2760
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Qy 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34  
Db 506 CCGGCGCGACGCTGGAGGTGGTGTGCCGCGCACTTCGGCGCGTCCAAAGGAGACGCTCAAGG 565  
Qy 35 ValLeuArgArgArg 39  
Db 566 CCGAGGCGGACGACGG 580

Search completed: April 2, 2006, 02:06:06  
Job time : 202.256 secs

GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 2, 2006, 01:09:48 ; Search time 121.78 Seconds  
(without alignments)

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Title: US-10-628-525a-37

Perfect score: 191

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Searched: 9263891 seqs, 1996499642 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA.New:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 2                  | 67    | 35.1        | 495    | 6  | US-09-925-065A-774283 |
| Sequence 26590, A  |       |             |        |    |                       |
| Sequence 774283, A |       |             |        |    |                       |

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| 67   | 35.1 | 495    | 6  | US-09-925-065A-837264 | Sequence 837264, A  |
| 67   | 35.1 | 1958   | 11 | US-11-096-568A-26982  | Sequence 26982, A   |
| 66   | 34.6 | 1437   | 14 | US-11-121-438-7       | Sequence 7, Appl1   |
| 6    | 33.5 | 3954   | 8  | US-10-750-185-42605   | Sequence 42605, A   |
| 64   | 33.5 | 3954   | 8  | US-10-750-623-42605   | Sequence 42605, A   |
| 62   | 32.5 | 201    | 8  | US-10-995-561-31039   | Sequence 31039, A   |
| 62   | 32.5 | 1258   | 11 | US-11-096-568A-11773  | Sequence 11773, A   |
| 62   | 32.5 | 103660 | 8  | US-10-995-561-13253   | Sequence 13253, A   |
| 61.5 | 32.2 | 2073   | 11 | US-11-096-568A-11714  | Sequence 11714, A   |
| 61   | 31.9 | 201    | 8  | US-10-995-561-31046   | Sequence 31046, A   |
| 60   | 31.4 | 1191   | 8  | US-10-750-185-34977   | Sequence 34977, A   |
| 60   | 31.4 | 1191   | 8  | US-10-750-623-34977   | Sequence 34977, A   |
| 60   | 31.4 | 1268   | 14 | US-11-037-243-23      | Sequence 23, Appl1  |
| 59.5 | 31.2 | 1930   | 11 | US-11-077-619-87      | Sequence 87, Appl1  |
| 59   | 30.9 | 508    | 6  | US-09-925-065A-371296 | Sequence 371296, A  |
| 59   | 30.9 | 523    | 10 | US-10-301-480-441295  | Sequence 441295, A  |
| 59   | 30.9 | 523    | 10 | US-10-301-480-1054704 | Sequence 1054704, A |
| 59   | 30.9 | 673    | 9  | US-10-301-480-39100   | Sequence 39100, A   |
| 59   | 30.9 | 673    | 10 | US-09-925-065A-652509 | Sequence 652509, A  |
| 59   | 30.9 | 800    | 6  | US-09-925-065A-39710  | Sequence 39710, A   |
| 59   | 30.9 | 800    | 9  | US-10-301-480-140948  | Sequence 140948, A  |
| 59   | 30.9 | 800    | 10 | US-10-301-480-754357  | Sequence 754357, A  |
| 59   | 30.9 | 962    | 11 | US-11-096-568A-15852  | Sequence 15852, A   |
| 59   | 30.9 | 1841   | 11 | US-11-096-568A-20625  | Sequence 20625, A   |
| 58.5 | 30.6 | 981    | 11 | US-11-096-568A-9238   | Sequence 9238, Ap   |
| 58.5 | 30.6 | 5189   | 14 | US-11-000-688-884     | Sequence 884, App   |
| 58   | 30.4 | 529    | 10 | US-10-301-480-362244  | Sequence 362244, A  |
| 58   | 30.4 | 529    | 10 | US-10-301-480-975653  | Sequence 975653, A  |
| 58   | 30.4 | 539    | 6  | US-09-925-065A-285243 | Sequence 285243, A  |
| 58   | 30.4 | 591    | 6  | US-09-925-065A-563303 | Sequence 563303, A  |
| 58   | 30.4 | 615    | 6  | US-09-925-065A-800272 | Sequence 800272, A  |
| 58   | 30.4 | 671    | 6  | US-09-925-065A-694569 | Sequence 694569, A  |
| 58   | 30.4 | 712    | 14 | US-09-925-065A-694570 | Sequence 694570, A  |
| 58   | 30.4 | 712    | 14 | US-11-108-172-354     | Sequence 354, App   |
| 58   | 30.4 | 903    | 10 | US-10-301-480-576910  | Sequence 576910, A  |
| 58   | 30.4 | 903    | 10 | US-10-301-480-1190319 | Sequence 1190319, A |
| 58   | 30.4 | 1064   | 9  | US-10-301-480-28301   | Sequence 28301, A   |
| 58   | 30.4 | 1064   | 10 | US-10-301-480-641710  | Sequence 641710, A  |
| 58   | 30.4 | 2898   | 14 | US-11-000-463-141     | Sequence 141, App   |
| 58   | 30.4 | 2898   | 14 | US-11-000-463-613     | Sequence 613, App   |
| 58   | 30.4 | 3851   | 14 | US-11-090-739-119     | Sequence 119, App   |
| 58   | 30.4 | 4104   | 14 | US-11-154-227-94      | Sequence 94, Appl   |
| 58   | 30.4 | 4650   | 14 | US-11-154-227-102     | Sequence 102, App   |
| 58   | 30.4 | 138627 | 9  | US-10-330-773-159     | Sequence 159, App   |
| 58   | 30.4 | 151169 | 14 | US-11-121-086-38      | Sequence 38, Appl   |
| 57.5 | 30.1 | 2894   | 14 | US-11-128-061-742     | Sequence 742, App   |
| 57.5 | 30.1 | 2894   | 14 | US-11-128-049-742     | Sequence 742, App   |
| 57.5 | 30.1 | 4358   | 8  | US-10-750-185-60148   | Sequence 60148, A   |
| 57.5 | 30.1 | 4358   | 8  | US-10-750-623-60148   | Sequence 60148, A   |
| 57   | 29.8 | 404    | 6  | US-09-925-065A-700432 | Sequence 700432, A  |
| 57   | 29.8 | 404    | 6  | US-09-925-065A-700433 | Sequence 700433, A  |
| 57   | 29.8 | 919    | 10 | US-10-301-480-560937  | Sequence 560937, A  |
| 57   | 29.8 | 919    | 10 | US-10-301-480-543371  | Sequence 543371, A  |
| 57   | 29.8 | 16382  | 14 | US-11-108-172-1112    | Sequence 1174346, A |
| 57   | 29.8 | 16382  | 14 | US-11-108-172-1112    | Sequence 1174346, A |
| 57   | 29.8 | 90120  | 9  | US-10-330-773-390     | Sequence 390, App   |
| 56.5 | 29.6 | 539    | 6  | US-09-925-065A-570109 | Sequence 570109, A  |
| 56.5 | 29.6 | 539    | 6  | US-09-925-065A-168746 | Sequence 168746, A  |
| 56.5 | 29.6 | 959    | 10 | US-10-301-480-543371  | Sequence 543371, A  |
| 56.5 | 29.6 | 959    | 10 | US-10-301-480-1156780 | Sequence 1156780, A |
| 56.5 | 29.6 | 1258   | 11 | US-11-096-568A-20425  | Sequence 20425, A   |
| 56.5 | 29.6 | 1720   | 11 | US-11-096-568A-12769  | Sequence 12769, A   |
| 56.5 | 29.6 | 512    | 14 | US-11-000-688-599     | Sequence 599, App   |
| 56   | 29.3 | 516    | 6  | US-09-925-065A-728639 | Sequence 728639, A  |
| 56   | 29.3 | 523    | 6  | US-09-925-065A-807927 | Sequence 807927, A  |
| 56   | 29.3 | 525    | 6  | US-09-925-065A-786401 | Sequence 786401, A  |
| 56   | 29.3 | 538    | 6  | US-09-925-065A-636233 | Sequence 636233, A  |
| 56   | 29.3 | 551    | 14 | US-11-181-587-23      | Sequence 23, Appl1  |
| 56   | 29.3 | 557    | 6  | US-09-925-065A-530374 | Sequence 530374, A  |
| 56   | 29.3 | 570    | 6  | US-09-925-065A-321873 | Sequence 321873, A  |
| 56   | 29.3 | 570    | 6  | US-09-925-065A-321874 | Sequence 321874, A  |
| 56   | 29.3 | 572    | 10 | US-10-301-480-396441  | Sequence 396441, A  |
| 56   | 29.3 | 572    | 10 | US-10-301-480-396442  | Sequence 396442, A  |

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| 76  | 56   | 29.3 | 572    | 10 | US-10-301-480-1009850 | Sequence 1009850, |
| 77  | 56   | 29.3 | 572    | 10 | US-10-301-480-1009851 | Sequence 1009851, |
| 78  | 56   | 29.3 | 635    | 6  | US-09-925-065A-52826  | Sequence 52826, A |
| 79  | 56   | 29.3 | 635    | 9  | US-10-301-480-154064  | Sequence 154064,  |
| 80  | 56   | 29.3 | 635    | 10 | US-10-301-480-767473  | Sequence 767473,  |
| 81  | 56   | 29.3 | 738    | 6  | US-09-925-065A-924492 | Sequence 924492,  |
| 82  | 56   | 29.3 | 810    | 8  | US-10-467-657-7099    | Sequence 7099, Ap |
| 83  | 56   | 29.3 | 888    | 8  | US-10-467-657-4293    | Sequence 4293, Ap |
| 84  | 56   | 29.3 | 1042   | 11 | US-11-096-568A-19268  | Sequence 19268, A |
| 85  | 56   | 29.3 | 1422   | 11 | US-11-096-568A-19469  | Sequence 19469, A |
| 86  | 56   | 29.3 | 1633   | 11 | US-11-096-568A-19469  | Sequence 19469, A |
| 87  | 56   | 29.3 | 2304   | 8  | US-10-775-169-191     | Sequence 191, App |
| 88  | 56   | 29.3 | 3789   | 11 | US-11-072-512-324     | Sequence 324, App |
| 89  | 56   | 29.3 | 168753 | 14 | US-11-181-234-1       | Sequence 1, Appl  |
| 90  | 56   | 29.3 | 169495 | 14 | US-11-121-086-61      | Sequence 61, Appl |
| 91  | 55.5 | 29.1 | 201    | 8  | US-10-995-561-20303   | Sequence 20303, A |
| 92  | 55.5 | 29.1 | 201    | 8  | US-10-995-561-20313   | Sequence 20313, A |
| 93  | 55.5 | 29.1 | 201    | 8  | US-10-995-561-20314   | Sequence 20314, A |
| 94  | 55.5 | 29.1 | 201    | 8  | US-10-995-561-20315   | Sequence 20315, A |
| 95  | 55.5 | 29.1 | 201    | 8  | US-10-995-561-20317   | Sequence 20317, A |
| 96  | 55.5 | 29.1 | 201    | 8  | US-10-995-561-20318   | Sequence 20318, A |
| 97  | 55.5 | 29.1 | 1437   | 9  | US-10-330-773-860     | Sequence 860, App |
| 98  | 55.5 | 29.1 | 2864   | 8  | US-10-750-185-48604   | Sequence 48604, A |
| 99  | 55.5 | 29.1 | 2864   | 8  | US-10-750-185-48604   | Sequence 48604, A |
| 100 | 55.5 | 29.1 | 5032   | 8  | US-10-750-185-31483   | Sequence 31483, A |
| 101 | 55.5 | 29.1 | 5032   | 8  | US-10-750-623-31483   | Sequence 31483, A |
| 102 | 55.5 | 29.1 | 21437  | 9  | US-10-330-773-859     | Sequence 859, App |
| 103 | 55.5 | 29.1 | 24054  | 8  | US-10-995-561-13373   | Sequence 13373, A |
| 104 | 55.5 | 29.1 | 25209  | 8  | US-10-995-561-13407   | Sequence 13407, A |
| 105 | 55.5 | 29.1 | 110608 | 8  | US-10-775-169-193     | Sequence 193, App |
| 106 | 55.5 | 29.1 | 380749 | 14 | US-10-995-561-13216   | Sequence 13216, A |
| 107 | 55   | 28.8 | 132    | 14 | US-11-043-752-2243    | Sequence 2243, Ap |
| 108 | 55   | 28.8 | 420    | 14 | US-11-043-752-2240    | Sequence 2240, Ap |
| 109 | 55   | 28.8 | 432    | 11 | US-11-087-099-203     | Sequence 203, App |
| 110 | 55   | 28.8 | 558    | 6  | US-09-925-065A-757719 | Sequence 757719,  |
| 111 | 55   | 28.8 | 589    | 6  | US-09-925-065A-126640 | Sequence 126640,  |
| 112 | 55   | 28.8 | 589    | 6  | US-09-925-065A-232930 | Sequence 232930,  |
| 113 | 55   | 28.8 | 589    | 6  | US-09-925-065A-232931 | Sequence 232931,  |
| 114 | 55   | 28.8 | 589    | 6  | US-09-925-065A-232931 | Sequence 232932,  |
| 115 | 55   | 28.8 | 590    | 6  | US-09-925-065A-232932 | Sequence 232932,  |
| 116 | 55   | 28.8 | 590    | 6  | US-09-925-065A-41977  | Sequence 41977, A |
| 117 | 55   | 28.8 | 590    | 10 | US-10-301-480-143215  | Sequence 143215,  |
| 118 | 55   | 28.8 | 602    | 14 | US-10-301-480-756624  | Sequence 756624,  |
| 119 | 55   | 28.8 | 602    | 10 | US-11-136-537-6102    | Sequence 6102, Ap |
| 120 | 55   | 28.8 | 602    | 10 | US-10-301-480-233880  | Sequence 233880,  |
| 121 | 55   | 28.8 | 602    | 10 | US-10-301-480-316177  | Sequence 316177,  |
| 122 | 55   | 28.8 | 602    | 10 | US-10-301-480-316178  | Sequence 316178,  |
| 123 | 55   | 28.8 | 602    | 10 | US-10-301-480-316179  | Sequence 316179,  |
| 124 | 55   | 28.8 | 602    | 10 | US-10-301-480-837289  | Sequence 837289,  |
| 125 | 55   | 28.8 | 602    | 10 | US-10-301-480-929586  | Sequence 929586,  |
| 126 | 55   | 28.8 | 602    | 10 | US-10-301-480-929587  | Sequence 929587,  |
| 127 | 55   | 28.8 | 602    | 10 | US-10-301-480-929588  | Sequence 929588,  |
| 128 | 55   | 28.8 | 637    | 9  | US-10-301-480-100754  | Sequence 100754,  |
| 129 | 55   | 28.8 | 637    | 10 | US-10-301-480-714163  | Sequence 714163,  |
| 130 | 55   | 28.8 | 914    | 6  | US-09-925-065A-700206 | Sequence 700206,  |
| 131 | 55   | 28.8 | 985    | 10 | US-10-301-480-565276  | Sequence 565276,  |
| 132 | 55   | 28.8 | 985    | 10 | US-10-301-480-1178685 | Sequence 1178685, |
| 133 | 55   | 28.8 | 1114   | 6  | US-09-925-065A-25142  | Sequence 25142, A |
| 134 | 55   | 28.8 | 1114   | 6  | US-09-925-065A-25143  | Sequence 25143, A |
| 135 | 55   | 28.8 | 1114   | 9  | US-09-925-065A-25144  | Sequence 25144, A |
| 136 | 55   | 28.8 | 1114   | 9  | US-10-301-480-126379  | Sequence 126379,  |
| 137 | 55   | 28.8 | 1114   | 9  | US-10-301-480-126380  | Sequence 126380,  |
| 138 | 55   | 28.8 | 1114   | 9  | US-10-301-480-126381  | Sequence 126381,  |
| 139 | 55   | 28.8 | 1114   | 10 | US-10-301-480-739788  | Sequence 739788,  |
| 140 | 55   | 28.8 | 1114   | 10 | US-10-301-480-739789  | Sequence 739789,  |
| 141 | 55   | 28.8 | 1114   | 10 | US-10-301-480-739790  | Sequence 739790,  |
| 142 | 55   | 28.8 | 1143   | 14 | US-11-136-537-2006    | Sequence 2006, Ap |
| 143 | 55   | 28.8 | 1160   | 9  | US-10-714-887-341     | Sequence 341, App |
| 144 | 55   | 28.8 | 1619   | 11 | US-11-096-568A-19148  | Sequence 19148, A |
| 145 | 55   | 28.8 | 1906   | 6  | US-09-925-065A-703230 | Sequence 703230,  |
| 146 | 55   | 28.8 | 1906   | 6  | US-09-925-065A-703231 | Sequence 703231,  |
| 147 | 55   | 28.8 | 2161   | 13 | US-11-033-764-94      | Sequence 94, Appl |
| 148 | 55   | 28.8 | 2703   | 14 | US-11-128-061-3433    | Sequence 3433, Ap |
| 149 | 55   | 28.8 | 2703   | 14 | US-11-128-049-3433    | Sequence 3433, Ap |

|     |    |      |      |   |                     |                   |
|-----|----|------|------|---|---------------------|-------------------|
| 149 | 55 | 28.8 | 3081 | 8 | US-10-514-863-1     | Sequence 1, Appl  |
| 150 | 55 | 28.8 | 3990 | 8 | US-10-750-185-46314 | Sequence 46314, A |

ALIGNMENTS

RESULT 1

US-11-096-568A-26590

Sequence 26590, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nikolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

FILE REFERENCE: 2750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 26590

LENGTH: 2970

TYPE: DNA

ORGANISM: Zea mays subsp. mays

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)..(2970)

OTHER INFORMATION: Ceres Seq. ID no. 13579604

US-11-096-568A-26590

Alignment Scores:

Pred. No.: 2,98e-13 Length: 2970

Score: 191.00 Matches: 38

Percent Similarity: 97.4% Conservative: 0

Best Local Similarity: 97.4% Mismatches: 1

Query Match: 100.0% Indels: 0

DB: 11 Gaps: 0

US-10-628-525A-37 (1-39) x US-11-096-568A-26590 (1-2970)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20

DB 602 ATGGCGACGCCCTCGCGCGTGGCGCGCGTCCCTCTCGCGCGCGCGCGCGCG 661

QY 21 AlaAlaValGlyAspArgAlaAlaArgProArgArgLeuGlnArgValLeuArgArg 39

DB 662 GCCGCGTGGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 718

RESULT 2

US-09-925-065A-774283/c

Sequence 774283, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

FILE REFERENCE: 109827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 774283

LENGTH: 495

TYPE: DNA

ORGANISM: Homo sapiens







```
QY 31 ArgLeuGlnArg 34
DB 90 AGGTTGAGCGG 79

RESULT 9
US-11-096-568A-11773
; Sequence 11773, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11773
; LENGTH: 1258
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1258)
; OTHER INFORMATION: Ceres Seq. ID no. 13656983
US-11-096-568A-11773

Alignment Scores:
Pred. No.: 505 Length: 1258
Score: 62.00 Matches: 21
Percent Similarity: 62.2% Conservative: 2
Best Local Similarity: 56.8% Mismatches: 8
Query Match: 32.5% Indels: 6
DB: 11 Gaps: 2

US-10-628-525A-37 (1-39) x US-11-096-568A-11773 (1-1258)

QY 8 GlyAlaAlaCysLeuLeuAlaArg-----***AlaTrpProAlaAla 22
DB 280 GCGCGCGCGGAGTCTCTCCAGCGACTTCGGCTGGAGCGCGCGCGCTCGCGCGC 339

QY 23 ValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
DB 340 GTCGCGCGCGCGCGCGCGCGCGACTT---CGAGTTCTCGTCGCGGAG 387

RESULT 10
US-10-995-561-13253/c
; Sequence 13253, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF DETECTION AND USES THEREOF
; FILE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13253
; LENGTH: 103660
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(103660)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-13253)
US-10-995-561-13253

Alignment Scores:
Pred. No.: 3,22e+04 Length: 103660
Score: 62.00 Matches: 11
Percent Similarity: 58.3% Conservative: 3

Best Local Similarity: 45.8% Mismatches: 10
Query Match: 32.5% Indels: 0
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-995-561-13253 (1-103660)

QY 11 CysLeuLeuAlaArg***AlaTrpProAlaAlaValGlyAspArgAlaArgProArg 30
DB 44152 TGTGCACTGGTAGTCCAGCTACTTGGAGCGCGAGTGGGAGAGATCACTGAGCCGAGG 44093

QY 31 ArgLeuGlnArg 34
DB 44092 AGGTTGAGCGG 44081

RESULT 11
US-11-096-568A-11714
; Sequence 11714, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11714
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2073)
; OTHER INFORMATION: Ceres Seq. ID no. 13656435
US-11-096-568A-11714

Alignment Scores:
Pred. No.: 929 Length: 2073
Score: 61.50 Matches: 20
Percent Similarity: 63.6% Conservative: 1
Best Local Similarity: 60.6% Mismatches: 5
Query Match: 32.2% Indels: 7
DB: 11 Gaps: 1

US-10-628-525A-37 (1-39) x US-11-096-568A-11714 (1-2073)

QY 7 ValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAlaAlaValGlyAsp--A 26
DB 564 GTTGGCGCGCACTGGCGCTGGCGCTCAGG-----CGCGCGCGCGAGCGC 608

QY 26 ArgAlaArgProArgArgLeuGlnArgValLeuArg 37
DB 609 GTGCTCGGCTCGACACTTCAACGCGTACTACGA 643

RESULT 12
US-10-995-561-31046/c
; Sequence 31046, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF DETECTION AND USES THEREOF
; FILE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31046
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-31046)
US-10-995-561-31046
```

```
Alignment Scores:
Pred. No.: 118 Length: 201
Score: 61.00 Matches: 11
Percent Similarity: 58.3% Conservative: 3
Best Local Similarity: 45.8% Mismatches: 10
Query Match: 31.9% Indels: 0
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-995-561-31046 (1-201)
QY 11 CysLeuLeuAlaArg***AlaTrpProAlaAlaValGlyAspArgAlaArgProArg 30
Db 157 TGTGCACTGGTAGTCCAGCTACTTGGGAGCGCGAGGTGGGAGATCACTTGGAGCKAGG 98
QY 31 ArgLeuGlnArg 34
Db 97 AGGTTGAGCGG 86

RESULT 13
US-10-750-185-34977
; Sequence 34977, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US/10750,185
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34977
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Bovine 19866881212167
US-10-750-185-34977

Alignment Scores:
Pred. No.: 836 Length: 1191
Score: 60.00 Matches: 13
Percent Similarity: 51.9% Conservative: 1
Best Local Similarity: 48.1% Mismatches: 13
Query Match: 31.4% Indels: 0
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-750-185-34977 (1-1191)
QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAla 21
Db 540 GCCGCTCGGCTCTGCCGCGCGCGCGCGCGCTCCCGCGCCCTCGTCGATGGCTCCA 599
QY 22 AlaValGlyAspArgAlaArg 28
Db 600 GCAGCTGGCAGCAGCAGCAG 620

RESULT 14
US-10-750-623-34977
; Sequence 34977, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US/10750,623
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 60437,482
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34977
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Bovine 19866881212167
US-10-750-623-34977

Alignment Scores:
Pred. No.: 836 Length: 1191
Score: 60.00 Matches: 13
Percent Similarity: 51.9% Conservative: 1
Best Local Similarity: 48.1% Mismatches: 13
Query Match: 31.4% Indels: 0
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-750-623-34977 (1-1191)
QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAla 21
Db 540 GCCGCTCGGCTCTGCCGCGCGCGCGCGCGCTCCCGCGCCCTCGTCGATGGCTCCA 599
QY 22 AlaValGlyAspArgAlaArg 28
Db 600 GCAGCTGGCAGCAGCAGCAG 620

RESULT 15
US-11-037-243-23/c
; Sequence 23, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERAED
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 2268
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-037-243-23

Alignment Scores:
Pred. No.: 1,53e+03 Length: 2268
Score: 60.00 Matches: 11
Percent Similarity: 59.1% Conservative: 2
Best Local Similarity: 50.0% Mismatches: 9
Query Match: 31.4% Indels: 0
DB: 14 Gaps: 0

US-10-628-525A-37 (1-39) x US-11-037-243-23 (1-2268)
QY 8 GlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAlaAlaValGlyAspArgAla 27
Db 8 GlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAlaAlaValGlyAspArgAla 27
```



QY 26 ArgAlaArgPro 29  
 DB 63 ATGGCCCCACCT 74

## RESULT 19

US-10-301-480-1054704  
 ; Sequence 1054704, Application US/10301480  
 ; Publication No. US20060057564A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
 ; FILE OF INVENTION: in the Human Genome  
 ; FILE REFERENCE: 108827.137  
 ; CURRENT APPLICATION NUMBER: US/10/301,480  
 ; PRIOR FILING DATE: 2002-11-21  
 ; PRIOR APPLICATION NUMBER: US 10/215,598  
 ; PRIOR FILING DATE: 2002-08-09  
 ; PRIOR APPLICATION NUMBER: US 60/311,695  
 ; PRIOR FILING DATE: 2001-08-10  
 ; NUMBER OF SEQ ID NOS: 1226818  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1054704  
 ; LENGTH: 523  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-301-480-1054704

Alignment Scores:  
 Pred. No.: 509 Length: 523  
 Score: 59.00 Matches: 11  
 Percent Similarity: 58.3% Conservative: 3  
 Best Local Similarity: 45.8% Mismatches: 10  
 Query Match: 30.9% Indels: 0  
 DB: 10 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-301-480-1054704 (1-523)

QY 6 AlavalGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpProAlaAlaValGlyAap 25  
 DB 3 GCAC TAGCAATATATGTTTAATTTGTTCAAAATTTATGGCCAGACGAGTAGGTGAC 62  
 QY 26 ArgAlaArgPro 29  
 DB 63 ATGGCCCCACCT 74

## RESULT 20

US-10-301-480-39100  
 ; Sequence 39100, Application US/10301480  
 ; Publication No. US20060057564A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
 ; FILE OF INVENTION: in the Human Genome  
 ; FILE REFERENCE: 108827.137  
 ; CURRENT APPLICATION NUMBER: US/10/301,480  
 ; PRIOR FILING DATE: 2002-11-21  
 ; PRIOR APPLICATION NUMBER: US 10/215,598  
 ; PRIOR FILING DATE: 2002-08-09  
 ; PRIOR APPLICATION NUMBER: US 60/311,695  
 ; PRIOR FILING DATE: 2001-08-10  
 ; NUMBER OF SEQ ID NOS: 1226818  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 39100  
 ; LENGTH: 673  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-301-480-39100

Alignment Scores:  
 Pred. No.: 645 Length: 673  
 Score: 59.00 Matches: 11  
 Percent Similarity: 58.3% Conservative: 3  
 Best Local Similarity: 45.8% Mismatches: 10

Query Match: 30.9% Indels: 0  
 DB: 9 Gaps: 0  
 US-10-628-525A-37 (1-39) x US-10-301-480-39100 (1-673)

QY 6 AlavalGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpProAlaAlaValGlyAap 25  
 DB 119 GCAC TAGCAATATATGTTTAATTTGTTCAAAATTTATGGCCAGACGAGTAGGTGAC 178  
 QY 26 ArgAlaArgPro 29  
 DB 179 ATGGCCCCACCT 190

## RESULT 21

US-10-301-480-652509  
 ; Sequence 652509, Application US/10301480  
 ; Publication No. US20060057564A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
 ; FILE OF INVENTION: in the Human Genome  
 ; FILE REFERENCE: 108827.137  
 ; CURRENT APPLICATION NUMBER: US/10/301,480  
 ; PRIOR FILING DATE: 2002-11-21  
 ; PRIOR APPLICATION NUMBER: US 10/215,598  
 ; PRIOR FILING DATE: 2002-08-09  
 ; PRIOR APPLICATION NUMBER: US 60/311,695  
 ; PRIOR FILING DATE: 2001-08-10  
 ; NUMBER OF SEQ ID NOS: 1226818  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 652509  
 ; LENGTH: 673  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-301-480-652509

Alignment Scores:  
 Pred. No.: 645 Length: 673  
 Score: 59.00 Matches: 11  
 Percent Similarity: 58.3% Conservative: 3  
 Best Local Similarity: 45.8% Mismatches: 10  
 Query Match: 30.9% Indels: 0  
 DB: 10 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-301-480-652509 (1-673)

QY 6 AlavalGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpProAlaAlaValGlyAap 25  
 DB 119 GCAC TAGCAATATATGTTTAATTTGTTCAAAATTTATGGCCAGACGAGTAGGTGAC 178  
 QY 26 ArgAlaArgPro 29  
 DB 179 ATGGCCCCACCT 190

## RESULT 22

US-09-925-065A-39710/C  
 ; Sequence 39710, Application US/09925065A  
 ; Publication No. US20040181048A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome  
 ; FILE OF INVENTION: 108827.135  
 ; CURRENT APPLICATION NUMBER: US/09/925,065A  
 ; CURRENT FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: US 60/243,096  
 ; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 60/252,147  
 ; PRIOR FILING DATE: 2000-11-20  
 ; PRIOR APPLICATION NUMBER: US 60/250,092  
 ; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: US 60/261,766  
 ; PRIOR FILING DATE: 2001-01-16

```
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39710
; LENGTH: 800
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-39710

Alignment Scores:
Pred. No.: 759          Length: 800
Score: 59.00           Matches: 11
Percent Similarity: 53.8% Conservatives: 3
Best Local Similarity: 42.3% Mismatches: 12
Query Match: 30.9%      Indels: 0
DB: 6                  Gaps: 0

US-10-628-525A-37 (1-39) x US-09-925-065A-39710 (1-800)

QY 8 GlyAlaAaCysLeuLeuAlaArg**AlaTrpProAlaAlaValGlyAspArgAla 27
Db 583 GGTGTTGTATGTATGCCACTTGTGCCAGCTACCTGGGAGGCTGAAGTGGGAGGACTGCTT 524
QY 28 ArgProArgArgLeuGln 33
Db 523 AAGCCCAAGAGGTTGAGG 506

RESULT 23
US-10-301-480-140948/c
; Sequence 140948, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US 60/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140948
; LENGTH: 800
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-140948

Alignment Scores:
Pred. No.: 759          Length: 800
Score: 59.00           Matches: 11
Percent Similarity: 53.8% Conservatives: 3
Best Local Similarity: 42.3% Mismatches: 12
Query Match: 30.9%      Indels: 0
DB: 9                  Gaps: 0

US-10-628-525A-37 (1-39) x US-10-301-480-140948 (1-800)

QY 8 GlyAlaAaCysLeuLeuAlaArg**AlaTrpProAlaAlaValGlyAspArgAla 27
Db 583 GGTGTTGTATGTATGCCACTTGTGCCAGCTACCTGGGAGGCTGAAGTGGGAGGACTGCTT 524
QY 28 ArgProArgArgLeuGln 33
Db 523 AAGCCCAAGAGGTTGAGG 506

RESULT 24
US-10-301-480-754357/c
; Sequence 754357, Application US/10301480
; Publication No. US20060057564A1
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; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 754357
; LENGTH: 800
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-754357

Alignment Scores:
Pred. No.: 759          Length: 800
Score: 59.00           Matches: 11
Percent Similarity: 53.8% Conservatives: 3
Best Local Similarity: 42.3% Mismatches: 12
Query Match: 30.9%      Indels: 0
DB: 10                 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-301-480-754357 (1-800)

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Db 583 GGTGTTGTATGTATGCCACTTGTGCCAGCTACCTGGGAGGCTGAAGTGGGAGGACTGCTT 524
QY 28 ArgProArgArgLeuGln 33
Db 523 AAGCCCAAGAGGTTGAGG 506

RESULT 25
US-11-096-568A-15852
; Sequence 15852, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 15852
; LENGTH: 962
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(962)
; OTHER INFORMATION: Ceres Seq. ID no. 12349152
US-11-096-568A-15852

Alignment Scores:
Pred. No.: 903          Length: 962
Score: 59.00           Matches: 19
Percent Similarity: 60.0% Conservatives: 2
Best Local Similarity: 54.3% Mismatches: 12
Query Match: 30.9%      Indels: 2
DB: 11                 Gaps: 1

US-10-628-525A-37 (1-39) x US-11-096-568A-15852 (1-962)

QY 5 SerAlaValGlyAlaAaCysLeuLeuAlaArg**AlaTrpProAlaAlaValGly 24
Db 306 GCTGAGTGGGCACTGTCAGCACTTCTCCCGCCGCGGCGAGCC-----GCAGCAGTACCG 359
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Job time : 131.78 secs

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; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 362244
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-362244

Alignment Scores:
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Score:          58.00    Matches:      15
Percent Similarity: 51.5% Conservative: 2
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DB:              10      Gaps:      0

US-10-628-525A-37 (1-39) x US-10-301-480-362244 (1-529)

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      |||||:::|||||:::|||||:::|||||
Db      301 CCTCTGCGTAGCGCCCGTCCGTATAGCCCTCCGCGTGTGAGCCGGGTGCTG 360

QY      24 GlyAspArgAlaArgProArgLeuGlnArgValLeu 36
      |||||:::|||||:::|||||
Db      361 GTTGTTCAGCGCGCCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 399

RESULT 30
US-10-301-480-975653
; Sequence 975653, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 975653
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-975653

Alignment Scores:
Pred. No.:      679      Length:      529
Score:          58.00    Matches:      15
Percent Similarity: 51.5% Conservative: 2
Best Local Similarity: 45.5% Mismatches: 16
Query Match:      30.4% Indels:      0
DB:              10      Gaps:      0

US-10-628-525A-37 (1-39) x US-10-301-480-975653 (1-529)

QY      4 ProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAlaAlaVal 23
      |||||:::|||||:::|||||:::|||||
Db      301 CCTCTGCGTAGCGCCCGTCCGTATAGCCCTCCGCGTGTGAGCCGGGTGCTG 360

QY      24 GlyAspArgAlaArgProArgLeuGlnArgValLeu 36
      |||||:::|||||:::|||||
Db      361 GTTGTTCAGCGCGCCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 399
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 20:18:18 ; Search time 1066.11 Seconds  
(without alignments)  
2022.653 Million cell updates/sec

Title: US-10-628-525A-37

Perfect score: 191

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2          | 191   | 100.0       | 153    | 28    | US-09-625-406-18  |
| 3          | 191   | 100.0       | 153    | 49    | US-10-336-753-58  |
| 4          | 191   | 100.0       | 153    | 53    | US-10-628-525-18  |
| 5          | 191   | 100.0       | 153    | 53    | US-10-628-525A-18 |
| 6          | 191   | 100.0       | 1415   | 74    | US-60-094-436-11  |
| 7          | 191   | 100.0       | 2008   | 74    | US-60-094-436-12  |

Sequence 58, Appl  
Sequence 18, Appl  
Sequence 58, Appl  
Sequence 18, Appl  
Sequence 11, Appl  
Sequence 12, Appl

|    |       |       |       |    |                       |                    |       |      |      |        |    |                       |                    |
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| 8  | 191   | 100.0 | 2491  | 74 | US-60-094-436-9       | Sequence 9, Appl1  | 81    | 67   | 35.1 | 1971   | 43 | US-10-219-999-17887   | Sequence 17887, A  |
| 9  | 191   | 100.0 | 2970  | 69 | US-11-096-568A-26590  | Sequence 26590, A  | 82    | 67   | 35.1 | 1971   | 51 | US-10-425-114-1331    | Sequence 1331, Ap  |
| 10 | 191   | 100.0 | 2991  | 42 | US-10-109-048-1142    | Sequence 1142, Ap  | 83    | 67   | 35.1 | 1971   | 51 | US-10-425-114A-1331   | Sequence 1331, Ap  |
| 11 | 191   | 100.0 | 3123  | 51 | US-10-425-115-54073   | Sequence 54073, A  | 84    | 67   | 35.1 | 2008   | 72 | US-11-218-305-2759    | Sequence 2759, Ap  |
| 12 | 190   | 99.5  | 2992  | 20 | US-09-077-564-1       | Sequence 1, Appl1  | c 85  | 67   | 35.1 | 174589 | 63 | US-10-932-348-5181    | Sequence 5181, Ap  |
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| 14 | 186   | 97.4  | 324   | 29 | US-09-654-617-338633  | Sequence 338633, A | c 87  | 67   | 35.1 | 174589 | 65 | US-10-990-328A-96782  | Sequence 96782, A  |
| 15 | 186   | 97.4  | 324   | 29 | US-09-684-016-338633  | Sequence 338633, A | c 88  | 67   | 35.1 | 174589 | 65 | US-10-990-328A-96782  | Sequence 96782, A  |
| 16 | 186   | 97.4  | 324   | 75 | US-60-145-485-2189    | Sequence 2189, Ap  | c 89  | 66.5 | 34.8 | 520    | 27 | US-09-565-306-13452   | Sequence 13452, A  |
| 17 | 186   | 92.1  | 462   | 75 | US-09-619-643-17333   | Sequence 17333, A  | c 90  | 66.5 | 34.8 | 610    | 83 | US-09-565-306-13452   | Sequence 13452, A  |
| 18 | 176   | 92.1  | 462   | 75 | US-60-145-148-845     | Sequence 845, App  | c 91  | 66.5 | 34.8 | 620    | 83 | US-60-723-596-54092   | Sequence 54092, A  |
| 19 | 176   | 92.1  | 1034  | 29 | US-09-654-617-269739  | Sequence 269739, A | c 92  | 66.5 | 34.8 | 662    | 40 | US-10-020-338-25465   | Sequence 25465, A  |
| 20 | 176   | 92.1  | 1034  | 29 | US-09-684-016-269739  | Sequence 269739, A | c 93  | 66.5 | 34.8 | 662    | 40 | US-10-020-338-25465   | Sequence 25465, A  |
| 21 | 143.5 | 75.1  | 370   | 33 | US-09-850-147-1953    | Sequence 1953, Ap  | c 94  | 66.5 | 34.8 | 681    | 29 | US-09-654-617-395550  | Sequence 395550, A |
| 22 | 143.5 | 75.1  | 370   | 76 | US-60-202-213-1953    | Sequence 1953, Ap  | c 95  | 66.5 | 34.8 | 681    | 29 | US-09-684-016-395550  | Sequence 395550, A |
| 23 | 143.5 | 75.1  | 376   | 29 | US-09-654-617-454633  | Sequence 454633, A | c 96  | 66.5 | 34.8 | 957    | 43 | US-10-259-165-401     | Sequence 401, App  |
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| 25 | 143.5 | 75.1  | 2670  | 61 | US-10-767-701-13043   | Sequence 13043, A  | c 98  | 66.5 | 34.8 | 1011   | 43 | US-10-259-165-389     | Sequence 289, App  |
| 26 | 74    | 38.7  | 7492  | 75 | US-60-171-627-1369    | Sequence 1369, Ap  | c 99  | 66.5 | 34.8 | 1012   | 61 | US-10-739-930-4312    | Sequence 4312, Ap  |
| 27 | 74    | 38.7  | 7492  | 75 | US-60-173-464-14199   | Sequence 14199, A  | c 100 | 66.5 | 34.8 | 1254   | 51 | US-10-449-902-4056    | Sequence 4056, Ap  |
| 28 | 74    | 38.7  | 7495  | 75 | US-60-167-217-17335   | Sequence 17335, A  | c 101 | 66.5 | 34.8 | 1254   | 51 | US-10-449-902-4056    | Sequence 4056, Ap  |
| 29 | 74    | 38.7  | 7495  | 75 | US-60-161-932-1834    | Sequence 1834, App | c 102 | 66.5 | 34.8 | 1284   | 51 | US-10-449-902-2148    | Sequence 2148, Ap  |
| 30 | 74    | 38.7  | 54580 | 25 | US-09-528-237A-965    | Sequence 965, App  | c 103 | 66.5 | 34.8 | 6297   | 42 | US-10-132-134-37      | Sequence 37, Appl  |
| 31 | 73    | 38.2  | 879   | 61 | US-10-767-701-12709   | Sequence 12709, A  | c 104 | 66.5 | 34.8 | 22010  | 28 | US-09-620-392-39017   | Sequence 39017, A  |
| 32 | 72    | 37.7  | 307   | 51 | US-10-425-115-6595    | Sequence 6595, Ap  | c 105 | 66   | 34.6 | 50543  | 42 | US-10-132-134-25      | Sequence 25, Appl  |
| 33 | 71.5  | 37.4  | 1501  | 33 | US-09-815-264-6521    | Sequence 6521, Ap  | c 106 | 66   | 34.6 | 218    | 29 | US-09-654-617-392245  | Sequence 392245, A |
| 34 | 71.5  | 37.4  | 7939  | 28 | US-09-620-392-59533   | Sequence 59533, A  | c 107 | 66   | 34.6 | 529    | 22 | US-09-684-016-392245  | Sequence 392245, A |
| 35 | 71.5  | 37.4  | 7939  | 31 | US-09-702-134-13746   | Sequence 13746, A  | c 108 | 66   | 34.6 | 1437   | 1  | US-09-270-849B-86754  | Sequence 86754, A  |
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| 37 | 71    | 37.2  | 1569  | 50 | US-10-369-493-35694   | Sequence 35694, A  | c 110 | 66   | 34.6 | 1437   | 35 | US-09-922-531-7       | Sequence 7, Appl   |
| 38 | 69.5  | 36.4  | 1013  | 78 | US-60-360-039-35694   | Sequence 35694, A  | c 111 | 66   | 34.6 | 1437   | 42 | US-10-170-235-32893   | Sequence 32893, A  |
| 39 | 69.5  | 36.4  | 1013  | 78 | US-10-198-846-13012   | Sequence 13012, A  | c 112 | 66   | 34.6 | 1437   | 70 | US-11-121-438-7       | Sequence 7, Appl   |
| 40 | 68    | 35.6  | 738   | 55 | US-10-703-032-15857   | Sequence 15857, A  | c 113 | 66   | 34.6 | 1437   | 79 | US-60-452-680-9770    | Sequence 9770, Ap  |
| 41 | 68    | 35.6  | 807   | 61 | US-10-767-701-12477   | Sequence 12477, A  | c 114 | 66   | 34.6 | 1440   | 42 | US-10-170-235-33577   | Sequence 33577, Ap |
| 42 | 67.5  | 35.3  | 835   | 51 | US-10-449-902-7791    | Sequence 7791, Ap  | c 115 | 66   | 34.6 | 1440   | 79 | US-60-452-680-9769    | Sequence 9769, Ap  |
| 43 | 67.5  | 35.3  | 1134  | 31 | US-09-703-708-10270   | Sequence 10270, A  | c 116 | 66   | 34.6 | 1725   | 31 | US-09-708-427-68283   | Sequence 68283, A  |
| 44 | 67.5  | 35.3  | 1134  | 31 | US-60-164-320-10270   | Sequence 10270, A  | c 117 | 66   | 34.6 | 2432   | 82 | US-60-680-473-45628   | Sequence 45628, A  |
| 45 | 67.5  | 35.3  | 1134  | 25 | US-60-183-791-10270   | Sequence 10270, A  | c 118 | 66   | 34.6 | 2432   | 82 | US-60-680-473-45628   | Sequence 45628, A  |
| 46 | 67.5  | 35.3  | 1143  | 72 | US-09-252-691-911     | Sequence 911, App  | c 119 | 66   | 34.6 | 2895   | 32 | US-11-218-305-9221    | Sequence 9221, Ap  |
| 47 | 67.5  | 35.3  | 1443  | 22 | US-09-252-691C-911    | Sequence 911, App  | c 120 | 66   | 34.6 | 45206  | 3  | US-09-565-306-12509-2 | Sequence 2, Appl   |
| 48 | 67.5  | 35.3  | 1443  | 51 | US-10-417-886-911     | Sequence 911, App  | c 121 | 65.5 | 34.3 | 365    | 24 | US-09-452-238-9       | Sequence 9, Appl   |
| 49 | 67.5  | 35.3  | 1501  | 33 | US-09-815-264-55837   | Sequence 55837, A  | c 122 | 65.5 | 34.3 | 365    | 66 | US-11-032-490-9       | Sequence 9, Appl   |
| 50 | 67.5  | 35.3  | 2000  | 34 | US-09-887-272A-5000   | Sequence 5000, Ap  | c 123 | 65.5 | 34.3 | 365    | 66 | US-11-032-643-9       | Sequence 9, Appl   |
| 51 | 67.5  | 35.3  | 5122  | 75 | US-60-171-627-1370    | Sequence 1370, Ap  | c 124 | 65.5 | 34.3 | 391    | 23 | US-09-304-517A-94387  | Sequence 94387, A  |
| 52 | 67.5  | 35.3  | 5122  | 75 | US-60-173-464-14200   | Sequence 14200, A  | c 125 | 65.5 | 34.3 | 391    | 23 | US-09-394-745-22874   | Sequence 22874, A  |
| 53 | 67.5  | 35.3  | 5125  | 75 | US-60-167-217-17336   | Sequence 17336, A  | c 126 | 65.5 | 34.3 | 391    | 27 | US-09-565-306-47903   | Sequence 47903, A  |
| 54 | 67.5  | 35.3  | 6288  | 28 | US-09-620-392-48042   | Sequence 48042, A  | c 127 | 65.5 | 34.3 | 391    | 39 | US-09-985-678-94387   | Sequence 94387, A  |
| 55 | 67.5  | 35.3  | 6288  | 33 | US-09-702-134-18295   | Sequence 18295, A  | c 128 | 65.5 | 34.3 | 400    | 28 | US-09-620-111B-2633   | Sequence 2633, Ap  |
| 56 | 67.5  | 35.3  | 6288  | 33 | US-09-815-264-82579   | Sequence 82579, A  | c 129 | 65.5 | 34.3 | 409    | 23 | US-09-304-517A-80269  | Sequence 80269, A  |
| 57 | 67.5  | 35.3  | 60842 | 75 | US-09-703-708-775     | Sequence 775, App  | c 130 | 65.5 | 34.3 | 409    | 23 | US-09-371-146A-80269  | Sequence 80269, A  |
| 58 | 67.5  | 35.3  | 60842 | 75 | US-60-164-320-775     | Sequence 775, App  | c 131 | 65.5 | 34.3 | 409    | 39 | US-09-985-678-80269   | Sequence 80269, A  |
| 59 | 67.5  | 35.3  | 60842 | 75 | US-60-183-791-775     | Sequence 775, App  | c 132 | 65.5 | 34.3 | 441    | 23 | US-09-394-745-778     | Sequence 778, App  |
| 60 | 67    | 35.1  | 359   | 23 | US-09-304-517A-94845  | Sequence 94845, A  | c 133 | 65.5 | 34.3 | 441    | 27 | US-09-565-306-5560    | Sequence 5560, Ap  |
| 61 | 67    | 35.1  | 359   | 23 | US-09-394-745-26050   | Sequence 26050, A  | c 134 | 65.5 | 34.3 | 450    | 23 | US-09-304-517A-94953  | Sequence 94953, A  |
| 62 | 67    | 35.1  | 359   | 29 | US-09-565-306-43602   | Sequence 43602, A  | c 135 | 65.5 | 34.3 | 450    | 23 | US-09-394-745-25728   | Sequence 25728, A  |
| 63 | 67    | 35.1  | 359   | 39 | US-09-985-678-94845   | Sequence 94845, A  | c 136 | 65.5 | 34.3 | 450    | 27 | US-09-565-306-43740   | Sequence 43740, A  |
| 64 | 67    | 35.1  | 364   | 29 | US-09-654-617-367613  | Sequence 367613, A | c 137 | 65.5 | 34.3 | 450    | 27 | US-09-985-678-94953   | Sequence 94953, A  |
| 65 | 67    | 35.1  | 364   | 29 | US-09-684-016-367613  | Sequence 367613, A | c 138 | 65.5 | 34.3 | 506    | 27 | US-09-565-306-12509   | Sequence 12509, A  |
| 66 | 67    | 35.1  | 405   | 55 | US-10-703-032-66897   | Sequence 66897, A  | c 139 | 65.5 | 34.3 | 517    | 30 | US-09-696-664A-15086  | Sequence 15086, A  |
| 67 | 67    | 35.1  | 455   | 76 | US-60-207-458-34870   | Sequence 34870, A  | c 140 | 65.5 | 34.3 | 529    | 27 | US-09-371-146A-94953  | Sequence 94953, A  |
| 68 | 67    | 35.1  | 459   | 29 | US-09-654-617-277287  | Sequence 277287, A | c 141 | 65.5 | 34.3 | 529    | 27 | US-09-565-306-14496   | Sequence 14496, A  |
| 69 | 67    | 35.1  | 459   | 36 | US-09-684-016-277287  | Sequence 277287, A | c 142 | 65.5 | 34.3 | 576    | 23 | US-09-371-146A-94387  | Sequence 94387, A  |
| 70 | 67    | 35.1  | 495   | 36 | US-09-925-065A-774283 | Sequence 774283, A | c 143 | 65.5 | 34.3 | 815    | 43 | US-10-219-999-6976    | Sequence 6976, Ap  |
| 71 | 67    | 35.1  | 495   | 36 | US-09-925-065A-837264 | Sequence 837264, A | c 144 | 65.5 | 34.3 | 815    | 51 | US-10-425-114-16430   | Sequence 16430, A  |
| 72 | 67    | 35.1  | 777   | 23 | US-09-371-146A-94845  | Sequence 94845, A  | c 145 | 65.5 | 34.3 | 815    | 51 | US-10-425-114A-16430  | Sequence 16430, A  |
| 73 | 67    | 35.1  | 778   | 50 | US-10-363-345A-15113  | Sequence 15113, A  | c 146 | 65.5 | 34.3 | 815    | 78 | US-60-312-544-2932    | Sequence 2932, Ap  |
| 74 | 67    | 35.1  | 778   | 50 | US-10-363-345A-15113  | Sequence 15113, A  | c 147 | 65.5 | 34.3 | 852    | 31 | US-09-708-427-50237   | Sequence 50237, Ap |
| 75 | 67    | 35.1  | 778   | 50 | US-10-363-483A-15113  | Sequence 15113, A  | c 148 | 65.5 | 34.3 | 852    | 31 | US-09-708-427-77300   | Sequence 77300, A  |
| 76 | 67    | 35.1  | 778   | 50 | US-10-363-483A-15114  | Sequence 15114, A  | c 149 | 65.5 | 34.3 | 855    | 29 | US-09-654-617-259710  | Sequence 259710, A |
| 77 | 67    | 35.1  | 1461  | 31 | US-09-760-495-263     | Sequence 263, App  | c 150 | 65.5 | 34.3 | 855    | 29 | US-09-654-617-259710  | Sequence 259710, A |
| 78 | 67    | 35.1  | 1461  | 42 | US-10-143-775-263     | Sequence 263, App  | c 150 | 65.5 | 34.3 | 855    | 29 | US-09-654-617-259710  | Sequence 259710, A |
| 79 | 67    | 35.1  | 1775  | 72 | US-11-218-305-17942   | Sequence 17942, A  |       |      |      |        |    |                       |                    |
| 80 | 67    | 35.1  | 1958  | 69 | US-11-096-568A-26982  | Sequence 26982, A  |       |      |      |        |    |                       |                    |

```
RESULT 1
US-09-402-254-58
; Sequence 58, Application US/09402254
; GENERAL INFORMATION:
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; FILE REFERENCE: 2461-52
; CURRENT APPLICATION NUMBER: US/09/402,254
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: PCT/US98/06660
; EARLIER FILING DATE: 1998-04-03
; EARLIER APPLICATION NUMBER: 60/042,939
; EARLIER FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 153
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(153)
US-09-402-254-58
Alignment Scores:
Pred. No.: 5.06e-17 Length: 153
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 24 Gaps: 0

US-10-628-525A-37 (1-39) x US-09-402-254-58 (1-153)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpPro 20
DB 1 ATGGCGACGCCCTCGGCGCGTGGCGCGCTGCTCTCTCTCGCGCGCGCGCTGCGCG 60
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
DB 61 GCCGCGCTCGGCGACCGCGCGCGCGCGCTCCAGCGCTCCAGCGCGCTGCTGCGCGCG 117

RESULT 2
US-09-625-406-18
; Sequence 18, Application US/09625406
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/625,406
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/941,445
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..153
US-09-625-406-18
Alignment Scores:
Pred. No.: 5.06e-17 Length: 153
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 28 Gaps: 0

US-10-628-525A-37 (1-39) x US-09-625-406-18 (1-153)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpPro 20
DB 1 ATGGCGACGCCCTCGGCGCGTGGCGCGCTGCTCTCTCTCGCGCGCGCGCTGCGCG 60
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
DB 61 GCCGCGCTCGGCGACCGCGCGCGCGCGCTCCAGCGCTCCAGCGCGCTGCTGCGCGCG 117

RESULT 3
US-10-336-753-58
; Sequence 58, Application US/10336753
; GENERAL INFORMATION:
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; FILE REFERENCE: 2461-52
; CURRENT APPLICATION NUMBER: US/10/336,753
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US/09/402,254
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/06660
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/042,939
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 153
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(153)
US-10-336-753-58
Alignment Scores:
Pred. No.: 5.06e-17 Length: 153
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
```



```
Alignment Scores:
Pred. No.: 9.78e-16 Length: 1415
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 74 Gaps: 0

US-10-628-525A-37 (1-39) x US-60-094-436-11 (1-1415)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpPro 20
Db 2 ATGCGAGCCCTCGGCGCGTGGGCGCGTGCCTCTCTCGGCGGCGCGCTGGCCG 61
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
Db 62 GCCGCGTGGCGACCGCGCGCGCGCGGCTCCAGCGCGTGTCTGCGCGCGCG 118

RESULT 7
US-60-094-436-12
; Sequence 12, Application US/60094436
; GENERAL INFORMATION:
; APPLICANT: Lightner, Jonathan E.
; APPLICANT: Broglie, Karen E.
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Modification of Starch Biosynthetic Enzyme Gene
; FILE REFERENCE: BB-1147-P1
; CURRENT APPLICATION NUMBER: US/60/094,436
; CURRENT FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 12
; LENGTH: 2008
; TYPE: DNA
; ORGANISM: Zea mays
US-60-094-436-12

Alignment Scores:
Pred. No.: 1.56e-15 Length: 2008
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 74 Gaps: 0

US-10-628-525A-37 (1-39) x US-60-094-436-12 (1-2008)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpPro 20
Db 2 ATGCGAGCCCTCGGCGCGTGGGCGCGTGCCTCTCTCGGCGGCGCGCTGGCCG 61
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
Db 62 GCCGCGTGGCGACCGCGCGCGCGCGGCTCCAGCGCGTGTCTGCGCGCGCG 118

RESULT 8
US-60-094-436-9
; Sequence 9, Application US/60094436
; GENERAL INFORMATION:
; APPLICANT: Lightner, Jonathan E.
; APPLICANT: Broglie, Karen E.
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Modification of Starch Biosynthetic Enzyme Gene
; FILE REFERENCE: BB-1147-P1
; CURRENT APPLICATION NUMBER: US/60/094,436
; CURRENT FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 9
; LENGTH: 2491
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; TYPE: DNA
; ORGANISM: Zea mays
US-60-094-436-9

Alignment Scores:
Pred. No.: 2.08e-15 Length: 2491
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 74 Gaps: 0

US-10-628-525A-37 (1-39) x US-60-094-436-9 (1-2491)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpPro 20
Db 145 ATGCGAGCCCTCGGCGCGTGGGCGCGTGCCTCTCTCGGCGGCGCGCTGGCCG 204
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
Db 205 GCCGCGTGGCGACCGCGCGCGCGCGGCTCCAGCGCGTGTCTGCGCGCGCG 261

RESULT 9
US-11-096-568A-26590
; Sequence 26590, Application US/11096568A
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26590
; LENGTH: 2970
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(2970)
; OTHER INFORMATION: Ceres Seq. ID no. 13579604
US-11-096-568A-26590

Alignment Scores:
Pred. No.: 2.62e-15 Length: 2970
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 69 Gaps: 0

US-10-628-525A-37 (1-39) x US-11-096-568A-26590 (1-2970)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpPro 20
Db 602 ATGCGAGCCCTCGGCGCGTGGGCGCGTGCCTCTCTCGGCGGCGCGCTGGCCG 661
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
Db 662 GCCGCGTGGCGACCGCGCGCGCGCGGCTCCAGCGCGTGTCTGCGCGCGCG 718

RESULT 10
US-10-109-048-1142
; Sequence 1142, Application US/10109048
; GENERAL INFORMATION:
; APPLICANT: COMMURI, PADMA
; APPLICANT: KEELING, PETER L.
; APPLICANT: RAMIREZ, NONA
; APPLICANT: MCKEAN, ANGELA
; APPLICANT: GAO, ZHONG
; APPLICANT: GUAN, HANPING
; TITLE OF INVENTION: GLUCAN CHAIN LENGTH DOMAINS
; FILE REFERENCE: 2461-76
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! CURRENT APPLICATION NUMBER: US/10/109,048  
! CURRENT FILING DATE: 2003-03-04  
! PRIOR APPLICATION NUMBER: 60/279,720  
! PRIOR FILING DATE: 2001-03-30  
! NUMBER OF SEQ ID NOS: 1154  
! SOFTWARE: Patent in Ver. 2.1  
! SEQ ID NO 1142  
! TYPE: DNA  
! ORGANISM: Zea mays  
! FEATURE:  
! NAME/KEY: modified\_base  
! LOCATION: (2709)  
! OTHER INFORMATION: a, t, c, g, other or unknown  
US-10-109-048-1142

Alignment Scores:  
Pred. No.: 2,65e-15 Length: 2991  
Score: 191.00 Matches: 38  
Percent Similarity: 97.4% Conservative: 0  
Best Local Similarity: 97.4% Mismatches: 1  
Query Match: 100.0% Indels: 0  
DB: 42 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-109-048-1142 (1-2991)

QY 1 MetaAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpPro 20  
Db 602 ATGGCGACCCCTCGGCGGTGGCGCGCGGCTCTCTCGCGCGCGCCCTGGCGG 661  
QY 21 AlaAlaValGlyAspArgAlaArgProArgGlnArgValLeuArgArg 39  
Db 662 GCCGCGGTGGCGACCGCGCGCGCGCGGCTCCAGCGGTCTGGCGCGCGG 718

## RESULT 11

US-10-425-115-54073/c  
! Sequence 54073, Application US/10425115  
! GENERAL INFORMATION:  
! APPLICANT: La Rosa, Thomas J.  
! APPLICANT: Kovalic, David K.  
! APPLICANT: Zhou, Yihua  
! APPLICANT: Cao, Yongwei  
! TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
! FILE REFERENCE: 38-21(53222)B  
! CURRENT APPLICATION NUMBER: US/10/425,115  
! CURRENT FILING DATE: 2003-04-28  
! NUMBER OF SEQ ID NOS: 369326  
! SEQ ID NO 54073  
! LENGTH: 3123  
! TYPE: DNA  
! ORGANISM: Zea mays  
! FEATURE:  
! NAME/KEY: unsure  
! LOCATION: (1)..(3123)  
! OTHER INFORMATION: unsure at all n locations  
! FEATURE:  
! OTHER INFORMATION: Clone ID: MRT4577\_149315C.1  
US-10-425-115-54073

Alignment Scores:  
Pred. No.: 2,81e-15 Length: 3123  
Score: 191.00 Matches: 38  
Percent Similarity: 97.4% Conservative: 0  
Best Local Similarity: 97.4% Mismatches: 1  
Query Match: 100.0% Indels: 0  
DB: 51 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-425-115-54073 (1-3123)

QY 1 MetaAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpPro 20  
Db 2390 ATGGCGACCCCTCGGCGGTGGCGCGCGGCTCTCTCTCGCGCGCGCCCTGGCGG 2331

QY 21 AlaAlaValGlyAspArgAlaArgProArgGlnArgValLeuArgArg 39  
Db 2330 GCCGCGGTGGCGACCGCGCGCGCGGCTCCAGCGGTCTGGCGCGCGG 2274

## RESULT 12

US-09-077-564-1  
! Sequence 1, Application US/09077564  
! GENERAL INFORMATION:  
! APPLICANT: Knight, Mary E.  
! APPLICANT: Keeling, Peter L.  
! TITLE OF INVENTION: Modification of Starch Synthesis in  
! TITLE OF INVENTION: Plants  
! NUMBER OF SEQUENCES: 32  
! CORRESPONDENCE ADDRESS:  
! ADDRESSEE: ZENECA Ag Products  
! STREET: 1800 Concord Pike  
! CITY: Wilmington  
! STATE: DE  
! COUNTRY: USA  
! ZIP: 19850  
! COMPUTER READABLE FORM:  
! MEDIUM TYPE: Floppy disk  
! COMPUTER: IBM PC compatible  
! OPERATING SYSTEM: PC-DOS/MS-DOS  
! SOFTWARE: Patent in Release #1.0, Version #1.25  
! CURRENT APPLICATION DATA:  
! APPLICATION NUMBER: US/09/077,564  
! FILING DATE: 14-DEC-1998  
! CLASSIFICATION: 800  
! PRIOR APPLICATION DATA:  
! APPLICATION NUMBER: PCT/GB96/02990  
! FILING DATE: 04-DEC-1996  
! PRIOR APPLICATION DATA:  
! APPLICATION NUMBER: GB 9524938.9  
! FILING DATE: 06-DEC-1995  
! ATTORNEY/AGENT INFORMATION:  
! NAME: Hohenschutz, Liza D.  
! REGISTRATION NUMBER: 33,712  
! REFERENCE/DOCKET NUMBER: SEE 45052/UST  
! TELECOMMUNICATION INFORMATION:  
! TELEPHONE: (302) 886-1699  
! INFORMATION FOR SEQ ID NO: 1:  
! SEQUENCE CHARACTERISTICS:  
! LENGTH: 2992 base pairs  
! TYPE: nucleic acid  
! STRANDEDNESS: single  
! TOPOLOGY: unknown  
! MOLECULE TYPE: cDNA  
! IMMEDIATE SOURCE:  
! CLONE: NUMBER 1  
US-09-077-564-1

Alignment Scores:  
Pred. No.: 3,68e-15 Length: 2992  
Score: 190.00 Matches: 39  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 99.5% Indels: 0  
DB: 20 Gaps: 0

US-10-628-525A-37 (1-39) x US-09-077-564-1 (1-2992)

QY 1 MetaAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpPro 20  
Db 602 ATGGCGACCCCTCGGCGGTGGCGCGCGGCTCTCTCTCGCGCGGNCCTGGCGG 661  
QY 21 AlaAlaValGlyAspArgAlaArgProArgGlnArgValLeuArgArg 39  
Db 662 GCCGCGGTGGCGACCGCGCGCGCGGCTCCAGCGGTCTGGCGCGCGG 718

## RESULT 13

US-09-619-643-9073



```
RESULT 17
US-09-619-643-17333
; Sequence 17333, Application US/09619643
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51230)B
; CURRENT APPLICATION NUMBER: US/09/619,643
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 17333
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3151-012-Q1-K1-E9
US-09-619-643-17333

Alignment Scores:
Pred. No.: 3,01e-14 Length: 462
Score: 176.00 Matches: 35
Percent Similarity: 89.7% Conservatives: 0
Best Local Similarity: 89.7% Mismatches: 4
Query Match: 92.1% Indels: 0
DB: 28 Gaps: 0

US-10-628-525A-37 (1-39) x US-09-619-643-17333 (1-462)
QY 1 MetaLthrProSexAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpPro 20
DB 69 ATGGCGACCCCTCGGCGCTGGGCGCGAGTGCCTCTCTCGGCGGCCGCGACTGGCGG 128
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
DB 129 GCCGGCGTGGCGACCGGCGCGCGCGCGCGCTCCAGCGGTGCTGCGCGCGCGG 185

RESULT 18
US-60-145-148-845
; Sequence 845, Application US/60145148
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Deng, Molian
; APPLICANT: Fisher, Dane K.
; APPLICANT: Miller, Philip W.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(51230)A
; CURRENT APPLICATION NUMBER: US/60/145,148
; CURRENT FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 3994
; SEQ ID NO 845
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3151-012-Q1-K1-E9
US-60-145-148-845

Alignment Scores:
Pred. No.: 3,01e-14 Length: 462
Score: 176.00 Matches: 35
Percent Similarity: 89.7% Conservatives: 0
Best Local Similarity: 89.7% Mismatches: 4
Query Match: 92.1% Indels: 0
DB: 75 Gaps: 0

US-10-628-525A-37 (1-39) x US-60-145-148-845 (1-462)
QY 1 MetaLthrProSexAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpPro 20
DB 69 ATGGCGACCCCTCGGCGCTGGGCGCGAGTGCCTCTCTCGGCGGCCGCGACTGGCGG 128
```

```
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
DB 129 GCCGGCGTGGCGACCGGCGCGCGCGCGCTCCAGCGGTGCTGCGCGCGCGG 185

RESULT 19
US-09-654-617-269739
; Sequence 269739, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 269739
; LENGTH: 1034
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION:
US-09-654-617-269739

Alignment Scores:
Pred. No.: 8,8e-14 Length: 1034
Score: 176.00 Matches: 35
Percent Similarity: 89.7% Conservatives: 0
Best Local Similarity: 89.7% Mismatches: 4
Query Match: 92.1% Indels: 0
DB: 29 Gaps: 0

US-10-628-525A-37 (1-39) x US-09-654-617-269739 (1-1034)
QY 1 MetaLthrProSexAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpPro 20
DB 69 ATGGCGACCCCTCGGCGCTGGGCGCGAGTGCCTCTCTCGGCGGCCGCGACTGGCGG 128
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
DB 129 GCCGGCGTGGCGACCGGCGCGCGCGCTCCAGCGGTGCTGCGCGCGCGG 185

RESULT 20
US-09-684-016-269739
; Sequence 269739, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 269739
; LENGTH: 1034
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION:
US-09-684-016-269739

Alignment Scores:
Pred. No.: 8,8e-14 Length: 1034
Score: 176.00 Matches: 35
Percent Similarity: 89.7% Conservatives: 0
Best Local Similarity: 89.7% Mismatches: 4
Query Match: 92.1% Indels: 0
DB: 29 Gaps: 0

US-10-628-525A-37 (1-39) x US-09-684-016-269739 (1-1034)
QY 1 MetaLthrProSexAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpPro 20
DB 69 ATGGCGACCCCTCGGCGCTGGGCGCGAGTGCCTCTCTCGGCGGCCGCGACTGGCGG 128
```

QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39  
Db 129 GCCGGCTGCGGACCGCGCGCGCGCGCGCTCCAGCGCTGCTGCGCGCGCG 185

RESULT 21  
US-09-850-147-1953  
; Sequence 1953, Application US/09850147  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(51914)B  
; CURRENT APPLICATION NUMBER: US/09/850,147  
; CURRENT FILING DATE: 2001-05-08  
; PRIOR FILING DATE: 2000-05-08  
; PRIOR APPLICATION NUMBER: US 60/202,213  
; PRIOR FILING DATE: 2000-05-08  
; PRIOR APPLICATION NUMBER: US 09/654,617  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: US 09/684,016  
; PRIOR FILING DATE: 2000-10-10  
; NUMBER OF SEQ ID NOS: 18014  
; SEQ ID NO 1953  
; LENGTH: 370  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; OTHER INFORMATION: Clone ID: LIB3476-015-P1-K1-B5  
US-09-850-147-1953

Alignment Scores:  
Pred. No.: 9.5e-10 Length: 370  
Score: 143.50 Matches: 32  
Percent Similarity: 77.3% Conservative: 2  
Best Local Similarity: 72.7% Mismatches: 5  
Query Match: 75.1% Indels: 5  
DB: 33 Gaps: 1

US-10-628-525A-37 (1-39) x US-09-850-147-1953 (1-370)  
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*Ala----- 18  
Db 129 ATGGCGAGCGCTCGGCGCGCGCGCGCTGCTGCTAGCGGAGCGCGCGCGG 188  
QY 19 -----TrpProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgVal 35  
Db 189 CTGGGCTTTGGCGCGCGCGCGCGCGATCGGCGCGCGCGCGCTCCAGCGGTG 248  
QY 36 LeuArgArgArg 39  
Db 249 GTGCGCAGGCGG 260

RESULT 22  
US-60-202-213-1950  
; Sequence 1950, Application US/60202213  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; FILE REFERENCE: 38-21(51914)A  
; CURRENT APPLICATION NUMBER: US/60/202,213  
; CURRENT FILING DATE: 2000-05-08  
; NUMBER OF SEQ ID NOS: 17986  
; SEQ ID NO 1950  
; LENGTH: 370  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; OTHER INFORMATION: Clone ID: LIB3476-015-P1-K1-B5  
US-60-202-213-1950

Alignment Scores:  
Pred. No.: 9.5e-10 Length: 370  
Score: 143.50 Matches: 32  
Percent Similarity: 77.3% Conservative: 2  
Best Local Similarity: 72.7% Mismatches: 5  
Query Match: 75.1% Indels: 5  
DB: 33 Gaps: 1

US-10-628-525A-37 (1-39) x US-09-850-147-1953 (1-370)  
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*Ala----- 18  
Db 129 ATGGCGAGCGCTCGGCGCGCGCGCGCTGCTGCTAGCGGAGCGCGCGCGG 188  
QY 19 -----TrpProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgVal 35  
Db 189 CTGGGCTTTGGCGCGCGCGCGCGATCGGCGCGCGCGCGCGCTCCAGCGGTG 248  
QY 36 LeuArgArgArg 39  
Db 249 GTGCGCAGGCGG 260

RESULT 23  
US-09-654-617-454633  
; Sequence 454633, Application US/09654617  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: Annotated Plant Genes  
; FILE REFERENCE: 38-21(15097)D  
; CURRENT APPLICATION NUMBER: US/09/654,617  
; CURRENT FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 463173  
; SEQ ID NO 454633  
; LENGTH: 376  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
US-09-654-617-454633

Alignment Scores:  
Pred. No.: 9.7e-10 Length: 376  
Score: 143.50 Matches: 32  
Percent Similarity: 77.3% Conservative: 2  
Best Local Similarity: 72.7% Mismatches: 5  
Query Match: 75.1% Indels: 5  
DB: 29 Gaps: 1

US-10-628-525A-37 (1-39) x US-09-654-617-454633 (1-376)  
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*Ala----- 18  
Db 135 ATGGCGAGCGCTCGGCGCGCGCGCTGCTGCTAGCGGAGCGCGCGCGG 194  
QY 19 -----TrpProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgVal 35  
Db 195 CTGGGCTTTGGCGCGCGCGCGCGATCGGCGCGCGCGCGCGCTCCAGCGGTG 254  
QY 36 LeuArgArgArg 39  
Db 255 GTGCGCAGGCGG 266

RESULT 24  
US-09-684-016-454633  
; Sequence 454633, Application US/09684016  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: Annotated Plant Genes  
; FILE REFERENCE: 38-21(15097)D  
; CURRENT APPLICATION NUMBER: US/09/684,016  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 09/654,617  
; PRIOR FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 463173  
; SEQ ID NO 454633  
; LENGTH: 376

Percent Similarity: 77.3% Conservative: 2  
Best Local Similarity: 72.7% Mismatches: 5  
Query Match: 75.1% Indels: 5  
DB: 76 Gaps: 1

US-10-628-525A-37 (1-39) x US-60-202-213-1950 (1-370)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*Ala----- 18  
Db 129 ATGGCGAGCGCTCGGCGCGCGCGCTGCTGCTAGCGGAGCGCGCGCGG 188  
QY 19 -----TrpProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgVal 35  
Db 189 CTGGGCTTTGGCGCGCGCGCGCGATCGGCGCGCGCGCGCTCCAGCGGTG 248  
QY 36 LeuArgArgArg 39  
Db 249 GTGCGCAGGCGG 260

RESULT 23  
US-09-654-617-454633  
; Sequence 454633, Application US/09654617  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: Annotated Plant Genes  
; FILE REFERENCE: 38-21(15097)D  
; CURRENT APPLICATION NUMBER: US/09/654,617  
; CURRENT FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 463173  
; SEQ ID NO 454633  
; LENGTH: 376  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
US-09-654-617-454633

Alignment Scores:  
Pred. No.: 9.7e-10 Length: 376  
Score: 143.50 Matches: 32  
Percent Similarity: 77.3% Conservative: 2  
Best Local Similarity: 72.7% Mismatches: 5  
Query Match: 75.1% Indels: 5  
DB: 29 Gaps: 1

US-10-628-525A-37 (1-39) x US-09-654-617-454633 (1-376)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*Ala----- 18  
Db 135 ATGGCGAGCGCTCGGCGCGCGCGCTGCTGCTAGCGGAGCGCGCGCGG 194  
QY 19 -----TrpProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgVal 35  
Db 195 CTGGGCTTTGGCGCGCGCGCGCGATCGGCGCGCGCGCGCGCTCCAGCGGTG 254  
QY 36 LeuArgArgArg 39  
Db 255 GTGCGCAGGCGG 266

RESULT 24  
US-09-684-016-454633  
; Sequence 454633, Application US/09684016  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: Annotated Plant Genes  
; FILE REFERENCE: 38-21(15097)D  
; CURRENT APPLICATION NUMBER: US/09/684,016  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 09/654,617  
; PRIOR FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 463173  
; SEQ ID NO 454633  
; LENGTH: 376

```
/ TYPE: DNA
/ ORGANISM: Sorghum bicolor
US-09-684-016-454633

Alignment Scores:
Pred. No.: 9.7e-10 Length: 376
Score: 143.50 Matches: 32
Percent Similarity: 77.3% Conservative: 2
Best Local Similarity: 72.7% Mismatches: 5
Query Match: 75.1% Indels: 5
DB: 29 Gaps: 1

US-10-628-525A-37 (1-39) x US-09-684-016-454633 (1-376)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***Ala----- 18
Db 135 ATGGCAGCCCTCGGCGCGCGCGCGTCTGCTCTAGCGGAGCCCGCGCGG 194
QY 19 -----TrpProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgVal 35
Db 195 CTTGGCTTGGCGCGCGCGCGCGATCGGCGCGCGCGCGGCTCCAGCGCGTG 254
QY 36 LeuArgArgArg 39
Db 255 GTGCGCAGCGCG 266

RESULT 25
US-10-767-701-13043
/ Sequence 13043, Application US/10767701
/ GENERAL INFORMATION:
/ APPLICANT: Kovacic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53535)B
/ CURRENT APPLICATION NUMBER: US/10/767,701
/ CURRENT FILING DATE: 2004-01-29
/ NUMBER OF SEQ ID NOS: 63128
/ SEQ ID NO 13043
/ LENGTH: 2670
/ TYPE: DNA
/ ORGANISM: Sorghum bicolor
/ FEATURE:
/ OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS52_1
US-10-767-701-13043

Alignment Scores:
Pred. No.: 1.32e-08 Length: 2670
Score: 143.50 Matches: 32
Percent Similarity: 77.3% Conservative: 2
Best Local Similarity: 72.7% Mismatches: 5
Query Match: 75.1% Indels: 5
DB: 61 Gaps: 1

US-10-628-525A-37 (1-39) x US-10-767-701-13043 (1-2670)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***Ala----- 18
Db 138 ATGGCAGCCCTCGGCGCGCGCGTCTGCTCTAGCGGAGCCCGCGCGG 197
QY 19 -----TrpProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgVal 35
Db 198 CTTGGCTTGGCGCGCGCGCGCGATCGGCGCGCGCGCGGCTCCAGCGCGTG 257
QY 36 LeuArgArgArg 39
Db 258 GTGCGCAGCGCG 269

RESULT 26
US-60-171-627-1369
/ Sequence 1369, Application US/60171627
/ GENERAL INFORMATION:
/ APPLICANT: Yandell, Mark
/ TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS ESSENTIAL
/ TITLE OF INVENTION: FOR SURVIVAL, NUCLEIC ACID MOLECULES ENCODING ESSENTIAL
/ FILE REFERENCE: CL000177
/ CURRENT APPLICATION NUMBER: US/60/171,627
/ CURRENT FILING DATE: 1999-12-23
/ NUMBER OF SEQ ID NOS: 2237
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1369
/ LENGTH: 7492
/ TYPE: DNA
/ ORGANISM: Drosophila
US-60-171-627-1369

Alignment Scores:
Pred. No.: 410 Length: 7492
Score: 74.00 Matches: 16
Percent Similarity: 56.8% Conservative: 5
Best Local Similarity: 43.2% Mismatches: 16
Query Match: 38.7% Indels: 0
DB: 75 Gaps: 0

US-10-628-525A-37 (1-39) x US-60-171-627-1369 (1-7492)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTTPPro 20
Db 4941 ATGGGCACCAAGCAGCTTGGGCAAAATAGTATTTCACCGCATCGCGAAGCCATGCGCG 5000
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 37
Db 5001 GCTGTGTCAGAGATAGGCTTAAAGCAGGAGTTTATAGTAGAATCTTCGC 5051

RESULT 27
US-60-173-464-14199
/ Sequence 14199, Application US/60173464
/ GENERAL INFORMATION:
/ APPLICANT: Li, Peter W. D.
/ TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR, PROTEINS AND USES
/ FILE REFERENCE: THEREOF
/ FILE REFERENCE: CL000173
/ CURRENT APPLICATION NUMBER: US/60/173,464
/ CURRENT FILING DATE: 1999-12-29
/ NUMBER OF SEQ ID NOS: 30269
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 14199
/ LENGTH: 7492
/ TYPE: DNA
/ ORGANISM: Drosophila
US-60-173-464-14199

Alignment Scores:
Pred. No.: 410 Length: 7492
Score: 74.00 Matches: 16
Percent Similarity: 56.8% Conservative: 5
Best Local Similarity: 43.2% Mismatches: 16
Query Match: 38.7% Indels: 0
DB: 75 Gaps: 0

US-10-628-525A-37 (1-39) x US-60-173-464-14199 (1-7492)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTTPPro 20
Db 4941 ATGGGCACCAAGCAGCTTGGGCAAAATAGTATTTCACCGCATCGCGAAGCCATGCGCG 5000
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 37
Db 5001 GCTGTGTCAGAGATAGGCTTAAAGCAGGAGTTTATAGTAGAATCTTCGC 5051

RESULT 28
US-60-167-217-17335
/ Sequence 17335, Application US/60167217
```

```
; GENERAL INFORMATION:
; APPLICANT: Li, Peter W. D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES
; FILE REFERENCE: CL000152
; CURRENT APPLICATION NUMBER: US/60/167,217
; CURRENT FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 23195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17335
; LENGTH: 7495
; TYPE: DNA
; ORGANISM: Drosophila
US-60-167-217-17335

Alignment Scores:
Pred. No.: 410 Length: 7495
Score: 74.00 Matches: 16
Percent Similarity: 56.8% Conservative: 5
Best Local Similarity: 43.2% Mismatches: 16
Query Match: 38.7% Indels: 0
DB: 75 Gaps: 0

US-10-628-525A-37 (1-39) x US-60-167-217-17335 (1-7495)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTtpPro 20
Db 4941 ATGGGCACAGAGAGAGCTGGGCAATAGTATTTCACCGCATCGCGAAGCCATGGCCG 5000

QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 37
Db 5001 GCTGTGTCAGAGATAGGCTAAAGCAGGGATTTTAGTAGAATTCTTCGC 5051

RESULT 29
US-60-161-932-184
; Sequence 184, Application US/60161932
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containin the Nucleic Acid Sequences
; FILE REFERENCE: CL000122
; CURRENT APPLICATION NUMBER: US/60/161,932
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 2626
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 53583
; TYPE: DNA
; ORGANISM: Drosophila
US-60-161-932-184

Alignment Scores:
Pred. No.: 5,63e+03 Length: 53583
Score: 74.00 Matches: 16
Percent Similarity: 56.8% Conservative: 5
Best Local Similarity: 43.2% Mismatches: 16
Query Match: 38.7% Indels: 0
DB: 75 Gaps: 0

US-10-628-525A-37 (1-39) x US-60-161-932-184 (1-53583)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTtpPro 20
Db 37623 ATGGGCACAGAGAGAGCTGGGCAATAGTATTTCACCGCATCGCGAAGCCATGGCCG 37682

QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 37
Db 37683 GCTGTGTCAGAGATAGGCTAAAGCAGGGATTTTAGTAGAATTCTTCGC 37733

RESULT 30
US-09-528-237A-965/c
```

```
; Sequence 965, Application US/09528237A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid
; TITLE OF INVENTION: Sequences and Uses Thereof
; FILE REFERENCE: CL000284
; CURRENT APPLICATION NUMBER: US/09/528,237A
; CURRENT FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 2926
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 965
; LENGTH: 54050
; TYPE: DNA
; ORGANISM: Drosophila
US-09-528-237A-965
```

```
Alignment Scores:
Pred. No.: 5,69e+03 Length: 54050
Score: 74.00 Matches: 16
Percent Similarity: 56.8% Conservative: 5
Best Local Similarity: 43.2% Mismatches: 16
Query Match: 38.7% Indels: 0
DB: 25 Gaps: 0
```

US-10-628-525A-37 (1-39) x US-09-528-237A-965 (1-54050)

```
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTtpPro 20
Db 15961 ATGGGCACAGAGAGAGCTGGGCAATAGTATTTCACCGCATCGCGAAGCCATGGCCG 15902

QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 37
Db 15901 GCTGTGTCAGAGATAGGCTAAAGCAGGGATTTTAGTAGAATTCTTCGC 15851
```

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Job time : 1078.11 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 21:21:57 ; Search time 72.9357 Seconds  
(without alignments)  
1603.719 Million cell updates/sec

Title: US-10-628-525A-37

Perfect score: 191

Sequence: 1 MATPSVAGAACILLARXPAVGDPRRLQVLRRR 39

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6698573 seqs, 1499593917 residues

Total number of hits satisfying chosen parameters: 13397146

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+p2n.model -DRV=xlh  
-Q=/abes/ABSSWEB spool/US10628525/runat\_31032006\_095132\_17106/app.query.fasta\_1  
-DB=Pending Patents NA New -QFMT=fastcap -SUFFIX=p2n.rnpn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=150 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abss06h  
-USER=US10628525 @CGN 1.1.1552 @runat\_31032006\_095132\_17106 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WAE TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA New:

1: /SID55/ptodata/2/pna/pct NEW COMB.seq.\*  
2: /SID55/ptodata/2/pna/US05 NEW COMB.seq.\*  
3: /SID55/ptodata/2/pna/US07 NEW COMB.seq.\*  
4: /SID55/ptodata/2/pna/US08 NEW COMB.seq.\*  
5: /SID55/ptodata/2/pna/US09 NEW COMB.seq.\*  
6: /SID55/ptodata/2/pna/US10 NEW COMB.seq.\*  
7: /SID55/ptodata/2/pna/US10 NEW COMB.seq.1.\*  
8: /SID55/ptodata/2/pna/US11 NEW COMB.seq.\*  
9: /SID55/ptodata/2/pna/US11 NEW COMB.seq.1.\*  
10: /SID55/ptodata/2/pna/US11 NEW COMB.seq.\*  
11: /SID55/ptodata/2/pna/US11 NEW COMB.seq.3.\*  
12: /SID55/ptodata/2/pna/US60 NEW COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description          |
|------------|-------|-------------|--------|----|----------------------|
| 1          | 191   | 100.0       | 324    | 8  | US-11-330-822-62     |
| 2          | 186   | 97.4        | 324    | 10 | US-11-227-183A-9073  |
| 3          | 176   | 92.1        | 462    | 10 | US-11-227-183A-17333 |
| 4          | 67    | 35.1        | 359    | 8  | US-11-353-150-43602  |
| 5          | 67    | 35.1        | 1958   | 7  | US-10-953-349-38532  |

|    |      |      |       |    |                       |                                     |
|----|------|------|-------|----|-----------------------|-------------------------------------|
| 6  | 67   | 35.1 | 1958  | 8  | US-11-056-355B-8207   | Sequence 8207, Ap                   |
| 7  | 67   | 35.1 | 1958  | 8  | US-11-056-355B-15424  | Sequence 15424, A                   |
| 8  | 66.5 | 34.8 | 520   | 8  | US-11-353-150-13452   | Sequence 13452, A                   |
| 9  | 65.5 | 34.3 | 391   | 8  | US-11-353-150-47903   | Sequence 47903, A                   |
| 10 | 65.5 | 34.3 | 441   | 8  | US-11-353-150-5560    | Sequence 5560, Ap                   |
| 11 | 65.5 | 34.3 | 450   | 8  | US-11-353-150-43740   | Sequence 43740, A                   |
| 12 | 65.5 | 34.3 | 506   | 8  | US-11-353-150-12500   | Sequence 12500, A                   |
| 13 | 65.5 | 34.3 | 517   | 8  | US-11-330-364-15086   | Sequence 15086, A                   |
| 14 | 65.5 | 34.3 | 549   | 8  | US-11-353-150-14496   | Sequence 14496, A                   |
| 15 | 64.5 | 33.8 | 452   | 8  | US-11-353-150-11403   | Sequence 11403, A                   |
| 16 | 64.5 | 33.8 | 12499 | 10 | US-11-266-748A-30547  | Sequence 30547, A                   |
| 17 | 64   | 33.5 | 502   | 10 | US-11-266-748A-13015  | Sequence 13015, A                   |
| 18 | 63   | 33.0 | 416   | 10 | US-11-314-008-3670    | Sequence 3670, Ap                   |
| 19 | 63   | 33.0 | 2869  | 12 | US-60-751-455-406     | Sequence 406, Appl                  |
| 20 | 63   | 33.0 | 8705  | 7  | US-10-240-851A-10     | Sequence 10, Appl                   |
| 21 | 62.5 | 32.7 | 334   | 8  | US-11-239-610A-7822   | Sequence 7822, Ap                   |
| 22 | 62.5 | 32.7 | 357   | 8  | US-11-239-610A-18886  | Sequence 18886, A                   |
| 23 | 62.5 | 32.7 | 379   | 8  | US-11-353-150-63898   | Sequence 63898, A                   |
| 24 | 62.5 | 32.7 | 395   | 8  | US-11-353-150-47816   | Sequence 47816, A                   |
| 25 | 62.5 | 32.7 | 755   | 7  | US-10-289-526-1524    | Sequence 1524, Ap                   |
| 26 | 62.5 | 32.7 | 2300  | 12 | US-60-762-056-17573   | Sequence 17573, A                   |
| 27 | 62.5 | 32.7 | 2300  | 12 | US-60-762-056-17574   | Sequence 17574, A                   |
| 28 | 62.5 | 32.7 | 2300  | 12 | US-60-762-056-41263   | Sequence 41263, A                   |
| 29 | 62   | 32.5 | 1000  | 10 | US-11-266-748A-395580 | Sequence 395580, Sequence 466626    |
| 30 | 62   | 32.5 | 1000  | 10 | US-11-266-748A-466626 | Sequence 466626, Sequence 65842, A  |
| 31 | 62   | 32.5 | 1258  | 8  | US-11-056-355B-65842  | Sequence 65842, A                   |
| 32 | 62   | 32.5 | 1383  | 12 | US-60-772-786-75      | Sequence 75, Appl                   |
| 33 | 62   | 32.5 | 2203  | 8  | US-11-360-355-81526   | Sequence 81526, A                   |
| 34 | 62   | 32.5 | 2300  | 12 | US-60-762-056-14174   | Sequence 14174, A                   |
| 35 | 62   | 32.5 | 3110  | 8  | US-11-360-355-2775    | Sequence 2775, Ap                   |
| 36 | 62   | 32.5 | 3521  | 8  | US-11-360-355-78416   | Sequence 78416, A                   |
| 37 | 62   | 32.5 | 3757  | 8  | US-11-360-355-14379   | Sequence 14379, A                   |
| 38 | 62   | 32.5 | 9288  | 10 | US-11-266-748A-22728  | Sequence 22728, A                   |
| 39 | 61.5 | 32.2 | 431   | 10 | US-11-227-183A-979    | Sequence 979, Appl                  |
| 40 | 61.5 | 32.2 | 461   | 7  | US-10-953-349-30799   | Sequence 30799, A                   |
| 41 | 61.5 | 32.2 | 2073  | 8  | US-11-056-355B-6583   | Sequence 6583, A                    |
| 42 | 61   | 31.9 | 844   | 10 | US-11-266-748A-94331  | Sequence 94331, A                   |
| 43 | 61   | 31.9 | 844   | 10 | US-11-266-748A-147142 | Sequence 147142, A                  |
| 44 | 61   | 31.9 | 1021  | 10 | US-11-266-748A-262513 | Sequence 262513, A                  |
| 45 | 61   | 31.9 | 1021  | 10 | US-11-266-748A-323030 | Sequence 323030, A                  |
| 46 | 61   | 31.9 | 1097  | 7  | US-10-953-349-33785   | Sequence 33785, A                   |
| 47 | 61   | 31.9 | 1097  | 8  | US-11-056-355B-3807   | Sequence 3807, Ap                   |
| 48 | 61   | 31.9 | 1097  | 8  | US-11-056-355B-5274   | Sequence 5274, Ap                   |
| 49 | 61   | 31.9 | 1097  | 8  | US-11-056-355B-11617  | Sequence 11617, A                   |
| 50 | 61   | 31.9 | 1097  | 8  | US-11-056-355B-13376  | Sequence 13376, A                   |
| 51 | 61   | 31.9 | 3213  | 10 | US-11-266-748A-57722  | Sequence 57722, A                   |
| 52 | 61   | 31.9 | 3640  | 12 | US-60-751-420-961     | Sequence 961, Appl                  |
| 53 | 60.5 | 31.7 | 266   | 12 | PCI-US05-47111-543    | Sequence 543, Appl                  |
| 54 | 60.5 | 31.7 | 266   | 12 | US-60-752-355-543     | Sequence 543, Appl                  |
| 55 | 60.5 | 31.7 | 535   | 6  | US-10-515-373-615     | Sequence 615, Appl                  |
| 56 | 60.5 | 31.7 | 1088  | 10 | US-11-266-748A-366896 | Sequence 366896, Sequence 450275, A |
| 57 | 60.5 | 31.7 | 1088  | 10 | US-11-266-748A-450275 | Sequence 450275, A                  |
| 58 | 60.5 | 31.7 | 2300  | 12 | US-60-762-056-16437   | Sequence 16437, A                   |
| 59 | 60.5 | 31.7 | 2300  | 12 | US-60-762-056-21708   | Sequence 21708, A                   |
| 60 | 60.5 | 31.7 | 2899  | 10 | US-11-266-748A-26672  | Sequence 26672, A                   |
| 61 | 60   | 31.4 | 279   | 8  | US-11-360-355-46316   | Sequence 46316, A                   |
| 62 | 60   | 31.4 | 436   | 8  | US-11-360-355-32867   | Sequence 32867, A                   |
| 63 | 60   | 31.4 | 718   | 10 | US-11-266-748A-214421 | Sequence 214421, A                  |
| 64 | 60   | 31.4 | 718   | 10 | US-11-266-748A-237041 | Sequence 237041, A                  |
| 65 | 60   | 31.4 | 936   | 7  | US-10-502-832-3       | Sequence 3, Appl                    |
| 66 | 60   | 31.4 | 1000  | 10 | US-11-266-748A-118260 | Sequence 118260, A                  |
| 67 | 60   | 31.4 | 1000  | 10 | US-11-266-748A-160424 | Sequence 160424, A                  |
| 68 | 60   | 31.4 | 1000  | 10 | US-11-266-748A-402945 | Sequence 402945, A                  |
| 69 | 60   | 31.4 | 1000  | 10 | US-11-266-748A-473991 | Sequence 473991, A                  |
| 70 | 60   | 31.4 | 1692  | 7  | US-10-567-728-9       | Sequence 9, Appl                    |
| 71 | 60   | 31.4 | 1758  | 8  | US-11-174-307B-3643   | Sequence 3643, Ap                   |
| 72 | 60   | 31.4 | 2075  | 8  | US-11-360-355-13119   | Sequence 13119, A                   |
| 73 | 60   | 31.4 | 2083  | 10 | US-11-266-748A-72831  | Sequence 72831, A                   |
| 74 | 60   | 31.4 | 2083  | 10 | US-11-266-748A-107509 | Sequence 107509, A                  |
| 75 | 60   | 31.4 | 2083  | 10 | US-11-266-748A-125642 | Sequence 125642, A                  |
| 76 | 60   | 31.4 | 2300  | 12 | US-60-762-056-31506   | Sequence 31506, A                   |
| 77 | 60   | 31.4 | 2307  | 10 | US-11-266-748A-27954  | Sequence 27954, A                   |
| 78 | 60   | 31.4 | 2669  | 10 | US-11-288-493-65      | Sequence 65, Appl                   |



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Best Local Similarity: 97.4% Mismatches: 1
Query Match: 97.4% Indels: 0
DB: 10 Gaps: 0

US-10-628-525A-37 (1-39) x US-11-227-183A-9073 (1-324)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpPro 20
Db 153 ATGGCGACGCCCTCGCGCGGTGGCGCGCGCTGCTCTTCTCGCGCGCGCGCTGGCCG 212
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 38
Db 213 GCCCGCGTGGCGACCGCGCGCGCGCGCGCGCTCCAGCGCGGTGCTGCGCGCGC 266

RESULT 3
US-11-227-183A-17333
; Sequence 17333, Application US/11227183A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalugudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated with
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US
; CURRENT APPLICATION NUMBER: US/11/227,183A
; CURRENT FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: US 09/619,643
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 17333
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3151-012-Q1-K1-E9
US-11-227-183A-17333

Alignment Scores:
Pred. No.: 7,25e-16 Length: 462
Score: 176.00 Matches: 35
Percent Similarity: 89.7% Conservative: 0
Best Local Similarity: 89.7% Mismatches: 4
Query Match: 92.1% Indels: 0
DB: 10 Gaps: 0

US-10-628-525A-37 (1-39) x US-11-227-183A-17333 (1-462)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpPro 20
Db 69 ATGGCGACGCCCTCGCGCGGTGGCGCGCGAGTGCCTCTCTCGCGCGCGCGCTGGCCG 128
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
Db 129 GCCCGCGTGGCGACCGCGCGCGCGCGCGCGCTCCAGCGGTGCTGCGCGCGCG 185

RESULT 4
US-11-353-150-43602
; Sequence 43602, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalugudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 43602
; LENGTH: 359
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; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3066-044-Q1-K1-F5
US-11-353-150-43602
```

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Alignment Scores:
Pred. No.: 3,62 Length: 359
Score: 67.00 Matches: 22
Percent Similarity: 51.1% Conservative: 1
Best Local Similarity: 48.9% Mismatches: 10
Query Match: 35.1% Indels: 12
DB: 8 Gaps: 2
```

US-10-628-525A-37 (1-39) x US-11-353-150-43602 (1-359)

```
QY 6 AlaValGlyAlaAlaCysLeu-----LeuLeuAla 15
Db 170 GCTGCAGCGCGTCTGCTCTTACCACTCTCCCTCGCGCTGCTCCGACTCTCGGCGC 229
QY 16 Arg***AlaTrpProAlaAlaVal-----GlyAspArgAlaArgProArgArgLeuGln 33
Db 230 CGCGCGTCCACCCACCGCTGTCCGCGAGGAGGTGAGCTCGCCCCCGCGCGCGC 289
```

```
QY 34 ArgValLeuArgArg 38
Db 290 CGGCATCGCGGTGG 304
```

#### RESULT 5

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US-10-953-349-38532
; Sequence 38532, Application US/10953349
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38532
; LENGTH: 1958
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (208)..(208)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (247)..(247)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-38532
```

```
Alignment Scores:
Pred. No.: 33,4 Length: 1958
Score: 67.00 Matches: 22
Percent Similarity: 51.1% Conservative: 1
Best Local Similarity: 48.9% Mismatches: 10
Query Match: 35.1% Indels: 12
DB: 7 Gaps: 2
```

US-10-628-525A-37 (1-39) x US-10-953-349-38532 (1-1958)

```
QY 6 AlaValGlyAlaAlaCysLeu-----LeuLeuAla 15
Db 472 GCTGCAGCGCGTCTGCTCTTACCACTCTCCCTCGCGCTGCTCCGACTCTCGGCGC 531
QY 16 Arg***AlaTrpProAlaAlaVal-----GlyAspArgAlaArgProArgArgLeuGln 33
Db 532 CGCGCGTCCACCCACCGCTGTCCGCGAGGAGGTGAGCTCGCCCCCGCGCGCGC 591
```

```
QY 34 ArgValLeuArgArg 38
|||
Db 592 CGGCATGCGGTCGG 606

RESULT 6
US-11-056-355B-8207
; Sequence 8207, Application US/11056355B
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 8207
; LENGTH: 1958
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1958)
; OTHER INFORMATION: Ceres Seq. ID no. 13636500
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1958)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177043
; OTHER INFORMATION: as cited in SEQ ID NO 57425
US-11-056-355B-8207

Alignment Scores:
Pred. No.: 33.4 Length: 1958
Score: 67.00 Matches: 22
Percent Similarity: 51.1% Conservative: 1
Best Local Similarity: 48.9% Mismatches: 10
Query Match: 35.1% Indels: 12
DB: 8 Gaps: 2

US-10-628-525A-37 (1-39) x US-11-056-355B-8207 (1-1958)
QY 6 AlaValGlyAlaAlaCysLeu-----LeuLeuAla 15
|||
Db 472 GCTGCAGGCGCTGCTCTACACAGTCTCCCTCGCGCCTCGCCTCGGACTCTCTGGCC 531
|||
QY 16 Arg***AlaTrpProAlaAlaVal-----GlyAspArgAlaArgProArgArgLeuGln 33
|||
Db 532 CGCGGCGTCCACCCACAGCTGTCCGCGGAGGAGTGTGAGCTCGCCCGCGCGCGCGC 591
|||
QY 34 ArgValLeuArgArg 38
|||
Db 592 CGGCATGCGGTCGG 606

RESULT 7
US-11-056-355B-15424
; Sequence 15424, Application US/11056355B
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 15424
; LENGTH: 1958
; TYPE: DNA
```

```
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1958)
; OTHER INFORMATION: Ceres Seq. ID no. 13636500
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1958)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177043
; OTHER INFORMATION: as cited in SEQ ID NO 57425
US-11-056-355B-15424

Alignment Scores:
Pred. No.: 33.4 Length: 1958
Score: 67.00 Matches: 22
Percent Similarity: 51.1% Conservative: 1
Best Local Similarity: 48.9% Mismatches: 10
Query Match: 35.1% Indels: 12
DB: 8 Gaps: 2

US-10-628-525A-37 (1-39) x US-11-056-355B-15424 (1-1958)
QY 6 AlaValGlyAlaAlaCysLeu-----LeuLeuAla 15
|||
Db 472 GCTGCAGGCGCTGCTCTACACAGTCTCCCTCGCGCCTCGCCTCGGACTCTCTGGCC 531
|||
QY 16 Arg***AlaTrpProAlaAlaVal-----GlyAspArgAlaArgProArgArgLeuGln 33
|||
Db 532 CGCGGCGTCCACCCACAGCTGTCCGCGGAGGAGTGTGAGCTCGCCCGCGCGCGCGC 591
|||
QY 34 ArgValLeuArgArg 38
|||
Db 592 CGGCATGCGGTCGG 606

RESULT 8
US-11-353-150-13452
; Sequence 13452, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalgudi, Raghunath V.
; FILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 13452
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: cC-zmpo14820021b07d1
US-11-353-150-13452

Alignment Scores:
Pred. No.: 6.95 Length: 520
Score: 66.50 Matches: 20
Percent Similarity: 51.1% Conservative: 3
Best Local Similarity: 44.4% Mismatches: 11
Query Match: 34.8% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-11-353-150-13452 (1-520)
QY 2 AlaThrProSerAlaValGlyAla-----AlaCysLeuLeuLeuAlaArg***AlaTrp 19
|||
Db 294 GCGACCCCTGCGCGCGCGGTTCTGAGACGAACGTGT-----CCAGGAGCGTGG 341
|||
```

```
QY 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
    |||||
Db 342 CCGCGCGCAGCGTGAGGTGGAGTGGCGCACTTCGCGCGGTCGAAGGACGCTCAAGG 401
    |||||
QY 35 ValLeuArgArgArg 39
    |||||
Db 402 CGGAGCGGACGACGG 416

RESULT 9
US-11-353-150-47903
; Sequence 47903, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 47903
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3066-028-Q1-K1-P2
US-11-353-150-47903

Alignment Scores:
Pred. No.: 6.69 Length: 391
Score: 65.50 Matches: 20
Percent Similarity: 48.9% Conservative: 2
Best Local Similarity: 44.4% Mismatches: 12
Query Match: 34.3% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-11-353-150-47903 (1-391)

QY 2 AlaThrProSerAlaValGlyAla-----AlaCysLeuLeuAlaArg***AlaTTrp 19
    |||||
Db 202 CGGACCCCTGCGCGCGGTTTCGAGACGAACTGT-----CCAGGAGCGTGG 249
    |||||
QY 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
    |||||
Db 250 CCGGCGCAGCGTGAGGTGGTGTGCGCGCACTTCGCGCGGTCGAAGGACGCTCAAGG 309
    |||||
QY 35 ValLeuArgArgArg 39
    |||||
Db 310 CGGAGCGGACGACGG 324

RESULT 10
US-11-353-150-5560
; Sequence 5560, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 5560
```

```
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB148-010-Q1-E1-H11
US-11-353-150-5560

Alignment Scores:
Pred. No.: 7.93 Length: 441
Score: 65.50 Matches: 20
Percent Similarity: 48.9% Conservative: 2
Best Local Similarity: 44.4% Mismatches: 12
Query Match: 34.3% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-11-353-150-5560 (1-441)

QY 2 AlaThrProSerAlaValGlyAla-----AlaCysLeuLeuAlaArg***AlaTTrp 19
    |||||
Db 228 CGGACCCCTGCGCGCGGTTTCGAGACGAACTGT-----CCAGGAGCGTGG 275
    |||||
QY 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
    |||||
Db 276 CCGGCGCAGCGTGAGGTGGTGTGCGCGCACTTCGCGCGGTCGAAGGACGCTCAAGG 335
    |||||
QY 35 ValLeuArgArgArg 39
    |||||
Db 336 CGGAGCGGACGACGG 350

RESULT 11
US-11-353-150-43740
; Sequence 43740, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 43740
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3066-048-Q1-K1-E5
US-11-353-150-43740

Alignment Scores:
Pred. No.: 8.04 Length: 450
Score: 65.50 Matches: 20
Percent Similarity: 48.9% Conservative: 2
Best Local Similarity: 44.4% Mismatches: 12
Query Match: 34.3% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-11-353-150-43740 (1-450)

QY 2 AlaThrProSerAlaValGlyAla-----AlaCysLeuLeuAlaArg***AlaTTrp 19
    |||||
Db 209 CGGACCCCTGCGCGCGGTTTCGAGACGAACTGT-----CCAGGAGCGTGG 256
    |||||
QY 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
    |||||
Db 257 CCGGCGCAGCGTGAGGTGGTGTGCGCGCACTTCGCGCGGTCGAAGGACGCTCAAGG 316
    |||||
QY 35 ValLeuArgArgArg 39
```



```
Db 302 CGGAGCGGACGACGG 316
|||||
RESULT 15
US-11-353-150-11403
; Sequence 11403, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Comer, Timothy W.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 16517,365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 11403
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: cC-zmpol48071b09b1
US-11-353-150-11403

Alignment Scores:
Pred. No.: 11.3 Length: 452
Score: 64.50 Matches: 20
Percent Similarity: 48.9% Conservative: 2
Best Local Similarity: 44.4% Mismatches: 12
Query Match: 33.8% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-11-353-150-11403 (1-452)
Qy 2 AlaThrProSerAlaValGlyAla-----AlaCysLeuLeuLeuAlaArg***AlaTTrp 19
|||||:|||||
Db 219 GCGACCCCTGCGCGCGGCTTCGAGACGAACGTGT-----CCAGGAGCGTGG 266
|||||
Qy 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
|||||
Db 267 CGGCGCGGACGGTGGAGGTGGTGTGCGGCACCTTTGCGCGCTCAAGGAGCGCTCAAGG 326
|||||
Qy 35 ValLeuArgArgArg 39
|||||
Db 327 CGGAGCGGACGACGG 341

RESULT 16
US-11-266-748A-30547/c
; Sequence 30547, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13015
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (332)..(332)
; OTHER INFORMATION: n is a, c, g, or t
```

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; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30547
; LENGTH: 12499
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-30547

Alignment Scores:
Pred. No.: 874 Length: 12499
Score: 64.50 Matches: 21
Percent Similarity: 40.7% Conservative: 3
Best Local Similarity: 35.6% Mismatches: 10
Query Match: 33.8% Indels: 25
DB: 10 Gaps: 2

US-10-628-525A-37 (1-39) x US-11-266-748A-30547 (1-12499)
Qy 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTrpProAla 21
|||||:|||||
Db 206 GCGTGGCGCGCTGCTCCAGCGCGAGCGTGT-----AGCGCGGAGAACAGCGCTCCA 156
|||||
Qy 22 AlaValGly----- 24
|||||
Db 155 GCTCTGGGCAAGCGAACTCTCTCGCAGCGCGCGCGCGCGCGCGCGCTTGTCCCGG 96
|||||
Qy 25 -----AspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 38
|||||
Db 95 CGCGCGCGCTCGGCGCGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCTTGTCCCGCGCG 39
|||||

RESULT 17
US-11-266-748A-13015/c
; Sequence 13015, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13015
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (332)..(332)
; OTHER INFORMATION: n is a, c, g, or t
```







```
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 47816
; LENGTH: 395
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3066-034-Q1-K1-E10
US-11-353-150-47816

Alignment Scores:
Pred. No.: 18.5 Length: 395
Score: 62.50 Matches: 19
Percent Similarity: 48.9% Conservative: 3
Best Local Similarity: 42.2% Mismatches: 12
Query Match: 32.7% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-11-353-150-47816 (1-395)

QY 2 AlatrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlatrP 19
|||||:|||||:|||||:|||||:|||||:
Db 207 GCGACCCCTGCGCGCGGTTGCGAGCGAGCGTGT-----CCAGGAGCGTGG 254
|||||:|||||:|||||:|||||:|||||:

QY 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
|||||:|||||:|||||:|||||:|||||:
Db 255 CCGGCGGACGGTGAGGTGGTGTCCGCGCACTTCGCGCGCTCCAAAGAGACGCTCAAGG 314
|||||:|||||:|||||:|||||:|||||:

QY 35 ValLeuArgArgArg 39
|||||:|||||:|||||:|||||:
Db 315 CGGAGCGGACGACGG 329
|||||:|||||:|||||:|||||:

RESULT 25
US-10-289-526-1524/c
; Sequence 1524, Application US/10289526
; GENERAL INFORMATION:
; APPLICANT: Askenazi, Manor
; APPLICANT: Driggers, Edward M.
; APPLICANT: Norman, Thea
; APPLICANT: Zimmer, Daniel P.
; APPLICANT: Royer, John C.
; APPLICANT: Salama, Sofie R.
; APPLICANT: Trusheart, Joshua
; APPLICANT: Madden, Kevin T.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING GENES REGULATING
; FILE OF INVENTION: METABOLITE PRODUCTION
; FILE REFERENCE: 14184-017001
; CURRENT APPLICATION NUMBER: US/10/289,526
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 60/332,903
; PRIOR FILING DATE: 2001-11-06
; NUMBER OF SEQ ID NOS: 1912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1524
; LENGTH: 755
; TYPE: DNA
; ORGANISM: Aspergillus terreus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) . - . (755)
; OTHER INFORMATION: n = A,T,C or G
US-10-289-526-1524

Alignment Scores:
Pred. No.: 43.2 Length: 755
```

```
Score: 62.50 Matches: 18
Percent Similarity: 48.9% Conservative: 4
Best Local Similarity: 40.0% Mismatches: 16
Query Match: 32.7% Indels: 7
DB: 7 Gaps: 2

US-10-628-525A-37 (1-39) x US-10-289-526-1524 (1-755)

QY 2 AlatrProSerAlaValGlyAlaAlaCysLeuLeu-----LeuAla 15
|||||:|||||:|||||:|||||:|||||:
Db 715 GCTGACGAGCGTGGCGCGCACCGCGGTGTACTGTCATCTTGCCCGCTTGGCGCGCTGGCC 656
|||||:|||||:|||||:|||||:|||||:

QY 16 Arg***AlatrProAlaAlaValGlyAspArgAlaArgPro---ArgArgLeuGlnArg 34
|||||:|||||:|||||:|||||:|||||:
Db 655 CGGCGAGTGTGGCTTGCAGACACCGACCGCGTGTGGTGTGGCTCCGCTGGAGGAGG 596
|||||:|||||:|||||:|||||:|||||:

QY 35 ValLeuArgArgArg 39
|||||:|||||:|||||:|||||:
Db 595 ACGATCGCGCGCGG 581
|||||:|||||:|||||:|||||:

RESULT 26
US-60-762-056-17573
; Sequence 17573, Application US/60762056
; GENERAL INFORMATION:
; APPLICANT: Trinklein, Nathan D
; APPLICANT: Aldred, Shelley Force
; APPLICANT: Cooper, Sara J
; APPLICANT: Myers, Richard M
; TITLE OF INVENTION: FUNCTIONAL ARRAYS FOR HIGH THROUGHPUT CHARACTERIZATION OF GENE
; FILE REFERENCE: 33102-701.102
; CURRENT APPLICATION NUMBER: US/60/762,056
; CURRENT FILING DATE: 2006-01-24
; NUMBER OF SEQ ID NOS: 45096
; SEQ ID NO 17573
; LENGTH: 2300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-762-056-17573

Alignment Scores:
Pred. No.: 186 Length: 2300
Score: 62.50 Matches: 18
Percent Similarity: 66.7% Conservative: 6
Best Local Similarity: 50.0% Mismatches: 10
Query Match: 32.7% Indels: 2
DB: 12 Gaps: 1

US-10-628-525A-37 (1-39) x US-60-762-056-17573 (1-2300)

QY 5 SerAlaValGlyAlaAlaCysLeuLeuAlaAlaArg***AlatrProAlaAlaValGly 24
|||||:|||||:|||||:|||||:|||||:
Db 1662 TCGCGCGCTGGTGGCGTGTCCGACGCTGGCT---CGCTCTATCCGCTTTGCTAGGG 1718
|||||:|||||:|||||:|||||:|||||:

QY 25 AspArgAla-ArgProArgArgLeuGlnArgValLeuArgArgArg 39
|||||:|||||:|||||:|||||:|||||:
Db 1719 GAGTGAGTCCGCGCGCGCGAACCAGCGGCTGAGGAGCGCGG 1764
|||||:|||||:|||||:|||||:|||||:

RESULT 27
US-60-762-056-17574
; Sequence 17574, Application US/60762056
; GENERAL INFORMATION:
; APPLICANT: Trinklein, Nathan D
; APPLICANT: Aldred, Shelley Force
; APPLICANT: Cooper, Sara J
; APPLICANT: Myers, Richard M
; TITLE OF INVENTION: FUNCTIONAL ARRAYS FOR HIGH THROUGHPUT CHARACTERIZATION OF GENE
; FILE REFERENCE: 33102-701.102
; CURRENT APPLICATION NUMBER: US/60/762,056
; CURRENT FILING DATE: 2006-01-24
; NUMBER OF SEQ ID NOS: 45096
; SEQ ID NO 17574
```

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; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 466626
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-466626

Alignment Scores:
Pred. No.:      73.8      Length:      1000
Score:          62.00     Matches:      14
Percent Similarity: 54.8%  Conservative: 3
Best Local Similarity: 45.2% Mismatches:    10
Query Match:      32.5%   Indels:         4
DB:               10      Gaps:          1

US-10-628-525A-37 (1-39) x US-11-266-748A-466626 (1-1000)

QY      4 ProSerAlaValGlyAlaAlaCysLeuLeu-----LeuAlaArg***AlaTrp 19
Db      333 CTGGAGTCTCTGGTTCTGCGCCCTTCTGCGCGCACCCTCTCGCGAGTCCACTGG 392

QY      20 ProAlaAlaValGlyAspArgAlaArgProArg 30
Db      393 GGGGCGCAGCGGCTCCAGAGCCAGCCCTCGG 425

Search completed: April 2, 2006, 04:06:47
Job time : 79.9357 secs

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